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(54) Title: METHODS OF DIAGNOSIS OF ANGIOGENESIS, COMPOSITIONS AND METHODS OF SCREENING FOR AN-
GIOGENESIS MODULATORS

(57) Abstract: Described herein are methods and compositions that can be used for diagnosis and treatment of angiogenic pheno-
types and angiogenesis-associated diseases. Also described herein are methods that can be used to identify modulators of angiogen-
esis.

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METHODS OF DIAGNOSIS OF ANGIOGENESIS, COMPOSITIONS AND METHODS OF SCREENING FOR ANGIOGENESIS MODULATORS

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CROSS-REFERENCES TO RELATED APPLICATIONS

This application claims priority to USSN 09/784,356, filed February 14 2001;
10 USSN 09/791,390, filed February 22, 2001; USSN 60/285,475, filed April 19, 2001, USSN
60/310,025, filed August 3, 2001, and USSN 60/334,244, filed November 29, 2001, each of
which is herein incorporated by reference in its entirety.

FIELD OF THE INVENTION

15 The invention relates to the identification of nucleic acid and protein
expression profiles and nucleic acids, products, and antibodies thereto that are involved in
angiogenesis; and to the use of such expression profiles and compositions in diagnosis and
therapy of angiogenesis. The invention further relates to methods for identifying and using
agents and/or targets that modulate angiogenesis.

20

BACKGROUND OF THE INVENTION

Both vasculogenesis, the development of an interactive vascular system
comprising arteries and veins, and angiogenesis, the generation of new blood vessels, play a
role in embryonic development. In contrast, angiogenesis is limited in a normal adult to the
25 placenta, ovary, endometrium and sites of wound healing. However, angiogenesis, or its
absence, plays an important role in the maintenance of a variety of pathological states. Some
of these states are characterized by neovascularization, *e.g.*, cancer, diabetic retinopathy,
glaucoma, and age related macular degeneration. Others, *e.g.*, stroke, infertility, heart
disease, ulcers, and scleroderma, are diseases of angiogenic insufficiency.

30 Angiogenesis has a number of stages (see, *e.g.*, Folkman, *J.Natl Cancer Inst.*
82:4-6, 1990; Firestein, *J Clin Invest.* 103:3-4, 1999; Koch, *Arthritis Rheum.* 41:951-62, 1998;
Carter, *Oncologist* 5(Suppl 1):51-4, 2000; Browder *et al.*, *Cancer Res.* 60:1878-86, 2000; and
Zhu and Witte, *Invest New Drugs* 17:195-212, 1999). The early stages of angiogenesis

include endothelial cell protease production, migration of cells, and proliferation. The early stages also appear to require some growth factors, with VEGF, TGF- α , angiostatin, and selected chemokines all putatively playing a role. Later stages of angiogenesis include population of the vessels with mural cells (pericytes or smooth muscle cells), basement
5 membrane production, and the induction of vessel bed specializations. The final stages of vessel formation include what is known as "remodeling", wherein a forming vasculature becomes a stable, mature vessel bed. Thus, the process is highly dynamic, often requiring coordinated spatial and temporal waves of gene expression.

Conversely, the complex process may be subject to disruption by interfering
10 with one or more critical steps. Thus, the lack of understanding of the dynamics of angiogenesis prevents therapeutic intervention in serious diseases such as those indicated. It is an object of the invention to provide methods that can be used to screen compounds for the ability to modulate angiogenesis. Additionally, it is an object to provide molecular targets for therapeutic intervention in disease states which either have an undesirable excess or a deficit
15 in angiogenesis. The present invention provides solutions to both.

SUMMARY OF THE INVENTION

The present invention provides compositions and methods for detecting or modulating angiogenesis associated sequences.

20 In one aspect, the invention provides a method of detecting an angiogenesis-associated transcript in a cell in a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridized to a sequence at least 80% identical to a sequence as shown in Tables 1-8. In one embodiment, the biological sample is a tissue sample. In another embodiment, the biological sample comprises isolated
25 nucleic acids, which are often mRNA.

In another embodiment, the method further comprises the step of amplifying nucleic acids before the step of contacting the biological sample with the polynucleotide. Often, the polynucleotide comprises a sequence as shown in Tables 1-8. The polynucleotide can be labeled, for example, with a fluorescent label and can be immobilized on a solid
30 surface.

In other embodiments the patient is undergoing a therapeutic regimen to treat a disease associated with angiogenesis or the patient is suspected of having an angiogenesis-associated disorder.

In another aspect, the invention comprises an isolated nucleic acid molecule consisting of a polynucleotide sequence as shown in Tables 1-8. The nucleic acid molecule can be labeled, for example, with a fluorescent label,

5 In other aspects, the invention provides an expression vector comprising an isolated nucleic acid molecule consisting of a polynucleotide sequence as shown in Tables 1-8 or a host cell comprising the expression vector.

In another embodiment, the isolated nucleic acid molecule encodes a polypeptide having an amino acid sequence as shown in Table 8.

10 In another aspect, the invention provides an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1-8. In one embodiment, the isolated polypeptide has an amino acid sequence as shown in Table 8.

15 In another embodiment, the invention provides an antibody that specifically binds a polypeptide that has an amino acid sequence as shown in Table 8 or which is encoded by a nucleotide sequence of Tables 1-8. The antibody can be conjugated or fused to an effector component such as a fluorescent label, a toxin, or a radioisotope. In some embodiments, the antibody is an antibody fragment or a humanized antibody.

20 In another aspect, the invention provides a method of detecting a cell undergoing angiogenesis in a biological sample from a patient, the method comprising contacting the biological sample with an antibody that specifically binds to a polypeptide that has an amino acid sequence as shown in Table 8 or which is encoded by a nucleotide sequence of Tables 1-8. In some embodiments, the antibody is further conjugated or fused to an effector component, for example, a fluorescent label.

25 In another embodiment, the invention provides a method of detecting antibodies specific to angiogenesis in a patient, the method comprising contacting a biological sample from the patient with a polypeptide which is encoded by a nucleotide sequence of Tables 1-8.

30 The invention also provides a method of identifying a compound that modulates the activity of an angiogenesis-associated polypeptide, the method comprising the steps of: (i) contacting the compound with a polypeptide that comprises at least 80% identity to an amino acid sequence as shown in Table 8 or which is encoded by a nucleotide sequence of Tables 1-8; and (ii) detecting an increase or a decrease in the activity of the polypeptide. In one embodiment, the polypeptide has an amino acid sequence as shown in Table 8 or is a

polypeptide encoded by a nucleotide sequence of Tables 1-8. In another embodiment, the polypeptide is expressed in a cell.

5 The invention also provides a method of identifying a compound that modulates angiogenesis, the method comprising steps of: (i) contacting the compound with a cell undergoing angiogenesis; and (ii) detecting an increase or a decrease in the expression of a polypeptide sequence as shown in Table 8 or a polypeptide which is encoded by a nucleotide sequence of Tables 1-8. In one embodiment, the detecting step comprises hybridizing a nucleic acid sample from the cell with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-8. In
10 another embodiment, the method further comprises detecting an increase or decrease in the expression of a second sequence as shown in Table 8 or a polypeptide which is encoded by a nucleotide sequence of Tables 1-8 .

In another embodiment, the invention provides a method of inhibiting angiogenesis in a cell that expresses a polypeptide at least 80% identical to a sequence as
15 shown in Table 8 or which is 80% identical to a polypeptide encoded by a nucleotide sequence of Tables 1-8 , the method comprising the step of contacting the cell with a therapeutically effective amount of an inhibitor of the polypeptide. In one embodiment, the polypeptide has an amino acid sequence shown in Table 8 or is a polypeptide which is encoded by a nucleotide sequence of Tables 1-8 . In another embodiment, the inhibitor is an
20 antibody.

In other embodiments, the invention provides a method of activating angiogenesis in a cell that expresses a polypeptide at least 80% identical to a sequence as shown in Table 8 or at least 80% identical to a polypeptide which is encoded by a nucleotide sequence of Tables 1-8 , the method comprising the step of contacting the cell with a
25 therapeutically effective amount of an activator of the polypeptide. In one embodiment, the polypeptide has an amino acid sequence shown in Table 8 or is a polypeptide which is encoded by a nucleotide sequence of Tables 1-8.

Other aspects of the invention will become apparent to the skilled artisan by the following description of the invention.

30 Tables 1-8 provide nucleotide sequence of genes that exhibit changes in expression levels as a function of time in tissue undergoing angiogenesis compared to tissue that is not.

DESCRIPTION OF THE SPECIFIC EMBODIMENTS

In accordance with the objects outlined above, the present invention provides novel methods for diagnosis and treatment of disorders associated with angiogenesis (sometimes referred to herein as angiogenesis disorders or AD), as well as methods for screening for compositions which modulate angiogenesis. By “disorder associated with angiogenesis” or “disease associated with angiogenesis” herein is meant a disease state which is marked by either an excess or a deficit of blood vessel development. Angiogenesis disorders associated with increased angiogenesis include, but are not limited to, cancer and proliferative diabetic retinopathy. Pathological states for which it may be desirable to increase angiogenesis include stroke, heart disease, infertility, ulcers, wound healing, ischemia, and sclerodoma. Solid tumors typically require angiogenesis to support or sustain growth, e.g., breast, colon, lung, brain, bladder, and prostate tumors. Other AD include, e.g., arthritis, inflammatory bowel disease, diabetes retinopathy, macular degeneration, atherosclerosis, and psoriasis. Also provided are methods for treating AD.

Definitions

The term “angiogenesis protein” or “angiogenesis polynucleotide” refers to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologs that: (1) have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% or greater amino acid sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more amino acids, to an angiogenesis protein sequence of Table 8; (2) bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence of Table 8, and conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to an anti-sense strand corresponding to a nucleic acid sequence of Tables 1-8 and conservatively modified variants thereof; (4) have a nucleic acid sequence that has greater than about 95%, preferably greater than about 96%, 97%, 98%, 99%, or higher nucleotide sequence identity, preferably over a region of at least about 25, 50, 100, 200, 500, 1000, or more nucleotides, to a sense sequence corresponding to one set out in Tables 1-8. A polynucleotide or polypeptide sequence is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or any mammal. An “angiogenesis polypeptide” and an “angiogenesis polynucleotide,” include both naturally occurring or recombinant.

A "full length" angiogenesis protein or nucleic acid refers to an angiogenesis polypeptide or polynucleotide sequence, or a variant thereof, that contains all of the elements normally contained in one or more naturally occurring, wild type angiogenesis polynucleotide or polypeptide sequences. The "full length" may be prior to, or after, various stages of post-translation processing.

"Biological sample" as used herein is a sample of biological tissue or fluid that contains nucleic acids or polypeptides, *e.g.*, of an angiogenic protein. Such samples include, but are not limited to, tissue isolated from primates, *e.g.*, humans, or rodents, *e.g.*, mice, and rats. Biological samples may also include sections of tissues such as biopsy and autopsy samples, and frozen sections taken for histologic purposes. A biological sample is typically obtained from a eukaryotic organism, most preferably a mammal such as a primate *e.g.*, chimpanzee or human; cow; dog; cat; a rodent, *e.g.*, guinea pig, rat, mouse; rabbit; or a bird; reptile; or fish.

"Providing a biological sample" means to obtain a biological sample for use in methods described in this invention. Most often, this will be done by removing a sample of cells from an animal, but can also be accomplished by using previously isolated cells (*e.g.*, isolated by another person, at another time, and/or for another purpose), or by performing the methods of the invention *in vivo*. Archival tissues, having treatment or outcome history, will be particularly useful.

The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same (*i.e.*, about 70% identity, preferably 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher identity over a specified region (*e.g.*, SEQ ID NOS:1-229), when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (see, *e.g.*, NCBI web site <http://www.ncbi.nlm.nih.gov/BLAST/> or the like). Such sequences are then said to be "substantially identical." This definition also refers to, or may be applied to, the complement of a test sequence. The definition also includes sequences that have deletions and/or additions, as well as those that have substitutions. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is 50-100 amino acids or nucleotides in length.

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Preferably, default
5 program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window", as used herein, includes reference to a segment of any one of the number of contiguous positions selected from the group consisting of from 20
10 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith & Waterman, *Adv. Appl. Math.* 2:482 (1981), by the homology alignment algorithm of Needleman & Wunsch, *J. Mol. Biol.* 48:443 (1970), by the search for similarity method of Pearson & Lipman, *Proc. Nat'l. Acad. Sci. USA* 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and
20 visual inspection (*see, e.g., Current Protocols in Molecular Biology* (Ausubel *et al.*, eds. 1995 supplement)).

A preferred example of algorithm that is suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul *et al.*, *Nuc. Acids Res.* 25:3389-3402 (1997) and Altschul *et al.*, *J. Mol. Biol.* 215:403-410 (1990), respectively. BLAST and BLAST 2.0 are used, with the
25 parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying
30 short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al.*, *supra*). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as

far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff, *Proc. Natl. Acad. Sci. USA* 89:10915 (1989)) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin & Altschul, *Proc. Nat'l. Acad. Sci. USA* 90:5873-5787 (1993)). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01, and most preferably less than about 0.001.

An indication that two nucleic acid sequences or polypeptides are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid, as described below. Thus, a polypeptide is typically substantially identical to a second polypeptide, for example, where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules or their complements hybridize to each other under stringent conditions, as described below. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequences.

A "host cell" is a naturally occurring cell or a transformed cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be cultured cells, explants, cells *in vivo*, and the like. Host cells may be

prokaryotic cells such as *E. coli*, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells such as CHO, HeLa, and the like (see, e.g., the American Type Culture Collection catalog or web site, www.atcc.org).

The terms "polypeptide," "peptide" and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers and non-naturally occurring amino acid polymer.

The term "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function in a manner similar to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, e.g., hydroxyproline, γ -carboxyglutamate, and O-phosphoserine. Amino acid analogs refers to compounds that have the same basic chemical structure as a naturally occurring amino acid, i.e., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs have modified R groups (e.g., norleucine) or modified peptide backbones, but retain the same basic chemical structure as a naturally occurring amino acid. Amino acid mimetics refers to chemical compounds that have a structure that is different from the general chemical structure of an amino acid, but that functions in a manner similar to a naturally occurring amino acid.

Amino acids may be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

"Conservatively modified variants" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode any given protein. For instance, the codons GCA, GCC, GCG and GCU all encode the amino acid alanine. Thus, at every position where an alanine is specified by a codon, the codon can be altered to any of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations," which are one species of conservatively modified

variations. Every nucleic acid sequence herein which encodes a polypeptide also describes every possible silent variation of the nucleic acid. One of skill will recognize that each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally identical molecule. Accordingly, each silent variation of a nucleic acid which encodes a polypeptide is implicit in each described sequence with respect to the expression product, but not with respect to actual probe sequences.

As to amino acid sequences, one of skill will recognize that individual substitutions, deletions or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known in the art. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention.

The following eight groups each contain amino acids that are conservative substitutions for one another: 1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S), Threonine (T); and 8) Cysteine (C), Methionine (M) (*see, e.g., Creighton, Proteins* (1984)).

Macromolecular structures such as polypeptide structures can be described in terms of various levels of organization. For a general discussion of this organization, *see, e.g., Alberts et al., Molecular Biology of the Cell* (3rd ed., 1994) and Cantor and Schimmel, *Biophysical Chemistry Part I: The Conformation of Biological Macromolecules* (1980). "Primary structure" refers to the amino acid sequence of a particular peptide. "Secondary structure" refers to locally ordered, three dimensional structures within a polypeptide. These structures are commonly known as domains. Domains are portions of a polypeptide that form a compact unit of the polypeptide and are typically 25 to approximately 500 amino acids long. Typical domains are made up of sections of lesser organization such as stretches of β -sheet and α -helices. "Tertiary structure" refers to the complete three dimensional structure of a polypeptide monomer. "Quaternary structure" refers to the three dimensional

structure formed, usually by the noncovalent association of independent tertiary units.

Anisotropic terms are also known as energy terms.

5 A "label" or a "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, chemical, or other physical means. For example, useful labels include ^{32}P , fluorescent dyes, electron-dense reagents, enzymes (*e.g.*, as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins which can be made detectable, *e.g.*, by incorporating a radiolabel into the peptide or used to detect antibodies specifically reactive with the peptide.

10 An "effector" or "effector moiety" or "effector component" is a molecule that is bound (or linked, or conjugated), either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds, to an antibody. The "effector" can be a variety of molecules including, for example, detection moieties including radioactive compounds, fluorescent compounds, an enzyme or substrate, tags such as epitope tags, a toxin; a chemotherapeutic agent; a lipase; an antibiotic; or a radioisotope emitting "hard" *e.g.*, beta radiation.

15 A "labeled nucleic acid probe or oligonucleotide" is one that is bound, either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe. Alternatively, method using high affinity interactions may achieve the same results where one of a pair of binding partners binds to the other, *e.g.*, biotin, streptavidin.

20 As used herein a "nucleic acid probe or oligonucleotide" is defined as a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (*i.e.*, A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, so long as it does not interfere with hybridization. Thus, for example, probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. It will be understood by one of skill in the art that probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are preferably directly labeled as with isotopes, chromophores, lumiphores, chromogens, or indirectly labeled such as with biotin to which a streptavidin

complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence.

The term "recombinant" when used with reference, *e.g.*, to a cell, or nucleic acid, protein, or vector, indicates that the cell, nucleic acid, protein or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a native nucleic acid or protein, or that the cell is derived from a cell so modified. Thus, for example, recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed or not expressed at all.

The term "heterologous" when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences from unrelated genes arranged to make a new functional nucleic acid, *e.g.*, a promoter from one source and a coding region from another source. Similarly, a heterologous protein indicates that the protein comprises two or more subsequences that are not found in the same relationship to each other in nature (*e.g.*, a fusion protein).

A "promoter" is defined as an array of nucleic acid control sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A "constitutive" promoter is a promoter that is active under most environmental and developmental conditions. An "inducible" promoter is a promoter that is active under environmental or developmental regulation. The term "operably linked" refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

An "expression vector" is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements that permit transcription of a particular nucleic acid in a host cell. The expression vector can be part of a plasmid, virus, or nucleic acid fragment. Typically, the expression vector includes a nucleic acid to be transcribed operably linked to a promoter.

The phrase “selectively (or specifically) hybridizes to” refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (e.g., total cellular or library DNA or RNA).

5 The phrase “stringent hybridization conditions” refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acids, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in
10 Tijssen, *Techniques in Biochemistry and Molecular Biology--Hybridization with Nucleic Probes*, “Overview of principles of hybridization and the strategy of nucleic acid assays” (1993). Generally, stringent conditions are selected to be about 5-10°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50%
15 of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m , 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes (e.g., 10 to
20 50 nucleotides) and at least about 60°C for long probes (e.g., greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is at least two times background, preferably 10 times background hybridization. Exemplary stringent hybridization conditions can be as following: 50% formamide, 5x SSC, and 1% SDS,
25 incubating at 42°C, or, 5x SSC, 1% SDS, incubating at 65°C, with wash in 0.2x SSC, and 0.1% SDS at 65°C. For PCR, a temperature of about 36°C is typical for low stringency amplification, although annealing temperatures may vary between about 32°C and 48°C depending on primer length. For high stringency PCR amplification, a temperature of about 62°C is typical, although high stringency annealing temperatures can range from about 50°C
30 to about 65°C, depending on the primer length and specificity. Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90°C - 95°C for 30 sec - 2 min., an annealing phase lasting 30 sec. - 2 min., and an extension phase of about 72°C for 1 - 2 min. Protocols and guidelines for low and high stringency amplification

reactions are provided, *e.g.*, in Innis *et al.* (1990) *PCR Protocols, A Guide to Methods and Applications*, Academic Press, Inc. N.Y.).

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical.

5 This occurs, for example, when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37°C, and a wash in 1X SSC at 45°C. A positive hybridization is at least twice
10 background. Those of ordinary skill will readily recognize that alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency. Additional guidelines for determining hybridization parameters are provided in numerous reference, *e.g.*, and Current Protocols in Molecular Biology, ed. Ausubel, *et al*

The phrase "functional effects" in the context of assays for testing compounds
15 that modulate activity of an angiogenesis protein includes the determination of a parameter that is indirectly or directly under the influence of the angiogenesis protein, *e.g.*, a functional, physical, or chemical effect, such as the ability to increase or decrease angiogenesis. It includes binding activity, the ability of cells to proliferate, expression in cells undergoing angiogenesis, and other characteristics of angiogenic cells. "Functional effects" include *in*
20 *vitro*, *in vivo*, and *ex vivo* activities.

By "determining the functional effect" is meant assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of an angiogenesis protein sequence, *e.g.*, functional, physical and chemical effects. Such functional effects can be measured by any means known to those skilled in the art, *e.g.*,
25 changes in spectroscopic characteristics (*e.g.*, fluorescence, absorbance, refractive index), hydrodynamic (*e.g.*, shape), chromatographic, or solubility properties for the protein, measuring inducible markers or transcriptional activation of the angiogenesis protein; measuring binding activity or binding assays, *e.g.* binding to antibodies, and measuring cellular proliferation, particularly endothelial cell proliferation, cell viability, cell division
30 especially of endothelial cells, lumen formation and capillary or vessel growth or formation. Determination of the functional effect of a compound on angiogenesis can also be performed using angiogenesis assays known to those of skill in the art such as an *in vitro* assays, *e.g.*, *in vitro* endothelial cell tube formation assays, and other assays such as the chick CAM assay, the mouse corneal assay, and assays that assess vascularization of an implanted tumor. The

functional effects can be evaluated by many means known to those skilled in the art, *e.g.*, microscopy for quantitative or qualitative measures of alterations in morphological features, *e.g.*, tube or blood vessel formation, measurement of changes in RNA or protein levels for angiogenesis-associated sequences, measurement of RNA stability, identification of downstream or reporter gene expression (CAT, luciferase, β -gal, GFP and the like), *e.g.*, via chemiluminescence, fluorescence, colorimetric reactions, antibody binding, inducible markers, and ligand binding assays.

“Inhibitors”, “activators”, and “modulators” of angiogenic polynucleotide and polypeptide sequences are used to refer to activating, inhibitory, or modulating molecules identified using *in vitro* and *in vivo* assays of angiogenic polynucleotide and polypeptide sequences. Inhibitors are compounds that, *e.g.*, bind to, partially or totally block activity, decrease, prevent, delay activation, inactivate, desensitize, or down regulate the activity or expression of angiogenesis proteins, *e.g.*, antagonists. “Activators” are compounds that increase, open, activate, facilitate, enhance activation, sensitize, agonize, or up regulate angiogenesis protein activity. Inhibitors, activators, or modulators also include genetically modified versions of angiogenesis proteins, *e.g.*, versions with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, antibodies, small chemical molecules and the like. Such assays for inhibitors and activators include, *e.g.*, expressing the angiogenic protein *in vitro*, in cells, or cell membranes, applying putative modulator compounds, and then determining the functional effects on activity, as described above. Activators and inhibitors of angiogenesis can also be identified by incubating angiogenic cells with the test compound and determining increases or decreases in the expression of 1 or more angiogenesis proteins, *e.g.*, 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 40, 50 or more angiogenesis proteins, such as angiogenesis proteins comprising the sequences set out in Table 8.

Samples or assays comprising angiogenesis proteins that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of inhibition. Control samples (untreated with inhibitors) are assigned a relative protein activity value of 100%. Inhibition of a polypeptide is achieved when the activity value relative to the control is about 80%, preferably 50%, more preferably 25-0%. Activation of an angiogenesis polypeptide is achieved when the activity value relative to the control (untreated with activators) is 110%, more preferably 150%, more preferably 200-500% (*i.e.*, two to five fold higher relative to the control), more preferably 1000-3000% higher.

“Antibody” refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD and IgE, respectively. Typically, the antigen-binding region of an antibody will be most critical in specificity and affinity of binding.

An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one “light” (about 25 kD) and one “heavy” chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The terms variable light chain (V_L) and variable heavy chain (V_H) refer to these light and heavy chains respectively.

Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, for example, pepsin digests an antibody below the disulfide linkages in the hinge region to produce $F(ab)'_2$, a dimer of Fab which itself is a light chain joined to V_H-C_H1 by a disulfide bond. The $F(ab)'_2$ may be reduced under mild conditions to break the disulfide linkage in the hinge region, thereby converting the $F(ab)'_2$ dimer into an Fab' monomer. The Fab' monomer is essentially Fab with part of the hinge region (see *Fundamental Immunology* (Paul ed., 3d ed. 1993)). While various antibody fragments are defined in terms of the digestion of an intact antibody, one of skill will appreciate that such fragments may be synthesized *de novo* either chemically or by using recombinant DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized *de novo* using recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries (see, e.g., McCafferty *et al.*, *Nature* 348:552-554 (1990)).

For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal antibodies, many technique known in the art can be used (see, e.g., Kohler & Milstein, *Nature* 256:495-497 (1975); Kozbor *et al.*, *Immunology Today* 4: 72 (1983); Cole *et al.*, pp. 77-96 in *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc. (1985); Coligan, *Current Protocols in Immunology* (1991); Harlow & Lane, *Antibodies, A Laboratory Manual* (1988); and Goding, *Monoclonal Antibodies: Principles and Practice* (2d ed. 1986)).

Techniques for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms such as other mammals, may be used to express humanized antibodies.

Alternatively, phage display technology can be used to identify antibodies and heteromeric Fab fragments that specifically bind to selected antigens (*see, e.g., McCafferty et al., Nature* 348:552-554 (1990); Marks *et al., Biotechnology* 10:779-783 (1992)).

A "chimeric antibody" is an antibody molecule in which (a) the constant region, or a portion thereof, is altered, replaced or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, *e.g.*, an enzyme, toxin, hormone, growth factor, drug, etc.; or (b) the variable region, or a portion thereof, is altered, replaced or exchanged with a variable region having a different or altered antigen specificity.

The detailed description of the invention includes discussion of the following

aspects of the invention:

- Expression of angiogenesis-associated sequences
- Informatics
- Angiogenesis-associated sequences
- Detection of angiogenesis sequence for diagnostic and therapeutic applications
- Modulators of angiogenesis
- Methods of identifying variant angiogenesis-associated sequences
- Administration of pharmaceutical and vaccine compositions
- Kits for use in diagnostic and/or prognostic applications.

Expression of angiogenesis-associated sequences

In one aspect, the expression levels of genes are determined in different patient samples for which diagnosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a "fingerprint" of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is unique to the state of the cell. That is, normal tissue may be distinguished from AD tissue. By comparing expression profiles of tissue in known different angiogenesis states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. The identification of sequences that are

differentially expressed in angiogenic versus non-angiogenic tissue allows the use of this information in a number of ways. For example, a particular treatment regime may be evaluated: does a chemotherapeutic drug act to down-regulate angiogenesis, and thus tumor growth or recurrence, in a particular patient. Similarly, diagnosis and treatment outcomes
5 may be done or confirmed by comparing patient samples with the known expression profiles. Angiogenic tissue can also be analyzed to determine the stage of angiogenesis in the tissue. Furthermore, these gene expression profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; for example, screening can be done for drugs that suppress the angiogenic expression profile. This may be
10 done by making biochips comprising sets of the important angiogenesis genes, which can then be used in these screens. These methods can also be done on the protein basis; that is, protein expression levels of the angiogenic proteins can be evaluated for diagnostic purposes or to screen candidate agents. In addition, the angiogenic nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense nucleic
15 acids, or the angiogenic proteins (including antibodies and other modulators thereof) administered as therapeutic drugs.

Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in angiogenesis, herein termed "angiogenesis sequences". As outlined below, angiogenesis sequences include those that are up-regulated (i.e. expressed at
20 a higher level) in disorders associated with angiogenesis, as well as those that are down-regulated (i.e. expressed at a lower level). In a preferred embodiment, the angiogenesis sequences are from humans; however, as will be appreciated by those in the art, angiogenesis sequences from other organisms may be useful in animal models of disease and drug evaluation; thus, other angiogenesis sequences are provided, from vertebrates, including
25 mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc). Angiogenesis sequences from other organisms may be obtained using the techniques outlined below.

Angiogenesis sequences can include both nucleic acid and amino acid sequences. In a preferred embodiment, the angiogenesis sequences are recombinant nucleic
30 acids. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed *in vitro*, in general, by the manipulation of nucleic acid *e.g.*, using polymerases and endonucleases, in a form not normally found in nature. Thus an isolated nucleic acid, in a linear form, or an expression vector formed *in vitro* by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is

understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, *i.e.* using the *in vivo* cellular machinery of the host cell rather than *in vitro* manipulations; however, such nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered recombinant for the purposes of the invention.

Similarly, a "recombinant protein" is a protein made using recombinant techniques, *i.e.* through the expression of a recombinant nucleic acid as depicted above. A recombinant protein is distinguished from naturally occurring protein by at least one or more characteristics. For example, the protein may be isolated or purified away from some or all of the proteins and compounds with which it is normally associated in its wild type host, and thus may be substantially pure. For example, an isolated protein is unaccompanied by at least some of the material with which it is normally associated in its natural state, preferably constituting at least about 0.5%, more preferably at least about 5% by weight of the total protein in a given sample. A substantially pure protein comprises at least about 75% by weight of the total protein, with at least about 80% being preferred, and at least about 90% being particularly preferred. The definition includes the production of an angiogenesis protein from one organism in a different organism or host cell. Alternatively, the protein may be made at a significantly higher concentration than is normally seen, through the use of an inducible promoter or high expression promoter, such that the protein is made at increased concentration levels. Alternatively, the protein may be in a form not normally found in nature, as in the addition of an epitope tag or amino acid substitutions, insertions and deletions, as discussed below.

In a preferred embodiment, the angiogenesis sequences are nucleic acids. As will be appreciated by those in the art and is more fully outlined below, angiogenesis sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids, as well as screening applications; for example, biochips comprising nucleic acid probes to the angiogenesis sequences can be generated. In the broadest sense, then, by "nucleic acid" or "oligonucleotide" or grammatical equivalents herein means at least two nucleotides covalently linked together. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, nucleic acid analogs are included that may have alternate backbones, comprising, for example, phosphoramidate, phosphorothioate, phosphorodithioate, or O-methylphosphoroamidite linkages (see Eckstein, *Oligonucleotides and Analogues: A Practical Approach*, Oxford University Press); and peptide nucleic acid backbones and linkages. Other

analog nucleic acids include those with positive backbones; non-ionic backbones, and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7, ASC Symposium Series 580, "Carbohydrate Modifications in Antisense Research", Ed. Y.S. Sanghui and P. Dan Cook. Nucleic acids containing one or
5 more carbocyclic sugars are also included within one definition of nucleic acids.

Modifications of the ribose-phosphate backbone may be done for a variety of reasons, for example to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip.

As will be appreciated by those in the art, nucleic acid analogs may find use in
10 the present invention. In addition, mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in
15 contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in two advantages. First, the PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (T_m) for mismatched versus perfectly matched basepairs. DNA and RNA typically exhibit a 2-4°C drop in T_m for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9°C. Similarly,
20 due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. As will be appreciated
25 by those in the art, the depiction of a single strand also defines the sequence of the complementary strand; thus the sequences described herein also provide the complement of the sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA or a hybrid, where the nucleic acid may contain combinations of deoxyribo- and ribo-nucleotides, and combinations of bases, including uracil, adenine, thymine, cytosine, guanine, inosine,
30 xanthine hypoxanthine, isocytosine, isoguanine, etc. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus for example the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

An angiogenesis sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the angiogenesis sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions.

For identifying angiogenesis-associated sequences, the angiogenesis screen typically includes comparing genes identified in a modification of an *in vitro* model of angiogenesis as described in Hiraoka, Cell 95:365 (1998) with genes identified in controls. Samples of normal tissue and tissue undergoing angiogenesis are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated as is known in the art for the preparation of mRNA. Suitable biochips are commercially available, for example from Affymetrix. Gene expression profiles as described herein are generated and the data analyzed.

In a preferred embodiment, the genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, including, but not limited to lung, heart, brain, liver, breast, kidney, muscle, prostate, small intestine, large intestine, spleen, bone and placenta. In a preferred embodiment, those genes identified during the angiogenesis screen that are expressed in any significant amount in other tissues are removed from the profile, although in some embodiments, this is not necessary. That is, when screening for drugs, it is usually preferable that the target be disease specific, to minimize possible side effects.

In a preferred embodiment, angiogenesis sequences are those that are up-regulated in angiogenesis disorders; that is, the expression of these genes is higher in the disease tissue as compared to normal tissue. "Up-regulation" as used herein means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred. All accession numbers herein are for the GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is known in the art, see, *e.g.*, Benson, DA, et al., Nucleic Acids Research 26:1-7 (1998) and <http://www.ncbi.nlm.nih.gov/>. Sequences are also available in other databases, *e.g.*, European Molecular Biology Laboratory (EMBL) and DNA Database of Japan (DDBJ). In addition, most preferred genes were found to be expressed in a limited amount or not at all in heart, brain, lung, liver, breast, kidney, prostate, small intestine and spleen.

In another preferred embodiment, angiogenesis sequences are those that are down-regulated in the angiogenesis disorder; that is, the expression of these genes is lower in angiogenic tissue as compared to normal tissue. "Down-regulation" as used herein means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred.

Angiogenesis sequences according to the invention may be classified into discrete clusters of sequences based on common expression profiles of the sequences. Expression levels of angiogenesis sequences may increase or decrease as a function of time in a manner that correlates with the induction of angiogenesis. Alternatively, expression levels of angiogenesis sequences may both increase and decrease as a function of time. For example, expression levels of some angiogenesis sequences are temporarily induced or diminished during the switch to the angiogenesis phenotype, followed by a return to baseline expression levels. Tables 1-8 provides genes, the mRNA expression of which varies as a function of time in angiogenesis tissue when compared to normal tissue.

In a particularly preferred embodiment, angiogenesis sequences are those that are induced for a period of time, typically by positive angiogenic factors, followed by a return to the baseline levels. Sequences that are temporarily induced provide a means to target angiogenesis tissue, for example neovascularized tumors, at a particular stage of angiogenesis, while avoiding rapidly growing tissue that require perpetual vascularization. Such positive angiogenic factors include α FGF, β FGF, VEGF, angiogenin and the like.

Induced angiogenesis sequences also are further categorized with respect to the timing of induction. For example, some angiogenesis genes may be induced at an early time period, such as within 10 minutes of the induction of angiogenesis. Others may be induced later, such as between 5 and 60 minutes, while yet others may be induced for a time period of about two hours or more followed by a return to baseline expression levels.

In another preferred embodiment are angiogenesis sequences that are inhibited or reduced as a function of time followed by a return to "normal" expression levels. Inhibitors of angiogenesis are examples of molecules that have this expression profile. These sequences also can be further divided into groups depending on the timing of diminished expression. For example, some molecules may display reduced expression within 10 minutes of the induction of angiogenesis. Others may be diminished later, such as between 5 and 60 minutes, while others may be diminished for a time period of about two hours or more

followed by a return to baseline. Examples of such negative angiogenic factors include thrombospondin and endostatin to name a few.

In yet another preferred embodiment are angiogenesis sequences that are induced for prolonged periods. These sequences are typically associated with induction of angiogenesis and may participate in induction and/or maintenance of the angiogenesis phenotype.

In another preferred embodiment are angiogenesis sequences, the expression of which is reduced or diminished for prolonged periods in angiogenic tissue. These sequences are typically angiogenesis inhibitors and their diminution is correlated with an increase in angiogenesis.

Informatics

The ability to identify genes that undergo changes in expression with time during angiogenesis can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, biosensor development, and other related areas. For example, the expression profiles can be used in diagnostic or prognostic evaluation of patients with angiogenesis-associated disease. Or as another example, subcellular toxicological information can be generated to better direct drug structure and activity correlation (*see*, Anderson, L., "Pharmaceutical Proteomics: Targets, Mechanism, and Function," paper presented at the IBC Proteomics conference, Coronado, CA (June 11-12, 1998)). Subcellular toxicological information can also be utilized in a biological sensor device to predict the likely toxicological effect of chemical exposures and likely tolerable exposure thresholds (*see*, U.S. Patent No. 5,811,231). Similar advantages accrue from datasets relevant to other biomolecules and bioactive agents (*e.g.*, nucleic acids, saccharides, lipids, drugs, and the like).

Thus, in another embodiment, the present invention provides a database that includes at least one set of data assay data. The data contained in the database is acquired, *e.g.*, using array analysis either singly or in a library format. The database can be in substantially any form in which data can be maintained and transmitted, but is preferably an electronic database. The electronic database of the invention can be maintained on any electronic device allowing for the storage of and access to the database, such as a personal computer, but is preferably distributed on a wide area network, such as the World Wide Web.

The focus of the present section on databases that include peptide sequence data is for clarity of illustration only. It will be apparent to those of skill in the art that similar databases can be assembled for any assay data acquired using an assay of the invention.

5 The compositions and methods for identifying and/or quantitating the relative and/or absolute abundance of a variety of molecular and macromolecular species from a biological sample undergoing angiogenesis, *i.e.*, the identification of angiogenesis-associated sequences described herein, provide an abundance of information, which can be correlated with pathological conditions, predisposition to disease, drug testing, therapeutic monitoring, gene-disease causal linkages, identification of correlates of immunity and physiological
10 status, among others. Although the data generated from the assays of the invention is suited for manual review and analysis, in a preferred embodiment, prior data processing using high-speed computers is utilized.

An array of methods for indexing and retrieving biomolecular information is known in the art. For example, U.S. Patents 6,023,659 and 5,966,712 disclose a relational
15 database system for storing biomolecular sequence information in a manner that allows sequences to be catalogued and searched according to one or more protein function hierarchies. U.S. Patent 5,953,727 discloses a relational database having sequence records containing information in a format that allows a collection of partial-length DNA sequences to be catalogued and searched according to association with one or more sequencing projects
20 for obtaining full-length sequences from the collection of partial length sequences. U.S. Patent 5,706,498 discloses a gene database retrieval system for making a retrieval of a gene sequence similar to a sequence data item in a gene database based on the degree of similarity between a key sequence and a target sequence. U.S. Patent 5,538,897 discloses a method using mass spectroscopy fragmentation patterns of peptides to identify amino acid sequences
25 in computer databases by comparison of predicted mass spectra with experimentally-derived mass spectra using a closeness-of-fit measure. U.S. Patent 5,926,818 discloses a multi-dimensional database comprising a functionality for multi-dimensional data analysis described as on-line analytical processing (OLAP), which entails the consolidation of projected and actual data according to more than one consolidation path or dimension. U.S.
30 Patent 5,295,261 reports a hybrid database structure in which the fields of each database record are divided into two classes, navigational and informational data, with navigational fields stored in a hierarchical topological map which can be viewed as a tree structure or as the merger of two or more such tree structures.

The present invention provides a computer database comprising a computer and software for storing in computer-retrievable form assay data records cross-tabulated, *e.g.*, with data specifying the source of the target-containing sample from which each sequence specificity record was obtained.

5 In an exemplary embodiment, at least one of the sources of target-containing sample is from a control tissue sample known to be free of pathological disorders. In a variation, at least one of the sources is a known pathological tissue specimen, *e.g.*, a neoplastic lesion or another tissue specimen to be analyzed for angiogenesis. In another variation, the assay records cross-tabulate one or more of the following parameters for each target species in a sample: (1) a unique identification code, which can include, *e.g.*, a target
10 molecular structure and/or characteristic separation coordinate (*e.g.*, electrophoretic coordinates); (2) sample source; and (3) absolute and/or relative quantity of the target species present in the sample.

The invention also provides for the storage and retrieval of a collection of
15 target data in a computer data storage apparatus, which can include magnetic disks, optical disks, magneto-optical disks, DRAM, SRAM, SGRAM, SDRAM, RDRAM, DDR RAM, magnetic bubble memory devices, and other data storage devices, including CPU registers and on-CPU data storage arrays. Typically, the target data records are stored as a bit pattern in an array of magnetic domains on a magnetizable medium or as an array of charge states or
20 transistor gate states, such as an array of cells in a DRAM device (*e.g.*, each cell comprised of a transistor and a charge storage area, which may be on the transistor). In one embodiment, the invention provides such storage devices, and computer systems built therewith, comprising a bit pattern encoding a protein expression fingerprint record comprising unique identifiers for at least 10 target data records cross-tabulated with target source.

25 When the target is a peptide or nucleic acid, the invention preferably provides a method for identifying related peptide or nucleic acid sequences, comprising performing a computerized comparison between a peptide or nucleic acid sequence assay record stored in or retrieved from a computer storage device or database and at least one other sequence. The comparison can include a sequence analysis or comparison algorithm or computer program
30 embodiment thereof (*e.g.*, FASTA, TFASTA, GAP, BESTFIT) and/or the comparison may be of the relative amount of a peptide or nucleic acid sequence in a pool of sequences determined from a polypeptide or nucleic acid sample of a specimen.

The invention also preferably provides a magnetic disk, such as an IBM-compatible (DOS, Windows, Windows95/98/2000, Windows NT, OS/2) or other format

(*e.g.*, Linux, SunOS, Solaris, AIX, SCO Unix, VMS, MV, Macintosh, *etc.*) floppy diskette or hard (fixed, Winchester) disk drive, comprising a bit pattern encoding data from an assay of the invention in a file format suitable for retrieval and processing in a computerized sequence analysis, comparison, or relative quantitation method.

5 The invention also provides a network, comprising a plurality of computing devices linked via a data link, such as an Ethernet cable (coax or 10BaseT), telephone line, ISDN line, wireless network, optical fiber, or other suitable signal transmission medium, whereby at least one network device (*e.g.*, computer, disk array, *etc.*) comprises a pattern of magnetic domains (*e.g.*, magnetic disk) and/or charge domains (*e.g.*, an array of DRAM
10 cells) composing a bit pattern encoding data acquired from an assay of the invention.

 The invention also provides a method for transmitting assay data that includes generating an electronic signal on an electronic communications device, such as a modem, ISDN terminal adapter, DSL, cable modem, ATM switch, or the like, wherein the signal includes (in native or encrypted format) a bit pattern encoding data from an assay or a
15 database comprising a plurality of assay results obtained by the method of the invention.

 In a preferred embodiment, the invention provides a computer system for comparing a query target to a database containing an array of data structures, such as an assay result obtained by the method of the invention, and ranking database targets based on the degree of identity and gap weight to the target data. A central processor is preferably
20 initialized to load and execute the computer program for alignment and/or comparison of the assay results. Data for a query target is entered into the central processor via an I/O device. Execution of the computer program results in the central processor retrieving the assay data from the data file, which comprises a binary description of an assay result.

 The target data or record and the computer program can be transferred to
25 secondary memory, which is typically random access memory (*e.g.*, DRAM, SRAM, SGRAM, or SDRAM). Targets are ranked according to the degree of correspondence between a selected assay characteristic (*e.g.*, binding to a selected affinity moiety) and the same characteristic of the query target and results are output via an I/O device. For example, a central processor can be a conventional computer (*e.g.*, Intel Pentium, PowerPC, Alpha,
30 PA-8000, SPARC, MIPS 4400, MIPS 10000, VAX, *etc.*); a program can be a commercial or public domain molecular biology software package (*e.g.*, UWGCG Sequence Analysis Software, Darwin); a data file can be an optical or magnetic disk, a data server, a memory device (*e.g.*, DRAM, SRAM, SGRAM, SDRAM, EPROM, bubble memory, flash memory, *etc.*); an I/O device can be a terminal comprising a video display and a keyboard, a modem,

an ISDN terminal adapter, an Ethernet port, a punched card reader, a magnetic strip reader, or other suitable I/O device.

The invention also preferably provides the use of a computer system, such as that described above, which comprises: (1) a computer; (2) a stored bit pattern encoding a collection of peptide sequence specificity records obtained by the methods of the invention, which may be stored in the computer; (3) a comparison target, such as a query target; and (4) a program for alignment and comparison, typically with rank-ordering of comparison results on the basis of computed similarity values.

10 *Angiogenesis-associated sequences*

Angiogenesis proteins of the present invention may be classified as secreted proteins, transmembrane proteins or intracellular proteins. In one embodiment, the angiogenesis protein is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus or associated with the intracellular side of the plasma membrane. Intracellular proteins are involved in all aspects of cellular function and replication (including, *e.g.*, signaling pathways); aberrant expression of such proteins often results in unregulated or disregulated cellular processes (see, *e.g.*, Molecular Biology of the Cell, 3rd Edition, Alberts, Ed., Garland Pub., 1994). For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase activity, polymerase activity and the like. Intracellular proteins also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

An increasingly appreciated concept in characterizing proteins is the presence in the proteins of one or more motifs for which defined functions have been attributed. In addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2 domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. As will be appreciated by one of ordinary skill in the art, these motifs can be identified on the basis of primary

sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate.

In another embodiment, the angiogenesis sequences are transmembrane proteins. Transmembrane proteins are molecules that span a phospholipid bilayer of a cell.

5 They may have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine
10 kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor
15 guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors such as G protein coupled receptors (GPCRs) are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Characteristics of
20 transmembrane domains include approximately 20 consecutive hydrophobic amino acids that may be followed or flanked by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the localization and number of transmembrane domains within the protein may be predicted (see, *e.g.* PSORT web site <http://psort.nibb.ac.jp/>).

The extracellular domains of transmembrane proteins are diverse; however,
25 conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are found on receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like.
30 For example, growth factors such as EGF, FGF and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, neurotrophic factors and the like. Extracellular domains also bind to cell-associated molecules. In this respect, they mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell for example via a glycosylphosphatidylinositol

(GPI) anchor, or may themselves be transmembrane proteins. Extracellular domains also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

Angiogenesis proteins that are transmembrane are particularly preferred in the present invention as they are readily accessible targets for immunotherapeutics, as are
5 described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities. Antibodies may be used to label such readily accessible proteins *in situ*. Alternatively, antibodies can also label intracellular proteins, in which case samples are typically permeabilized to provide access to intracellular proteins.

It will also be appreciated by those in the art that a transmembrane protein can
10 be made soluble by removing transmembrane sequences, for example through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

In another embodiment, the angiogenesis proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins have a signal
15 peptide or signal sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; by virtue of their circulating nature, they serve to transmit signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor) or an endocrine manner (acting
20 on cells at a distance). Thus secreted molecules find use in modulating or altering numerous aspects of physiology. Angiogenesis proteins that are secreted proteins are particularly preferred in the present invention as they serve as good targets for diagnostic markers, *e.g.*, for blood or serum tests.

An angiogenesis sequence is typically initially identified by substantial nucleic
25 acid and/or amino acid sequence homology or linkage to the angiogenesis sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions. Typically, linked sequences on a mRNA are found on the same molecule.

30 As detailed in the definitions, percent identity can be determined using an algorithm such as BLAST. A preferred method utilizes the BLASTN module of WU-BLAST-2 set to the default parameters, with overlap span and overlap fraction set to 1 and 0.125, respectively. The alignment may include the introduction of gaps in the sequences to be aligned. In addition, for sequences which contain either more or fewer nucleotides than

those of the nucleic acids of the figures, it is understood that the percentage of homology will be determined based on the number of homologous nucleosides in relation to the total number of nucleosides. Thus, for example, homology of sequences shorter than those of the sequences identified herein and as discussed below, will be determined using the number of nucleosides in the shorter sequence.

In one embodiment, the nucleic acid homology is determined through hybridization studies. Thus, *e.g.*, nucleic acids which hybridize under high stringency to a nucleic acid of Tables 1-8, or its complement, or is also found on naturally occurring mRNAs is considered an angiogenesis sequence. In another embodiment, less stringent hybridization conditions are used; for example, moderate or low stringency conditions may be used, as are known in the art; see Ausubel, *supra*, and Tijssen, *supra*.

In addition, the angiogenesis nucleic acid sequences of the invention, *e.g.*, the sequence in Tables 1-8, are fragments of larger genes, *i.e.* they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, as will be appreciated by those in the art, using the sequences provided herein, extended sequences, in either direction, of the angiogenesis genes can be obtained, using techniques well known in the art for cloning either longer sequences or the full length sequences; see Ausubel, *et al.*, *supra*. Much can be done by informatics and many sequences can be clustered to include multiple sequences, *e.g.*, systems such as UniGene (see, <http://www.ncbi.nlm.nih.gov/UniGene/>).

Once the angiogenesis nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire angiogenesis nucleic acid coding regions or the entire mRNA sequence. Once isolated from its natural source, *e.g.*, contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant angiogenesis nucleic acid can be further-used as a probe to identify and isolate other angiogenesis nucleic acids, for example extended coding regions. It can also be used as a "precursor" nucleic acid to make modified or variant angiogenesis nucleic acids and proteins.

The angiogenesis nucleic acids of the present invention are used in several ways. In a first embodiment, nucleic acid probes to the angiogenesis nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, for example for gene therapy, vaccine, and/or antisense applications. Alternatively, the angiogenesis nucleic acids that include coding regions of angiogenesis

proteins can be put into expression vectors for the expression of angiogenesis proteins, again for screening purposes or for administration to a patient.

5 In a preferred embodiment, nucleic acid probes to angiogenesis nucleic acids (both the nucleic acid sequences outlined in the figures and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the angiogenesis nucleic acids, *i.e.* the target sequence (either the target sequence of the sample or to other probe sequences, for example in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under normal reaction conditions, particularly high stringency conditions, as outlined herein.

20 A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8 to about 100 bases long, with from about 10 to about 80 bases being preferred, and from about 30 to about 50 bases being particularly preferred. That is, generally whole genes are not used. In some embodiments, much longer nucleic acids can be used, up to hundreds of bases.

25 In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a particular target. The probes can be overlapping (*i.e.* have some sequence in common), or separate. In some cases, PCR primers may be used to amplify signal for higher sensitivity.

30 As will be appreciated by those in the art, nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined below. The binding can typically be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is meant one or more of electrostatic,

hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent attachment of a molecule, such as, streptavidin to the support and the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

In general, the probes are attached to the biochip in a wide variety of ways, as will be appreciated by those in the art. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant a material that can be modified to contain discrete individual sites appropriate for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. As will be appreciated by those in the art, the number of possible substrates are very large, and include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, Teflon, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably fluoresce. A preferred substrate is described in copending application entitled Reusable Low Fluorescent Plastic Biochip, U.S. Application Serial No. 09/270,214, filed March 15, 1999, herein incorporated by reference in its entirety.

Generally the substrate is planar, although as will be appreciated by those in the art, other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube, for flow-through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, for example, the biochip is derivatized with a chemical functional group including, but not

limited to, amino groups, carboxy groups, oxo groups and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, for example using linkers as are known in the art; for example, homo-or hetero-bifunctional linkers as are well known (see 1994 Pierce
5 Chemical Company catalog, technical section on cross-linkers, pages 155-200, incorporated herein by reference). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, oligonucleotides are synthesized as is known in the art, and then attached to the surface of the solid support. As will be appreciated by those skilled
10 in the art, either the 5' or 3' terminus may be attached to the solid support, or attachment may be via an internal nucleoside.

In another embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which
15 bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface, as is known in the art. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized in situ, using well known photolithographic techniques, such as those described
20 in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affimetrix GeneChip™ technology.

Often, amplification-based assays are performed to measure the expression level of angiogenesis-associated sequences. These assays are typically performed in
25 conjunction with reverse transcription. In such assays, an angiogenesis-associated nucleic acid sequence acts as a template in an amplification reaction (*e.g.*, Polymerase Chain Reaction, or PCR). In a quantitative amplification, the amount of amplification product will be proportional to the amount of template in the original sample. Comparison to appropriate controls provides a measure of the amount of angiogenesis-associated RNA. Methods of
30 quantitative amplification are well known to those of skill in the art. Detailed protocols for quantitative PCR are provided, *e.g.*, in Innis *et al.* (1990) *PCR Protocols, A Guide to Methods and Applications*, Academic Press, Inc. N.Y.).

In some embodiments, a TaqMan based assay is used to measure expression. TaqMan based assays use a fluorogenic oligonucleotide probe that contains a 5' fluorescent

dye and a 3' quenching agent. The probe hybridizes to a PCR product, but cannot itself be extended due to a blocking agent at the 3' end. When the PCR product is amplified in subsequent cycles, the 5' nuclease activity of the polymerase, *e.g.*, AmpliTaq, results in the cleavage of the TaqMan probe. This cleavage separates the 5' fluorescent dye and the 3' quenching agent, thereby resulting in an increase in fluorescence as a function of amplification (*see*, for example, literature provided by Perkin-Elmer, *e.g.*, www2.perkin-elmer.com).

Other suitable amplification methods include, but are not limited to, ligase chain reaction (LCR) (*see*, Wu and Wallace (1989) *Genomics* 4: 560, Landegren *et al.* (1988) *Science* 241: 1077, and Barringer *et al.* (1990) *Gene* 89: 117), transcription amplification (Kwoh *et al.* (1989) *Proc. Natl. Acad. Sci. USA* 86: 1173), self-sustained sequence replication (Guatelli *et al.* (1990) *Proc. Nat. Acad. Sci. USA* 87: 1874), dot PCR, and linker adapter PCR, *etc.*

In a preferred embodiment, angiogenesis nucleic acids, *e.g.*, encoding angiogenesis proteins are used to make a variety of expression vectors to express angiogenesis proteins which can then be used in screening assays, as described below. Expression vectors and recombinant DNA technology are well known to those of skill in the art (*see, e.g.*, Ausubel, *supra*, and Gene Expression Systems, Fernandez & Hoeffler, Eds, Academic Press, 1999) and are used to express proteins. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the angiogenesis protein. The term "control sequences" refers to DNA sequences used for the expression of an operably linked coding sequence in a particular host organism. Control sequences that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous,

and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is typically accomplished by ligation at convenient restriction sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. Transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the angiogenesis protein; for example, transcriptional and translational regulatory nucleic acid sequences from *Bacillus* are preferably used to express the angiogenesis protein in *Bacillus*. Numerous types of appropriate expression vectors, and suitable regulatory sequences are known in the art for a variety of host cells.

In general, transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences encode either constitutive or inducible promoters. The promoters may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known in the art, and are useful in the present invention.

In addition, an expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two organisms, for example in mammalian or insect cells for expression and in a procaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are well known in the art (*e.g.*, Fernandez & Hoeffler, *supra*). See also Kitamura, et al. (1995) PNAS 92:9146-9150.

In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known in the art and will vary with the host cell used.

The angiogenesis proteins of the present invention are produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding an angiogenesis protein, under the appropriate conditions to induce or cause expression of the

angiogenesis protein. Conditions appropriate for angiogenesis protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained by one skilled in the art through routine experimentation or optimization. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

Appropriate host cells include yeast, bacteria, archaeobacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are *Saccharomyces cerevisiae* and other yeasts, *E. coli*, *Bacillus subtilis*, Sf9 cells, C129 cells, 293 cells, *Neurospora*, BHK, CHO, COS, HeLa cells, HUVEC (human umbilical vein endothelial cells), THP1 cells (a macrophage cell line) and various other human cells and cell lines.

In a preferred embodiment, the angiogenesis proteins are expressed in mammalian cells. Mammalian expression systems are also known in the art, and include retroviral and adenoviral systems. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter (see, e.g., Fernandez & Hoeffler, *supra*). Typically, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenylation signals include those derived from SV40.

The methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, is well known in the art, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

In a preferred embodiment, angiogenesis proteins are expressed in bacterial systems. Bacterial expression systems are well known in the art. Promoters from bacteriophage may also be used and are known in the art. In addition, synthetic promoters

and hybrid promoters are also useful; for example, the tac promoter is a hybrid of the trp and lac promoter sequences. Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The expression vector may also include a signal peptide sequence that provides for secretion of the angiogenesis protein in bacteria. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known in the art, and include vectors for *Bacillus subtilis*, *E. coli*, *Streptococcus cremoris*, and *Streptococcus lividans*, among others (e.g., Fernandez & Hoeffler, *supra*). The bacterial expression vectors are transformed into bacterial host cells using techniques well known in the art, such as calcium chloride treatment, electroporation, and others.

In one embodiment, angiogenesis proteins are produced in insect cells.

Expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors, are well known in the art.

In a preferred embodiment, angiogenesis protein is produced in yeast cells.

Yeast expression systems are well known in the art, and include expression vectors for *Saccharomyces cerevisiae*, *Candida albicans* and *C. maltosa*, *Hansenula polymorpha*, *Kluyveromyces fragilis* and *K. lactis*, *Pichia guilliermondii* and *P. pastoris*, *Schizosaccharomyces pombe*, and *Yarrowia lipolytica*.

The angiogenesis protein may also be made as a fusion protein, using techniques well known in the art. Thus, for example, for the creation of monoclonal antibodies, if the desired epitope is small, the angiogenesis protein may be fused to a carrier protein to form an immunogen. Alternatively, the angiogenesis protein may be made as a fusion protein to increase expression, or for other reasons. For example, when the angiogenesis protein is an angiogenesis peptide, the nucleic acid encoding the peptide may be linked to another nucleic acid for expression purposes. Fusion with detection epitope tags can be made, e.g., with FLAG, His 6, myc, HA, etc.

In one embodiment, the angiogenesis nucleic acids, proteins and antibodies of the invention are labeled. By "labeled" herein is meant that a compound has at least one element, isotope or chemical compound attached to enable the detection of the compound. In general, labels fall into three classes: a) isotopic labels, which may be radioactive or heavy isotopes; b) immune labels, which may be antibodies, antigens, or epitope tags and c) colored or fluorescent dyes. The labels may be incorporated into the angiogenesis nucleic acids, proteins and antibodies at any position. For example, the label should be capable of producing, either directly or indirectly, a detectable signal. The detectable moiety may be a radioisotope, such as ^3H , ^{14}C , ^{32}P , ^{35}S , or ^{125}I , a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin, or an enzyme, such as alkaline phosphatase, beta-galactosidase or horseradish peroxidase. Any method known in the art for conjugating the antibody to the label may be employed, including those methods described by Hunter et al., *Nature*, 144:945 (1962); David et al., *Biochemistry*, 13:1014 (1974); Pain et al., *J. Immunol. Meth.*, 40:219 (1981); and Nygren, *J. Histochem. and Cytochem.*, 30:407 (1982).

Accordingly, the present invention also provides angiogenesis protein sequences. An angiogenesis protein of the present invention may be identified in several ways. "Protein" in this sense includes proteins, polypeptides, and peptides. As will be appreciated by those in the art, the nucleic acid sequences of the invention can be used to generate protein sequences. There are a variety of ways to do this, including cloning the entire gene and verifying its frame and amino acid sequence, or by comparing it to known sequences to search for homology to provide a frame, assuming the angiogenesis protein has an identifiable motif or homology to some protein in the database being used. Generally, the nucleic acid sequences are input into a program that will search all three frames for homology. This is done in a preferred embodiment using the following NCBI Advanced BLAST parameters. The program is blastx or blastn. The database is nr. The input data is as "Sequence in FASTA format". The organism list is "none". The "expect" is 10; the filter is default. The "descriptions" is 500, the "alignments" is 500, and the "alignment view" is pairwise. The "Query Genetic Codes" is standard (1). The matrix is BLOSUM62; gap existence cost is 11, per residue gap cost is 1; and the lambda ratio is .85 default. This results in the generation of a putative protein sequence.

Also included within one embodiment of angiogenesis proteins are amino acid variants of the naturally occurring sequences, as determined herein. Preferably, the variants are preferably greater than about 75% homologous to the wild-type sequence, more

preferably greater than about 80%, even more preferably greater than about 85% and most preferably greater than 90%. In some embodiments the homology will be as high as about 93 to 95 or 98%. As for nucleic acids, homology in this context means sequence similarity or identity, with identity being preferred. This homology will be determined using standard techniques well known in the art as are outlined above for the nucleic acid homologies.

Angiogenesis proteins of the present invention may be shorter or longer than the wild type amino acid sequences. Thus, in a preferred embodiment, included within the definition of angiogenesis proteins are portions or fragments of the wild type sequences herein. In addition, as outlined above, the angiogenesis nucleic acids of the invention may be used to obtain additional coding regions, and thus additional protein sequence, using techniques known in the art.

In a preferred embodiment, the angiogenesis proteins are derivative or variant angiogenesis proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative angiogenesis peptide will often contain at least one amino acid substitution, deletion or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion or deletion may occur at any residue within the angiogenesis peptide.

Also included within one embodiment of angiogenesis proteins of the present invention are amino acid sequence variants. These variants typically fall into one or more of three classes: substitutional, insertional or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the angiogenesis protein, using cassette or PCR mutagenesis or other techniques well known in the art, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above. However, variant angiogenesis protein fragments having up to about 100-150 residues may be prepared by in vitro synthesis using established techniques. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the angiogenesis protein amino acid sequence. The variants typically exhibit the same qualitative biological activity as the naturally occurring analogue, although variants can also be selected which have modified characteristics as will be more fully outlined below.

While the site or region for introducing an amino acid sequence variation is predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed angiogenesis variants screened for

the optimal combination of desired activity. Techniques for making substitution mutations at predetermined sites in DNA having a known sequence are well known, for example, M13 primer mutagenesis and PCR mutagenesis. Screening of the mutants is done using assays of angiogenesis protein activities.

5 Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1 to 20 amino acids, although considerably larger insertions may be tolerated. Deletions range from about 1 to about 20 residues, although in some cases deletions may be much larger.

10 Substitutions, deletions, insertions or any combination thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to minimize the alteration of the molecule. However, larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of the angiogenesis protein are desired, substitutions are generally made in accordance with the amino acid substitution chart provided in the definition section.

15 Substantial changes in function or immunological identity are made by selecting substitutions that are less conservative than those provided in the definition of "conservative substitution". For example, substitutions may be made which more significantly affect: the structure of the polypeptide backbone in the area of the alteration, for example the alpha-helical or beta-sheet structure; the charge or hydrophobicity of the molecule at the target site; or the bulk of the side chain. The substitutions which in general
20 are expected to produce the greatest changes in the polypeptide's properties are those in which (a) a hydrophilic residue, *e.g.* seryl or threonyl, is substituted for (or by) a hydrophobic residue, *e.g.* leucyl, isoleucyl, phenylalanyl, valyl or alanyl; (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue having an electropositive side chain,
25 *e.g.* lysyl, arginyl, or histidyl, is substituted for (or by) an electronegative residue, *e.g.* glutamyl or aspartyl; or (d) a residue having a bulky side chain, *e.g.* phenylalanine, is substituted for (or by) one not having a side chain, *e.g.* glycine.

30 The variants typically exhibit the same qualitative biological activity and will elicit the same immune response as the naturally-occurring analog, although variants also are selected to modify the characteristics of the angiogenesis proteins as needed. Alternatively, the variant may be designed such that the biological activity of the angiogenesis protein is altered. For example, glycosylation sites may be altered or removed.

Covalent modifications of angiogenesis polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino

acid residues of an angiogenesis polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N-or C-terminal residues of an angiogenesis polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking angiogenesis polypeptides to a water-insoluble support matrix or surface for use in the method for purifying anti-angiogenesis polypeptide antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, *e.g.*, 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-[(p-azidophenyl)dithio]propioimide.

Other modifications include deamidation of glutamyl and asparaginyll residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl, threonyl or tyrosyl residues, methylation of the γ -amino groups of lysine, arginine, and histidine side chains [T.E. Creighton, *Proteins: Structure and Molecular Properties*, W.H. Freeman & Co., San Francisco, pp. 79-86 (1983)], acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the angiogenesis polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence angiogenesis polypeptide, and/or adding one or more glycosylation sites that are not present in the native sequence angiogenesis polypeptide. Glycosylation patterns can be altered in many ways. For example the use of different cell types to express angiogenesis-associated sequences can result in different glycosylation patterns.

Addition of glycosylation sites to angiogenesis polypeptides may also be accomplished by altering the amino acid sequence thereof. The alteration may be made, for example, by the addition of, or substitution by, one or more serine or threonine residues to the native sequence angiogenesis polypeptide (for O-linked glycosylation sites). The angiogenesis amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the angiogenesis polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the angiogenesis polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330 published 11 September 1987, and in Aplin and Wriston, *CRC Crit. Rev. Biochem.*, pp. 259-306 (1981).

5 Removal of carbohydrate moieties present on the angiogenesis polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, et al., *Arch. Biochem. Biophys.*, 259:52 (1987) and by Edge et al., *Anal. Biochem.*, 118:131
10 (1981). Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo-and exo-glycosidases as described by Thotakura et al., *Meth. Enzymol.*, 138:350 (1987).

Another type of covalent modification of angiogenesis comprises linking the angiogenesis polypeptide to one of a variety of nonproteinaceous polymers, e.g.,
15 polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337.

Angiogenesis polypeptides of the present invention may also be modified in a way to form chimeric molecules comprising an angiogenesis polypeptide fused to another, heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric
20 molecule comprises a fusion of an angiogenesis polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino-or carboxyl-terminus of the angiogenesis polypeptide. The presence of such epitope-tagged forms of an angiogenesis polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the
25 angiogenesis polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of an angiogenesis polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

30 Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; HIS6 and metal chelation tags, the flu HA tag polypeptide and its antibody 12CA5 [Field *et al.*, *Mol. Cell. Biol.*, 8:2159-2165 (1988)]; the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies thereto [Evan *et al.*, *Molecular and Cellular Biology*, 5:3610-3616 (1985)];

and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody [*Paborsky et al., Protein Engineering*, 3(6):547-553 (1990)]. Other tag polypeptides include the Flag-peptide [*Hopp et al., BioTechnology*, 6:1204-1210 (1988)]; the KT3 epitope peptide [*Martin et al., Science*, 255:192-194 (1992)]; tubulin epitope peptide [*Skinner et al., J. Biol. Chem.*, 266:15163-15166 (1991)]; and the T7 gene 10 protein peptide tag [*Lutz-Freyermuth et al., Proc. Natl. Acad. Sci. USA*, 87:6393-6397 (1990)].

Also included with an embodiment of angiogenesis protein are other angiogenesis proteins of the angiogenesis family, and angiogenesis proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related angiogenesis proteins from humans or other organisms. As will be appreciated by those in the art, particularly useful probe and/or PCR primer sequences include the unique areas of the angiogenesis nucleic acid sequence. As is generally known in the art, preferred PCR primers are from about 15 to about 35 nucleotides in length, with from about 20 to about 30 being preferred, and may contain inosine as needed. The conditions for the PCR reaction are well known in the art (*e.g.*, Innis, PCR Protocols, *supra*).

In addition, as is outlined herein, angiogenesis proteins can be made that are longer than those encoded by the nucleic acids of the figures, *e.g.*, by the elucidation of extended sequences, the addition of epitope or purification tags, the addition of other fusion sequences, etc.

Angiogenesis proteins may also be identified as being encoded by angiogenesis nucleic acids. Thus, angiogenesis proteins are encoded by nucleic acids that will hybridize to the sequences of the sequence listings, or their complements, as outlined herein.

In a preferred embodiment, when the angiogenesis protein is to be used to generate antibodies, *e.g.*, for immunotherapy or immunodiagnosis, the angiogenesis protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is typically meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller angiogenesis protein will be able to bind to the full-length protein, particularly linear epitopes. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity. In a preferred embodiment, the epitope is selected from a protein sequence set out in Table 8.

Methods of preparing polyclonal antibodies are known to the skilled artisan (e.g., Coligan, *supra*; and Harlow & Lane, *supra*). Polyclonal antibodies can be raised in a mammal, e.g., by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include a protein encoded by a nucleic acid of the figures or fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art without undue experimentation.

The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein, *Nature*, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized in vitro. The immunizing agent will typically include a polypeptide encoded by a nucleic acid of Tables 1-8, or fragment thereof, or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell [Goding, *Monoclonal Antibodies: Principles and Practice*, Academic Press, (1986) pp. 59-103]. Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens or that have binding specificities for two epitopes on the same antigen. In one embodiment, one of the binding specificities is for a protein encoded by a nucleic acid Tables 1-8 or a fragment thereof, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific. Alternatively, tetramer-type technology may create multivalent reagents.

In a preferred embodiment, the antibodies to angiogenesis protein are capable of reducing or eliminating a biological function of an angiogenesis protein, as is described below. That is, the addition of anti-angiogenesis protein antibodies (either polyclonal or preferably monoclonal) to angiogenic tissue (or cells containing angiogenesis) may reduce or eliminate the angiogenesis activity. Generally, at least a 25% decrease in activity is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

In a preferred embodiment the antibodies to the angiogenesis proteins are humanized antibodies (*e.g.*, Xenex Biosciences, Mederex, Inc., Abgenix, Inc., Protein Design Labs, Inc.) Humanized forms of non-human (*e.g.*, murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues form a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, a humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework (FR) regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human

immunoglobulin [Jones et al., *Nature*, 321:522-525 (1986); Riechmann et al., *Nature*, 332:323-329 (1988); and Presta, *Curr. Op. Struct. Biol.*, 2:593-596 (1992)].

Methods for humanizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from
5 a source which is non-human. These non-human amino acid residues are often referred to as import residues, which are typically taken from an import variable domain. Humanization can be essentially performed following the method of Winter and co-workers [Jones et al., *Nature*, 321:522-525 (1986); Riechmann et al., *Nature*, 332:323-327 (1988); Verhoeyen et al., *Science*, 239:1534-1536 (1988)], by substituting rodent CDRs or CDR sequences for the
10 corresponding sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from
15 analogous sites in rodent antibodies.

Human antibodies can also be produced using various techniques known in the art, including phage display libraries [Hoogenboom and Winter, *J. Mol. Biol.*, 227:381 (1991); Marks et al., *J. Mol. Biol.*, 222:581 (1991)]. The techniques of Cole et al. and Boerner et al. are also available for the preparation of human monoclonal antibodies (Cole et al.,
20 *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, p. 77 (1985) and Boerner et al., *J. Immunol.*, 147(1):86-95 (1991)]. Similarly, human antibodies can be made by introducing of human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in
25 humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks et al., *Bio/Technology* 10, 779-783 (1992); Lonberg et al., *Nature* 368 856-859 (1994); Morrison, *Nature* 368, 812-13 (1994); Fishwild et al., *Nature Biotechnology* 14, 845-51
30 (1996); Neuberger, *Nature Biotechnology* 14, 826 (1996); Lonberg and Huszar, *Intern. Rev. Immunol.* 13 65-93 (1995).

By immunotherapy is meant treatment of angiogenesis with an antibody raised against angiogenesis proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient

(patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. As appreciated by one of ordinary skill in the art, the antigen may be provided by injecting a polypeptide against which antibodies are
5 desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen, leading to an immune response.

In a preferred embodiment the angiogenesis proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory,
10 antibodies used for treatment, bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted angiogenesis protein.

In another preferred embodiment, the angiogenesis protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment, bind the extracellular domain of the angiogenesis protein and prevent it from
15 binding to other proteins, such as circulating ligands or cell-associated molecules. The antibody may cause down-regulation of the transmembrane angiogenesis protein. As will be appreciated by one of ordinary skill in the art, the antibody may be a competitive, non-competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the angiogenesis protein. The antibody is also an antagonist of the angiogenesis protein.

Further, the antibody prevents activation of the transmembrane angiogenesis protein. In one aspect, when the antibody prevents the binding of other molecules to the angiogenesis
20 protein, the antibody prevents growth of the cell. The antibody may also be used to target or sensitize the cell to cytotoxic agents, including, but not limited to TNF- α , TNF- β , IL-1, INF- γ and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody belongs to a sub-type that
25 activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity or antigen-dependent cytotoxicity (ADCC). Thus, angiogenesis is treated by administering to a patient antibodies directed against the transmembrane angiogenesis protein. Antibody-labeling may activate a co-toxin, localize a toxin payload, or
30 otherwise provide means to locally ablate cells.

In another preferred embodiment, the antibody is conjugated or fused to an effector moiety. The effector moiety can be any number of molecules, including labelling moieties such as radioactive labels or fluorescent labels, or can be a therapeutic moiety. In

one aspect the therapeutic moiety is a small molecule that modulates the activity of the angiogenesis protein. In another aspect the therapeutic moiety modulates the activity of molecules associated with or in close proximity to the angiogenesis protein. The therapeutic moiety may inhibit enzymatic activity such as protease or collagenase activity associated with angiogenesis, or be an attractant of other cells, such as NK cells.

In a preferred embodiment, the therapeutic moiety can also be a cytotoxic agent. In this method, targeting the cytotoxic agent to angiogenesis tissue or cells, results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with angiogenesis. Cytotoxic agents are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin and the like. Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against angiogenesis proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane angiogenesis proteins not only serves to increase the local concentration of therapeutic moiety in the angiogenesis afflicted area, but also serves to reduce deleterious side effects that may be associated with the therapeutic moiety.

In another preferred embodiment, the angiogenesis protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated or fused to a protein which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the angiogenesis protein can be targeted within a cell, i.e., the nucleus, an antibody thereto contains a signal for that target localization, i.e., a nuclear localization signal.

The angiogenesis antibodies of the invention specifically bind to angiogenesis proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a K_d of at least about 0.1 mM, more usually at least about 1 μ M, preferably at least about 0.1 μ M or better, and most preferably, 0.01 μ M or better. Selectivity of binding is also important.

In a preferred embodiment, the angiogenesis protein is purified or isolated after expression. Angiogenesis proteins may be isolated or purified in a variety of ways known to those skilled in the art depending on what other components are present in the sample. Standard purification methods include electrophoretic, molecular, immunological

and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the angiogenesis protein may be purified using a standard anti-angiogenesis protein antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. For
5 general guidance in suitable purification techniques, see Scopes, R., Protein Purification, Springer-Verlag, NY (1982). The degree of purification necessary will vary depending on the use of the angiogenesis protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the angiogenesis proteins and nucleic acids are useful in a number of applications. They may be used as immunoselection
10 reagents, as vaccine reagents, as screening agents, etc.

Detection of angiogenesis sequence for diagnostic and therapeutic applications

In one aspect, the RNA expression levels of genes are determined for different cellular states in the angiogenesis phenotype. Expression levels of genes in normal tissue
15 (*i.e.*, not undergoing angiogenesis) and in angiogenesis tissue (and in some cases, for varying severities of angiogenesis that relate to prognosis, as outlined below) are evaluated to provide expression profiles. An expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state. While two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the
20 generation of a gene expression profile that is reflective of the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be performed or confirmed to determine whether a tissue sample has the gene expression profile of normal or angiogenic tissue. This will provide
25 for molecular diagnosis of related conditions.

"Differential expression," or grammatical equivalents as used herein, refers to qualitative or quantitative differences in the temporal and/or cellular gene expression patterns within and among cells and tissue. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, *e.g.*,
30 normal versus angiogenic tissue. Genes may be turned on or turned off in a particular state, relative to another state thus permitting comparison of two or more states. A qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques. Some genes will be expressed in one state or cell type, but not in both. Alternatively, the difference in expression may be quantitative, *e.g.*, in that

expression is increased or decreased; *i.e.*, gene expression is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays, Lockhart, Nature Biotechnology, 14:1675-1680 (1996), hereby expressly incorporated by reference. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR, Northern analysis and RNase protection. As outlined above, preferably the change in expression (*i.e.*, upregulation or downregulation) is at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably at least about 200%, with from 300 to at least 1000% being especially preferred.

Evaluation may be at the gene transcript, or the protein level. The amount of gene expression may be monitored using nucleic acid probes to the DNA or RNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, *e.g.*, with antibodies to the angiogenesis protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Proteins corresponding to angiogenesis genes, *i.e.*, those identified as being important in an angiogenesis phenotype, can be evaluated in an angiogenesis diagnostic test.

In a preferred embodiment, gene expression monitoring is performed simultaneously on a number of genes. Multiple protein expression monitoring can be performed as well. Similarly, these assays may be performed on an individual basis as well.

In this embodiment, the angiogenesis nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of angiogenesis sequences in a particular cell. The assays are further described below in the example. PCR techniques can be used to provide greater sensitivity.

In a preferred embodiment nucleic acids encoding the angiogenesis protein are detected. Although DNA or RNA encoding the angiogenesis protein may be detected, of particular interest are methods wherein an mRNA encoding an angiogenesis protein is detected. Probes to detect mRNA can be a nucleotide/deoxynucleotide probe that is complementary to and hybridizes with the mRNA and includes, but is not limited to, oligonucleotides, cDNA or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is

detected. In another method detection of the mRNA is performed in situ. In this method permeabilized cells or tissue samples are contacted with a detectably labeled nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxigenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding an angiogenesis protein is detected by binding the digoxigenin with an anti-digoxigenin secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl phosphate.

In a preferred embodiment, various proteins from the three classes of proteins as described herein (secreted, transmembrane or intracellular proteins) are used in diagnostic assays. The angiogenesis proteins, antibodies, nucleic acids, modified proteins and cells containing angiogenesis sequences are used in diagnostic assays. This can be performed on an individual gene or corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

As described and defined herein, angiogenesis proteins, including intracellular, transmembrane or secreted proteins, find use as markers of angiogenesis. Detection of these proteins in putative angiogenesis tissue allows for detection or diagnosis of angiogenesis. In one embodiment, antibodies are used to detect angiogenesis proteins. A preferred method separates proteins from a sample by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be another type of gel, including isoelectric focusing gels and the like). Following separation of proteins, the angiogenesis protein is detected, e.g., by immunoblotting with antibodies raised against the angiogenesis protein. Methods of immunoblotting are well known to those of ordinary skill in the art.

In another preferred method, antibodies to the angiogenesis protein find use in *in situ* imaging techniques, e.g., in histology (e.g., *Methods in Cell Biology: Antibodies in Cell Biology*, volume 37 (Asai, ed. 1993)). In this method cells are contacted with from one to many antibodies to the angiogenesis protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a detectable label. In another method the primary antibody to the angiogenesis protein(s) contains a detectable label, for example an enzyme marker that can act on a substrate. In another preferred embodiment each one of multiple primary antibodies contains a distinct and

detectable label. This method finds particular use in simultaneous screening for a plurality of angiogenesis proteins. As will be appreciated by one of ordinary skill in the art, many other histological imaging techniques are also provided by the invention.

5 In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

In another preferred embodiment, antibodies find use in diagnosing angiogenesis from biological samples, such as blood, urine, sputum, or other bodily fluids. As previously described, certain angiogenesis proteins are secreted/circulating molecules. 10 Blood samples, therefore, are useful as samples to be probed or tested for the presence of secreted angiogenesis proteins. Antibodies can be used to detect an angiogenesis protein by previously described immunoassay techniques including ELISA, immunoblotting (Western blotting), immunoprecipitation, BIACORE technology and the like. Conversely, the presence of antibodies may indicate an immune response against an endogenous angiogenesis protein.

15 In a preferred embodiment, *in situ* hybridization of labeled angiogenesis nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including angiogenesis tissue and/or normal tissue, are made. *In situ* hybridization (*see, e.g., Ausubel, supra*) is then performed. When comparing the fingerprints between an individual and a standard, the skilled artisan can make a diagnosis, a prognosis, or a prediction based on the 20 findings. It is further understood that the genes which indicate the diagnosis may differ from those which indicate the prognosis and molecular profiling of the condition of the cells may lead to distinctions between responsive or refractory conditions or may be predictive of outcomes.

In a preferred embodiment, the angiogenesis proteins, antibodies, nucleic 25 acids, modified proteins and cells containing angiogenesis sequences are used in prognosis assays. As above, gene expression profiles can be generated that correlate to angiogenesis severity, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. As above, angiogenesis probes may be attached to biochips for the detection and quantification of angiogenesis sequences in a tissue or 30 patient. The assays proceed as outlined above for diagnosis. PCR method may provide more sensitive and accurate quantification.

In a preferred embodiment members of the three classes of proteins as described herein are used in drug screening assays. The angiogenesis proteins, antibodies, nucleic acids, modified proteins and cells containing angiogenesis sequences are used in drug

screening assays or by evaluating the effect of drug candidates on a “gene expression profile” or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent (e.g.,
5 Zlokarnik, et al., Science 279, 84-8 (1998); Heid, *Genome Res* 6:986-94, 1996).

In a preferred embodiment, the angiogenesis proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified angiogenesis proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the angiogenesis phenotype or an identified physiological
10 function of an angiogenesis protein. As above, this can be done on an individual gene level or by evaluating the effect of drug candidates on a “gene expression profile”. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, *supra*.

15 Having identified the differentially expressed genes herein, a variety of assays may be executed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene as up regulated in angiogenesis, test compounds can be screened for the ability to modulate gene expression or for binding to the angiogenic protein. “Modulation” thus includes both an increase and a decrease in gene
20 expression. The preferred amount of modulation will depend on the original change of the gene expression in normal versus tissue undergoing angiogenesis, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4-fold increase in angiogenic tissue compared to normal tissue, a decrease of about four-fold is often desired; similarly, a 10-fold decrease in
25 angiogenic tissue compared to normal tissue often provides a target value of a 10-fold increase in expression to be induced by the test compound.

The amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be monitored, e.g., through the use of antibodies to the angiogenesis protein and standard
30 immunoassays. Proteomics and separation techniques may also allow quantification of expression.

In a preferred embodiment, gene expression or protein monitoring of a number of entities, i.e., an expression profile, is monitored simultaneously. Such profiles will typically involve a plurality of those entities described herein..

In this embodiment, the angiogenesis nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of angiogenesis sequences in a particular cell. Alternatively, PCR may be used. Thus, a series, e.g., of microtiter plate, may be used with dispensed primers in desired wells. A PCR reaction can then be performed and analyzed for each well.

Modulators of angiogenesis

Expression monitoring can be performed to identify compounds that modify the expression of one or more angiogenesis-associated sequences, e.g., a polynucleotide sequence set out in Tables 1-8. Generally, in a preferred embodiment, a test modulator is added to the cells prior to analysis. Moreover, screens are also provided to identify agents that modulate angiogenesis, modulate angiogenesis proteins, bind to an angiogenesis protein, or interfere with the binding of an angiogenesis protein and an antibody or other binding partner.

The term "test compound" or "drug candidate" or "modulator" or grammatical equivalents as used herein describes any molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to directly or indirectly alter the angiogenesis phenotype or the expression of an angiogenesis sequence, e.g., a nucleic acid or protein sequence. In preferred embodiments, modulators alter expression profiles, or expression profile nucleic acids or proteins provided herein. In one embodiment, the modulator suppresses an angiogenesis phenotype, for example to a normal tissue fingerprint. In another embodiment, a modulator induced an angiogenesis phenotype. Generally, a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, i.e., at zero concentration or below the level of detection.

In one aspect, a modulator will neutralize the effect of an angiogenesis protein. By "neutralize" is meant that activity of a protein is inhibited or blocked and thereby has substantially no effect on a cell.

In certain embodiments, combinatorial libraries of potential modulators will be screened for an ability to bind to an angiogenesis polypeptide or to modulate activity. Conventionally, new chemical entities with useful properties are generated by identifying a chemical compound (called a "lead compound") with some desirable property or activity, e.g., inhibiting activity, creating variants of the lead compound, and evaluating the property

and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis.

In one preferred embodiment, high throughput screening methods involve providing a library containing a large number of potential therapeutic compounds (candidate compounds). Such "combinatorial chemical libraries" are then screened in one or more assays to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library, such as a polypeptide (*e.g.*, mutein) library, is formed by combining a set of chemical building blocks called amino acids in every possible way for a given compound length (*i.e.*, the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks (Gallop *et al.* (1994) *J. Med. Chem.* 37(9): 1233-1251).

Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (*see, e.g.*, U.S. Patent No. 5,010,175, Furka (1991) *Int. J. Pept. Prot. Res.*, 37: 487-493, Houghton *et al.* (1991) *Nature*, 354: 84-88), peptoids (PCT Publication No WO 91/19735, 26 Dec. 1991), encoded peptides (PCT Publication WO 93/20242, 14 Oct. 1993), random bio-oligomers (PCT Publication WO 92/00091, 9 Jan. 1992), benzodiazepines (U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs *et al.*, (1993) *Proc. Nat. Acad. Sci. USA* 90: 6909-6913), vinylogous polypeptides (Hagihara *et al.* (1992) *J. Amer. Chem. Soc.* 114: 6568), nonpeptidal peptidomimetics with a Beta-D-Glucose scaffolding (Hirschmann *et al.*, (1992) *J. Amer. Chem. Soc.* 114: 9217-9218), analogous organic syntheses of small compound libraries (Chen *et al.* (1994) *J. Amer. Chem. Soc.* 116: 2661), oligocarbamates (Cho, *et al.*, (1993) *Science* 261:1303), and/or peptidyl phosphonates (Campbell *et al.*, (1994) *J. Org. Chem.* 59: 658). *See, generally*, Gordon *et al.*, (1994) *J. Med. Chem.* 37:1385, nucleic acid libraries (*see, e.g.*, Strategene, Corp.), peptide nucleic acid libraries (*see, e.g.*, U.S. Patent 5,539,083), antibody libraries (*see, e.g.*, Vaughn *et al.* (1996) *Nature Biotechnology*, 14(3): 309-314), and PCT/US96/10287), carbohydrate libraries (*see, e.g.*, Liang *et al.*, (1996) *Science*, 274: 1520-1522, and U.S. Patent No. 5,593,853), and small organic molecule libraries (*see, e.g.*, benzodiazepines, Baum (1993)

C&EN, Jan 18, page 33; isoprenoids, U.S. Patent No. 5,569,588; thiazolidinones and metathiazanones, U.S. Patent No. 5,549,974; pyrrolidines, U.S. Patent Nos. 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent No. 5,506,337; benzodiazepines, U.S. Patent No. 5,288,514; and the like).

5 Devices for the preparation of combinatorial libraries are commercially available (*see, e.g.*, 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY, Symphony, Rainin, Woburn, MA, 433A Applied Biosystems, Foster City, CA, 9050 Plus, Millipore, Bedford, MA).

10 A number of well known robotic systems have also been developed for solution phase chemistries. These systems include automated workstations like the automated synthesis apparatus developed by Takeda Chemical Industries, LTD. (Osaka, Japan) and many robotic systems utilizing robotic arms (Zymate II, Zymark Corporation, Hopkinton, Mass.; Orca, Hewlett-Packard, Palo Alto, Calif.), which mimic the manual synthetic operations performed by a chemist. Any of the above devices are suitable for use
15 with the present invention. The nature and implementation of modifications to these devices (if any) so that they can operate as discussed herein will be apparent to persons skilled in the relevant art. In addition, numerous combinatorial libraries are themselves commercially available (*see, e.g.*, ComGenex, Princeton, N.J., Asinex, Moscow, Ru, Tripos, Inc., St. Louis, MO, ChemStar, Ltd, Moscow, RU, 3D Pharmaceuticals, Exton, PA, Martek Biosciences,
20 Columbia, MD, *etc.*).

 The assays to identify modulators are amenable to high throughput screening. Preferred assays thus detect enhancement or inhibition of angiogenesis gene transcription, inhibition or enhancement of polypeptide expression, and inhibition or enhancement of polypeptide activity.

25 High throughput assays for the presence, absence, quantification, or other properties of particular nucleic acids or protein products are well known to those of skill in the art. Similarly, binding assays and reporter gene assays are similarly well known. Thus, for example, U.S. Patent No. 5,559,410 discloses high throughput screening methods for proteins, U.S. Patent No. 5,585,639 discloses high throughput screening methods for nucleic
30 acid binding (*i.e.*, in arrays), while U.S. Patent Nos. 5,576,220 and 5,541,061 disclose high throughput methods of screening for ligand/antibody binding.

 In addition, high throughput screening systems are commercially available (*see, e.g.*, Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman Instruments, Inc. Fullerton, CA; Precision Systems, Inc., Natick, MA, *etc.*). These systems

typically automate entire procedures, including all sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. The manufacturers of such systems provide
5 detailed protocols for various high throughput systems. Thus, for example, Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like.

In one embodiment, modulators are proteins, often naturally occurring proteins or fragments of naturally occurring proteins. Thus, *e.g.*, cellular extracts containing
10 proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of proteins may be made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred. Particularly useful test compound will be directed to the class of proteins to which
15 the target belongs, *e.g.*, substrates for enzymes or ligands and receptors.

In a preferred embodiment, modulators are peptides of from about 5 to about 30 amino acids, with from about 5 to about 20 amino acids being preferred, and from about 7 to about 15 being particularly preferred. The peptides may be digests of naturally occurring proteins as is outlined above, random peptides, or "biased" random peptides. By
20 "randomized" or grammatical equivalents herein is meant that each nucleic acid and peptide consists of essentially random nucleotides and amino acids, respectively. Since generally these random peptides (or nucleic acids, discussed below) are chemically synthesized, they may incorporate any nucleotide or amino acid at any position. The synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the formation of all or
25 most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a
30 limited number of possibilities. For example, in a preferred embodiment, the nucleotides or amino acid residues are randomized within a defined class, for example, of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking,

prolines for SH-3 domains, serines, threonines, tyrosines or histidines for phosphorylation sites, etc., or to purines, etc.

Modulators of angiogenesis can also be nucleic acids, as defined above.

As described above generally for proteins, nucleic acid modulating agents may
5 be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. For example, digests of procaryotic or eucaryotic genomes may be used as is outlined above for proteins.

In a preferred embodiment, the candidate compounds are organic chemical moieties, a wide variety of which are available in the literature.

10 After the candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing a target sequence to be analyzed is added to the biochip. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR performed as appropriate. For example,
15 an *in vitro* transcription with labels covalently attached to the nucleotides is performed. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

In a preferred embodiment, the target sequence is labeled with, for example, a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme,
20 such as, alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin. For the example of biotin, the
25 streptavidin is labeled as described above, thereby, providing a detectable signal for the bound target sequence. Unbound labeled streptavidin is typically removed prior to analysis.

As will be appreciated by those in the art, these assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos. 5,681,702, 5,597,909, 5,545,730,
30 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670, 5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246 and 5,681,697, all of which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

A variety of hybridization conditions may be used in the present invention, including high, moderate and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allows formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

The reactions outlined herein may be accomplished in a variety of ways. Components of the reaction may be added simultaneously, or sequentially, in different orders, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents. These include salts, buffers, neutral proteins, *e.g.* albumin, detergents, *etc.* which may be used to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, *etc.*, may also be used as appropriate, depending on the sample preparation methods and purity of the target.

The assay data are analyzed to determine the expression levels, and changes in expression levels as between states, of individual genes, forming a gene expression profile.

Screens are performed to identify modulators of the angiogenesis phenotype. In one embodiment, screening is performed to identify modulators that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. In another embodiment, *e.g.*, for diagnostic applications, having identified differentially expressed genes important in a particular state, screens can be performed to identify modulators that alter expression of individual genes. In another embodiment, screening is performed to identify modulators that alter a biological function of the expression product of a differentially expressed gene. Again, having identified the importance of a gene in a particular state, screens are performed to identify agents that bind and/or modulate the biological activity of the gene product.

In addition screens can be done for genes that are induced in response to a candidate agent. After identifying a modulator based upon its ability to suppress an angiogenesis expression pattern leading to a normal expression pattern, or to modulate a single angiogenesis gene expression profile so as to mimic the expression of the gene from

normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated angiogenesis tissue reveals genes that are not expressed in normal tissue or angiogenesis tissue, but are expressed in agent treated tissue. These agent-specific sequences can be identified and used by methods described herein for angiogenesis genes or proteins. In particular these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics to the treated angiogenesis tissue sample.

Thus, in one embodiment, a test compound is administered to a population of angiogenic cells, that have an associated angiogenesis expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (*i.e.*, a peptide) may be put into a viral construct such as an adenoviral or retroviral construct, and added to the cell, such that expression of the peptide agent is accomplished, *e.g.*, PCT US97/01019. Regulatable gene therapy systems can also be used.

Once the test compound has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

Thus, for example, angiogenesis tissue may be screened for agents that modulate, *e.g.*, induce or suppress the angiogenesis phenotype. A change in at least one gene, preferably many, of the expression profile indicates that the agent has an effect on angiogenesis activity. By defining such a signature for the angiogenesis phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein need to change.

Measure of angiogenesis polypeptide activity, or of angiogenesis or the angiogenic phenotype can be performed using a variety of assays. For example, the effects of the test compounds upon the function of the angiogenesis polypeptides can be measured by examining parameters described above. A suitable physiological change that affects activity can be used to assess the influence of a test compound on the polypeptides of this invention.

When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as, in the case of angiogenesis associated with tumors, tumor growth, neovascularization, hormone release, transcriptional changes to both known and uncharacterized genetic markers (*e.g.*, northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as cGMP. In the assays of the invention, mammalian angiogenesis polypeptide is typically used, *e.g.*, mouse, preferably human.

A variety of angiogenesis assays are known to those of skill in the art. Various models have been employed to evaluate angiogenesis (*e.g.*, Croix *et al.*, *Science* 289:1197-1202, 2000 and Kahn *et al.*, *Amer. J. Pathol.* 156:1887-1900). Assessment of angiogenesis in the presence of a potential modulator of angiogenesis can be performed using cell-culture-based angiogenesis assays, *e.g.*, endothelial cell tube formation assays, as well as other bioassays such as the chick CAM assay, the mouse corneal assay, and assays measuring the effect of administering potential modulators on implanted tumors. The chick CAM assay is described by O'Reilly, *et al.* *Cell* 79: 315-328, 1994. Briefly, 3 day old chicken embryos with intact yolks are separated from the egg and placed in a petri dish. After 3 days of incubation, a methylcellulose disc containing the protein to be tested is applied to the CAM of individual embryos. After about 48 hours of incubation, the embryos and CAMs are observed to determine whether endothelial growth has been inhibited. The mouse corneal assay involves implanting a growth factor-containing pellet, along with another pellet containing the suspected endothelial growth inhibitor, in the cornea of a mouse and observing the pattern of capillaries that are elaborated in the cornea. Angiogenesis can also be measured by determining the extent of neovascularization of a tumor. For example, carcinoma cells can be subcutaneously inoculated into athymic nude mice and tumor growth then monitored. The cancer cells are treated with an angiogenesis inhibitor, such as an antibody, or other compound that is exogenously administered, or can be transfected prior to inoculation with a polynucleotide inhibitor of angiogenesis. Immunoassays using endothelial cell-specific antibodies are typically used to stain for vascularization of tumor and the number of vessels in the tumor.

Assays to identify compounds with modulating activity can be performed *in vitro*. For example, an angiogenesis polypeptide is first contacted with a potential modulator and incubated for a suitable amount of time, *e.g.*, from 0.5 to 48 hours. In one embodiment, the angiogenesis polypeptide levels are determined *in vitro* by measuring the level of protein or mRNA. The level of protein is measured using immunoassays such as western blotting,

ELISA and the like with an antibody that selectively binds to the angiogenesis polypeptide or a fragment thereof. For measurement of mRNA, amplification, e.g., using PCR, LCR, or hybridization assays, e.g., northern hybridization, RNase protection, dot blotting, are preferred. The level of protein or mRNA is detected using directly or indirectly labeled
5 detection agents, e.g., fluorescently or radioactively labeled nucleic acids, radioactively or enzymatically labeled antibodies, and the like, as described herein.

Alternatively, a reporter gene system can be devised using the angiogenesis protein promoter operably linked to a reporter gene such as luciferase, green fluorescent protein, CAT, or β -gal. The reporter construct is typically transfected into a cell. After
10 treatment with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques known to those of skill in the art.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of the
15 expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "angiogenesis proteins". In preferred embodiments the angiogenesis protein comprises a sequence shown in Table 8. The angiogenesis protein may be a fragment, or alternatively, be the full length protein to a fragment shown herein.

20 Preferably, the angiogenesis protein is a fragment of approximately 14 to 24 amino acids long. More preferably the fragment is a soluble fragment. In one embodiment an angiogenesis protein is conjugated or fused to an immunogenic agent or BSA.

In one embodiment, screening for modulators of expression of specific genes is performed. Typically, the expression of only one or a few genes are evaluated. In another
25 embodiment, screens are designed to first find compounds that bind to differentially expressed proteins. These compounds are then evaluated for the ability to modulate differentially expressed activity. Moreover, once initial candidate compounds are identified, variants can be further screened to better evaluate structure activity relationships.

In a preferred embodiment, binding assays are done. In general, purified or
30 isolated gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the angiogenesis proteins can be used in the assays.

Thus, in a preferred embodiment, the methods comprise combining an angiogenesis protein and a candidate compound, and determining the binding of the compound to the angiogenesis protein. Preferred embodiments utilize the human angiogenesis protein, although other mammalian proteins may also be used, for example for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative angiogenesis proteins may be used.

Generally, in a preferred embodiment of the methods herein, the angiogenesis protein or the candidate agent is non-diffusably bound to an insoluble support having isolated sample receiving areas (e.g. a microtiter plate, an array, etc.). The insoluble supports may be made of any composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface of such supports may be solid or porous and of any convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflon™, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular manner of binding of the composition is not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition and is nondiffusable. Preferred methods of binding include the use of antibodies (which do not sterically block either the ligand binding site or activation sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein or other innocuous protein or other moiety.

In a preferred embodiment, the angiogenesis protein is bound to the support, and a test compound is added to the assay. Alternatively, the candidate agent is bound to the support and the angiogenesis protein is added. Novel binding agents include specific antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled in vitro protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.) and the like.

The determination of the binding of the test modulating compound to the angiogenesis protein may be done in a number of ways. In a preferred embodiment, the compound is labelled, and binding determined directly, *e.g.*, by attaching all or a portion of the angiogenesis protein to a solid support, adding a labelled candidate agent (*e.g.*, a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and washing steps may be utilized as appropriate.

By "labeled" herein is meant that the compound is either directly or indirectly labeled with a label which provides a detectable signal, *e.g.* radioisotope, fluorescers, enzyme, antibodies, particles such as magnetic particles, chemiluminescers, or specific binding molecules, etc. Specific binding molecules include pairs, such as biotin and streptavidin, digoxin and antidigoxin, etc. For the specific binding members, the complementary member would normally be labeled with a molecule which provides for detection, in accordance with known procedures, as outlined above. The label can directly or indirectly provide a detectable signal.

In some embodiments, only one of the components is labeled, *e.g.*, the proteins (or proteinaceous candidate compounds) can be labeled. Alternatively, more than one component can be labeled with different labels, *e.g.*, ^{125}I for the proteins and a fluorophore for the compound. Proximity reagents, *e.g.*, quenching or energy transfer reagents are also useful.

In one embodiment, the binding of the test compound is determined by competitive binding assay. The competitor is a binding moiety known to bind to the target molecule (*i.e.* an angiogenesis protein), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding between the compound and the binding moiety, with the binding moiety displacing the compound. In one embodiment, the test compound is labeled. Either the compound, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at a temperature which facilitates optimal activity, typically between 4 and 40°C. Incubation periods are typically optimized, *e.g.*, to facilitate rapid high throughput screening. Typically between 0.1 and 1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

In a preferred embodiment, the competitor is added first, followed by the test compound. Displacement of the competitor is an indication that the test compound is binding to the angiogenesis protein and thus is capable of binding to, and potentially modulating, the

activity of the angiogenesis protein. In this embodiment, either component can be labeled. Thus, for example, if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent. Alternatively, if the test compound is labeled, the presence of the label on the support indicates displacement.

5 In an alternative embodiment, the test compound is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the test compound is bound to the angiogenesis protein with a higher affinity. Thus, if the test compound is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the test compound is
10 capable of binding to the angiogenesis protein.

In a preferred embodiment, the methods comprise differential screening to identity agents that are capable of modulating the activity of the angiogenesis proteins. In this embodiment, the methods comprise combining an angiogenesis protein and a competitor in a first sample. A second sample comprises a test compound, an angiogenesis protein, and
15 a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the angiogenesis protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the angiogenesis protein.

20 Alternatively, differential screening is used to identify drug candidates that bind to the native angiogenesis protein, but cannot bind to modified angiogenesis proteins. The structure of the angiogenesis protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect the activity of an angiogenesis protein are also identified by screening drugs for the ability to either enhance or
25 reduce the activity of the protein.

Positive controls and negative controls may be used in the assays. Preferably control and test samples are performed in at least triplicate to obtain statistically significant results. Incubation of all samples is for a time sufficient for the binding of the agent to the protein. Following incubation, samples are washed free of non-specifically bound material
30 and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, *e.g.* albumin, detergents, *etc.* which may be used

to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in an order that provides for the requisite binding.

5 In a preferred embodiment, the invention provides methods for screening for a compound capable of modulating the activity of an angiogenesis protein. The methods comprise adding a test compound, as defined above, to a cell comprising angiogenesis proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes an angiogenesis protein. In a preferred embodiment, a library of
10 candidate agents are tested on a plurality of cells.

In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, for example hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including chemotherapeutics, radiation, carcinogenics, or other cells (i.e. cell-cell contacts). In another
15 example, the determinations are determined at different stages of the cell cycle process.

In this way, compounds that modulate angiogenesis agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the angiogenesis protein. Once identified, similar structures are evaluated to identify critical structural feature of the compound.

20 In one embodiment, a method of inhibiting angiogenic cell division is provided. The method comprises administration of an angiogenesis inhibitor. In another embodiment, a method of inhibiting angiogenesis is provided. The method comprises administration of an angiogenesis inhibitor. In a further embodiment, methods of treating cells or individuals with angiogenesis are provided. The method comprises administration of
25 an angiogenesis inhibitor.

In one embodiment, an angiogenesis inhibitor is an antibody as discussed above. In another embodiment, the angiogenesis inhibitor is an antisense molecule.

Polynucleotide modulators of angiogenesis

30 *Antisense Polynucleotides*

In certain embodiments, the activity of an angiogenesis-associated protein is downregulated, or entirely inhibited, by the use of antisense polynucleotide, *i.e.*, a nucleic acid complementary to, and which can preferably hybridize specifically to, a coding mRNA nucleic acid sequence, *e.g.*, an angiogenesis protein mRNA, or a subsequence thereof.

Binding of the antisense polynucleotide to the mRNA reduces the translation and/or stability of the mRNA.

In the context of this invention, antisense polynucleotides can comprise naturally-occurring nucleotides, or synthetic species formed from naturally-occurring subunits or their close homologs. Antisense polynucleotides may also have altered sugar moieties or inter-sugar linkages. Exemplary among these are the phosphorothioate and other sulfur containing species which are known for use in the art. Analogs are comprehended by this invention so long as they function effectively to hybridize with the angiogenesis protein mRNA. See, *e.g.*, Isis Pharmaceuticals, Carlsbad, CA; Sequitor, Inc., Natick, MA.

Such antisense polynucleotides can readily be synthesized using recombinant means, or can be synthesized *in vitro*. Equipment for such synthesis is sold by several vendors, including Applied Biosystems. The preparation of other oligonucleotides such as phosphorothioates and alkylated derivatives is also well known to those of skill in the art.

Antisense molecules as used herein include antisense or sense oligonucleotides. Sense oligonucleotides can, *e.g.*, be employed to block transcription by binding to the anti-sense strand. The antisense and sense oligonucleotide comprise a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for angiogenesis molecules. A preferred antisense molecule is for an angiogenesis sequences in Tables 1-8, or for a ligand or activator thereof. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, for example, Stein and Cohen (Cancer Res. 48:2659, 1988) and van der Krol et al. (BioTechniques 6:958, 1988).

Ribozymes

In addition to antisense polynucleotides, ribozymes can be used to target and inhibit transcription of angiogenesis-associated nucleotide sequences. A ribozyme is an RNA molecule that catalytically cleaves other RNA molecules. Different kinds of ribozymes have been described, including group I ribozymes, hammerhead ribozymes, hairpin ribozymes, RNase P, and axhead ribozymes (*see, e.g.*, Castanotto *et al.* (1994) *Adv. in Pharmacology* 25: 289-317 for a general review of the properties of different ribozymes).

The general features of hairpin ribozymes are described, *e.g.*, in Hampel *et al.* (1990) *Nucl. Acids Res.* 18: 299-304; Hampel *et al.* (1990) European Patent Publication No. 0

360 257; U.S. Patent No. 5,254,678. Methods of preparing are well known to those of skill in the art (*see, e.g.,* Wong-Staal *et al.*, WO 94/26877; Ojwang *et al.* (1993) *Proc. Natl. Acad. Sci. USA* 90: 6340-6344; Yamada *et al.* (1994) *Human Gene Therapy* 1: 39-45; Leavitt *et al.* (1995) *Proc. Natl. Acad. Sci. USA* 92: 699-703; Leavitt *et al.* (1994) *Human Gene Therapy* 5: 1151-120; and Yamada *et al.* (1994) *Virology* 205: 121-126).

Polynucleotide modulators of angiogenesis may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a polynucleotide modulator of angiogenesis may be introduced into a cell containing the target nucleic acid sequence, *e.g.,* by formation of an polynucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

Thus, in one embodiment, methods of modulating angiogenesis in cells or organisms are provided. In one embodiment, the methods comprise administering to a cell an anti-angiogenesis antibody that reduces or eliminates the biological activity of an endogenous angiogenesis protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic acid encoding an angiogenesis protein. This may be accomplished in any number of ways. In a preferred embodiment, for example when the angiogenesis sequence is down-regulated in angiogenesis, such state may be reversed by increasing the amount of angiogenesis gene product in the cell. This can be accomplished, *e.g.,* by overexpressing the endogenous angiogenesis gene or administering a gene encoding the angiogenesis sequence, using known gene-therapy techniques, for example. In a preferred embodiment, the gene therapy techniques include the incorporation of the exogenous gene using enhanced homologous recombination (EHR), for example as described in PCT/US93/03868, hereby incorporated by reference in its entirety. Alternatively, for example when the angiogenesis sequence is up-regulated in angiogenesis, the activity of the endogenous angiogenesis gene is decreased, for example by the administration of a angiogenesis antisense nucleic acid or other inhibitor, such as RNAi.

In one embodiment, the angiogenesis eproteins of the present invention may be used to generate polyclonal and monoclonal antibodies to angiogenesis proteins. Similarly, the angiogenesis proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify angiogenesis antibodies useful for production, diagnostic, or therapeutic purposes. In a preferred embodiment, the antibodies are generated to epitopes unique to a angiogenesis protein; that is, the antibodies show little or no cross-reactivity to other proteins. The angiogenesis antibodies may be coupled to standard affinity chromatography columns and used to purify angiogenesis proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the angiogenesis protein.

Methods of identifying variant angiogenesis-associated sequences

Without being bound by theory, expression of various angiogenesis sequences is correlated with angiogenesis. Accordingly, disorders based on mutant or variant angiogenesis genes may be determined. In one embodiment, the invention provides methods for identifying cells containing variant angiogenesis genes, *e.g.*, determining all or part of the sequence of at least one endogeneous angiogenesis genes in a cell. This may be accomplished using any number of sequencing techniques. In a preferred embodiment, the invention provides methods of identifying the angiogenesis genotype of an individual, *e.g.*, determining all or part of the sequence of at least one angiogenesis gene of the individual. This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced angiogenesis gene to a known angiogenesis gene, *i.e.*, a wild-type gene.

The sequence of all or part of the angiogenesis gene can then be compared to the sequence of a known angiogenesis gene to determine if any differences exist. This can be done using any number of known homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a a difference in the sequence between the angiogenesis gene of the patient and the known angiogenesis gene correlates with a disease state or a propensity for a disease state, as outlined herein.

In a preferred embodiment, the angiogenesis genes are used as probes to determine the number of copies of the angiogenesis gene in the genome.

In another preferred embodiment, the angiogenesis genes are used as probes to determine the chromosomal localization of the angiogenesis genes. Information such as

chromosomal localization finds use in providing a diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in the angiogenesis gene locus.

5 *Administration of pharmaceutical and vaccine compositions*

In one embodiment, a therapeutically effective dose of an angiogenesis protein or modulator thereof, is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using
10 known techniques (*e.g.*, Ansel *et al.*, *Pharmaceutical Dosage Forms and Drug Delivery*, Lippincott, Williams & Wilkins Publishers, ISBN:0683305727; Lieberman (1992) *Pharmaceutical Dosage Forms* (vols. 1-3), Dekker, ISBN 0824770846, 082476918X, 0824712692, 0824716981; Lloyd (1999) *The Art, Science and Technology of Pharmaceutical Compounding*, Amer. Pharmaceutical Assn, ISBN 0917330889; and Pickar (1999) *Dosage*
15 *Calculations*, Delmar Pub, ISBN 0766805042). As is known in the art, adjustments for angiogenesis degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration, drug interaction and the severity of the condition may be necessary, and will be ascertainable with routine experimentation by those skilled in the art.

20 A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals. Thus the methods are applicable to both human therapy and veterinary applications. In the preferred embodiment the patient is a mammal, preferably a primate, and in the most preferred embodiment the patient is human.

The administration of the angiogenesis proteins and modulators thereof of the
25 present invention can be done in a variety of ways as discussed above, including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, or intraocularly. In some instances, for example, in the treatment of wounds and inflammation, the angiogenesis proteins and modulators may be directly applied as a solution or spray.

30 The pharmaceutical compositions of the present invention comprise an angiogenesis protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain

the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid and the like. "Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose, lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol.

The pharmaceutical compositions can be administered in a variety of unit dosage forms depending upon the method of administration. For example, unit dosage forms suitable for oral administration include, but are not limited to, powder, tablets, pills, capsules and lozenges. It is recognized that angiogenesis protein modulators (*e.g.*, antibodies, antisense constructs, ribozymes, small organic molecules, *etc.*) when administered orally, should be protected from digestion. This is typically accomplished either by complexing the molecule(s) with a composition to render it resistant to acidic and enzymatic hydrolysis, or by packaging the molecule(s) in an appropriately resistant carrier, such as a liposome or a protection barrier. Means of protecting agents from digestion are well known in the art.

The compositions for administration will commonly comprise an angiogenesis protein modulator dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers can be used, *e.g.*, buffered saline and the like. These solutions are sterile and generally free of undesirable matter. These compositions may be sterilized by conventional, well known sterilization techniques. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents

and the like, for example, sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate and the like. The concentration of active agent in these formulations can vary widely, and will be selected primarily based on fluid volumes, viscosities, body weight and the like in accordance with the particular mode of administration selected and the patient's needs (*e.g.*, *Remington's Pharmaceutical Science*, 15th ed., Mack Publishing Company, Easton, Pennsylvania (1980) and Goodman and Gillman, *The Pharmacological Basis of Therapeutics*, (Hardman, J.G, Limbird, L.E, Molinoff, P.B., Ruddon, R.W, and Gilman, A.G., eds) The McGraw-Hill Companies, Inc., 1996).

Thus, a typical pharmaceutical composition for intravenous administration would be about 0.1 to 10 mg per patient per day. Dosages from 0.1 up to about 100 mg per patient per day may be used, particularly when the drug is administered to a secluded site and not into the blood stream, such as into a body cavity or into a lumen of an organ. Substantially higher dosages are possible in topical administration. Actual methods for preparing parenterally administrable compositions will be known or apparent to those skilled in the art, *e.g.*, *Remington's Pharmaceutical Science* and Goodman and Gillman, *The Pharmacological Basis of Therapeutics*, *supra*.

The compositions containing modulators of angiogenesis proteins can be administered for therapeutic or prophylactic treatments. In therapeutic applications, compositions are administered to a patient suffering from a disease (*e.g.*, a cancer) in an amount sufficient to cure or at least partially arrest the disease and its complications. An amount adequate to accomplish this is defined as a "therapeutically effective dose." Amounts effective for this use will depend upon the severity of the disease and the general state of the patient's health. Single or multiple administrations of the compositions may be administered depending on the dosage and frequency as required and tolerated by the patient. In any event, the composition should provide a sufficient quantity of the agents of this invention to effectively treat the patient. An amount of modulator that is capable of preventing or slowing the development of cancer in a mammal is referred to as a "prophylactically effective dose." The particular dose required for a prophylactic treatment will depend upon the medical condition and history of the mammal, the particular cancer being prevented, as well as other factors such as age, weight, gender, administration route, efficiency, *etc.* Such prophylactic treatments may be used, *e.g.*, in a mammal who has previously had cancer to prevent a recurrence of the cancer, or in a mammal who is suspected of having a significant likelihood of developing cancer.

It will be appreciated that the present angiogenesis protein-modulating compounds can be administered alone or in combination with additional angiogenesis modulating compounds or with other therapeutic agent, *e.g.*, other anti-cancer agents or treatments.

5 In numerous embodiments, one or more nucleic acids, *e.g.*, polynucleotides comprising nucleic acid sequences set forth in Tables 1-8, such as antisense polynucleotides or ribozymes, will be introduced into cells, *in vitro* or *in vivo*. The present invention provides methods, reagents, vectors, and cells useful for expression of angiogenesis-associated polypeptides and nucleic acids using *in vitro* (cell-free), *ex vivo* or *in vivo* (cell or
10 organism-based) recombinant expression systems.

The particular procedure used to introduce the nucleic acids into a host cell for expression of a protein or nucleic acid is application specific. Many procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, spheroplasts, electroporation, liposomes, microinjection,
15 plasma vectors, viral vectors and any of the other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell (*see, e.g.*, Berger and Kimmel, *Guide to Molecular Cloning Techniques, Methods in Enzymology* volume 152 Academic Press, Inc., San Diego, CA (Berger), F.M. Ausubel *et al.*, eds., *Current Protocols*, a joint venture between Greene Publishing Associates, Inc. and John Wiley &
20 Sons, Inc., (supplemented through 1999), and Sambrook *et al.*, *Molecular Cloning - A Laboratory Manual* (2nd Ed.), Vol. 1-3, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, 1989.

In a preferred embodiment, angiogenesis proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly,
25 angiogenesis genes (including both the full-length sequence, partial sequences, or regulatory sequences of the angiogenesis coding regions) can be administered in a gene therapy application. These angiogenesis genes can include antisense applications, either as gene therapy (*i.e.* for incorporation into the genome) or as antisense compositions, as will be appreciated by those in the art.

30 Angiogenesis polypeptides and polynucleotides can also be administered as vaccine compositions to stimulate HTL, CTL and antibody responses.. Such vaccine compositions can include, for example, lipidated peptides (*e.g.*, Vitiello, A. *et al.*, *J. Clin. Invest.* 95:341, 1995), peptide compositions encapsulated in poly(DL-lactide-co-glycolide) ("PLG") microspheres (*see, e.g.*, Eldridge, *et al.*, *Molec. Immunol.* 28:287-294, 1991; Alonso

et al., *Vaccine* 12:299-306, 1994; Jones et al., *Vaccine* 13:675-681, 1995), peptide compositions contained in immune stimulating complexes (ISCOMS) (see, e.g., Takahashi et al., *Nature* 344:873-875, 1990; Hu et al., *Clin Exp Immunol.* 113:235-243, 1998), multiple antigen peptide systems (MAPs) (see e.g., Tam, J. P., *Proc. Natl. Acad. Sci. U.S.A.* 85:5409-5413, 1988; Tam, J.P., *J. Immunol. Methods* 196:17-32, 1996), peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, M. E. et al., In: *Concepts in vaccine development*, Kaufmann, S. H. E., ed., p. 379, 1996; Chakrabarti, S. et al., *Nature* 320:535, 1986; Hu, S. L. et al., *Nature* 320:537, 1986; Kieny, M.-P. et al., *AIDS Bio/Technology* 4:790, 1986; Top, F. H. et al., *J. Infect. Dis.* 124:148, 1971; Chanda, P. K. et al., *Virology* 175:535, 1990), particles of viral or synthetic origin (e.g., Kofler, N. et al., *J. Immunol. Methods.* 192:25, 1996; Eldridge, J. H. et al., *Sem. Hematol.* 30:16, 1993; Falo, L. D., Jr. et al., *Nature Med.* 7:649, 1995), adjuvants (Warren, H. S., Vogel, F. R., and Chedid, L. A. *Annu. Rev. Immunol.* 4:369, 1986; Gupta, R. K. et al., *Vaccine* 11:293, 1993), liposomes (Reddy, R. et al., *J. Immunol.* 148:1585, 1992; Rock, K. L., *Immunol. Today* 17:131, 1996), or, naked or particle absorbed cDNA (Ulmer, J. B. et al., *Science* 259:1745, 1993; Robinson, H. L., Hunt, L. A., and Webster, R. G., *Vaccine* 11:957, 1993; Shiver, J. W. et al., In: *Concepts in vaccine development*, Kaufmann, S. H. E., ed., p. 423, 1996; Cease, K. B., and Berzofsky, J. A., *Annu. Rev. Immunol.* 12:923, 1994 and Eldridge, J. H. et al., *Sem. Hematol.* 30:16, 1993). Toxin-targeted delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

Vaccine compositions often include adjuvants. Many adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis* derived proteins. Certain adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

Vaccines can be administered as nucleic acid compositions wherein DNA or RNA encoding one or more of the polypeptides, or a fragment thereof, is administered to a patient. This approach is described, for instance, in Wolff *et. al.*, *Science* 247:1465 (1990) as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; WO 98/04720; and in more detail below. Examples of DNA-based delivery technologies include “naked DNA”, facilitated (bupivacaine, polymers, peptide-mediated) delivery, cationic lipid complexes, and particle-mediated (“gene gun”) or pressure-mediated delivery (*see, e.g.*, U.S. Patent No. 5,922,687).

For therapeutic or prophylactic immunization purposes, the peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus, for example, as a vector to express nucleotide sequences that encode angiogenic polypeptides or polypeptide fragments. Upon introduction into a host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, *e.g.*, U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover *et al.*, *Nature* 351:456-460 (1991). A wide variety of other vectors useful for therapeutic administration or immunization *e.g.* adeno and adeno-associated virus vectors, retroviral vectors, *Salmonella typhi* vectors, detoxified anthrax toxin vectors, and the like, will be apparent to those skilled in the art from the description herein (*see, e.g.*, Shata *et al.* (2000) *Mol Med Today*, 6: 66-71; Shedlock *et al.*, *J Leukoc Biol* 68,:793-806, 2000; Hipp *et al.*, *In Vivo* 14:571-85, 2000).

Methods for the use of genes as DNA vaccines are well known, and include placing an angiogenesis gene or portion of an angiogenesis gene under the control of a regulatable promoter or a tissue-specific promoter for expression in an angiogenesis patient. The angiogenesis gene used for DNA vaccines can encode full-length angiogenesis proteins, but more preferably encodes portions of the angiogenesis proteins including peptides derived from the angiogenesis protein. In one embodiment, a patient is immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived from an angiogenesis gene. For example, angiogenesis-associated genes or sequence encoding subfragments of an angiogenesis protein are introduced into expression vectors and tested for their immunogenicity in the context of Class I MHC and an ability to generate cytotoxic T cell responses. This procedure provides for production of cytotoxic T cell responses against cells which present antigen, including intracellular epitopes.

In a preferred embodiment, the DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the angiogenesis polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are available.

5 In another preferred embodiment angiogenesis genes find use in generating animal models of angiogenesis. When the angiogenesis gene identified is repressed or diminished in angiogenic tissue, gene therapy technology, *e.g.*, wherein antisense RNA directed to the angiogenesis gene will also diminish or repress expression of the gene. Animal models of angiogenesis find use in screening for modulators of an angiogenesis-associated sequence or modulators of angiogenesis. Similarly, transgenic animal technology
10 including gene knockout technology, for example as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence or increased expression of the angiogenesis protein. When desired, tissue-specific expression or knockout of the angiogenesis protein may be necessary.

15 It is also possible that the angiogenesis protein is overexpressed in angiogenesis. As such, transgenic animals can be generated that overexpress the angiogenesis protein. Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression
20 level of the transgene. Animals generated by such methods find use as animal models of angiogenesis and are additionally useful in screening for modulators to treat angiogenesis or to evaluate a therapeutic entity.

Kits for Use in Diagnostic and/or Prognostic Applications

25 For use in diagnostic, research, and therapeutic applications suggested above, kits are also provided by the invention. In the diagnostic and research applications such kits may include any or all of the following: assay reagents, buffers, angiogenesis-specific nucleic acids or antibodies, hybridization probes and/or primers, antisense polynucleotides, ribozymes, dominant negative angiogenesis polypeptides or polynucleotides, small molecules
30 inhibitors of angiogenesis-associated sequences *etc.* A therapeutic product may include sterile saline or another pharmaceutically acceptable emulsion and suspension base.

In addition, the kits may include instructional materials containing directions (*i.e.*, protocols) for the practice of the methods of this invention. While the instructional materials typically comprise written or printed materials they are not limited to such. Any

medium capable of storing such instructions and communicating them to an end user is contemplated by this invention. Such media include, but are not limited to electronic storage media (e.g., magnetic discs, tapes, cartridges, chips), optical media (e.g., CD ROM), and the like. Such media may include addresses to internet sites that provide such instructional materials.

The present invention also provides for kits for screening for modulators of angiogenesis-associated sequences. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise one or more of the following materials: an angiogenesis-associated polypeptide or polynucleotide, reaction tubes, and instructions for testing angiogenic-associated activity. Optionally, the kit contains biologically active angiogenesis protein. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user. Diagnosis would typically involve evaluation of a plurality of genes or products. The genes will be selected based on correlations with important parameters in disease which may be identified in historical or outcome data.

It is understood that the examples described above in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All publications, sequences of accession numbers, and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference.

EXAMPLES

Example 1: Tissue Preparation, Labeling Chips, and Fingerprints

Purify total RNA from tissue using TRIzol Reagent

Homogenize tissue samples in 1ml of TRIzol per 50mg of tissue using a Polytron 3100 homogenizer. The generator/probe used depends upon the tissue size. A generator that is too large for the amount of tissue to be homogenized will cause a loss of sample and lower RNA yield. TRIzol is added directly to frozen tissue, which is then homogenize. Following homogenization, insoluble material is removed by centrifugation at 7500 x g for 15 min in a Sorvall superspeed or 12,000 x g for 10 min. in an Eppendorf centrifuge at 4°C. The clear homogenate is transferred to a new tube for use. The samples may be frozen now at -60° to -70°C (and kept for at least one month). The homogenate is

mixed with 0.2ml of chloroform per 1ml of TRIzol reagent used in the original homogenization and incubated at room temp. for 2-3 minutes. The aqueous phase is then separated by centrifugation and transferred to a fresh tube and the RNA precipitated using isopropyl alcohol. The pellet is isolated by centrifugation, washed, air-dried, resuspended in an appropriate volume of DEPC H₂O, and the absorbance measured.

Purification of poly A+ mRNA from total RNA is performed as follows. Heat an oligotex suspension to 37°C and mixing immediately before adding to RNA. The Elution Buffer is heated at 70°C. Warm up 2 x Binding Buffer at 65°C if there is precipitate in the buffer. Mix total RNA with DEPC-treated water, 2 x Binding Buffer, and Oligotex according to Table 2 on page 16 of the Oligotex Handbook. Incubate for 3 minutes at 65°C. Incubate for 10 minutes at room temperature. Centrifuge for 2 minutes at 14,000 to 18,000 g. Remove supernatant without disturbing Oligotex pellet. A little bit of solution can be left behind to reduce the loss of Oligotex. Gently resuspend in Wash Buffer OW2 and pipet onto spin column. Centrifuge the spin column at full speed for 1 minute. Transfer spin column to a new collection tube and gently resuspend in Wash Buffer OW2 and centrifuge as describe herein. Transfer spin column to a new tube and elute with 20 to 100 ul of preheated (70°C) Elution Buffer. Gently resuspend Oligotex resin by pipetting up and down. Centrifuge as above. Repeat elution with fresh elution buffer or use first eluate to keep the elution volume low. Read absorbance, using diluted Elution Buffer as the blank. Before proceeding with cDNA synthesis, precipitate the mRNA as follows: add 0.4 vol. of 7.5 M NH₄OAc + 2.5 vol. of cold 100% ethanol. Precipitate at -20°C 1 hour to overnight (or 20-30 min. at -70°C). Centrifuge at 14,000-16,000 x g for 30 minutes at 4°C. Wash pellet with 0.5ml of 80% ethanol (-20°C) then centrifuge at 14,000-16,000 x g for 5 minutes at room temperature.. Repeat 80% ethanol wash. Air dry the ethanol from the pellet in the hood.. Suspend pellet in DEPC H₂O at 1ug/ul concentration.

To further Clean up total RNA using Qiagen's RNeasy kit, add no more than 100ug to an RNeasy column. Adjust sample to a volume of 100ul with RNase-free water. Add 350ul Buffer RLT then 250ul ethanol (100%) to the sample. Mix by pipetting (do not centrifuge) then apply sample to an RNeasy mini spin column. Centrifuge for 15 sec at >10,000rpm. Transfer column to a new 2-ml collection tube. Add 500ul Buffer RPE and centrifuge for 15 sec at >10,000rpm. Discard flowthrough. Add 500ul Buffer RPE and centrifuge for 15 sec at >10,000rpm. Discard flowthrough then centrifuge for 2 min at maximum speed to dry column membrane. Transfer column to a new 1.5-ml collection tube

and apply 30-50ul of RNase-free water directly onto column membrane. Centrifuge 1 min at >10,000rpm. Repeat elution. and read absorbance.

cDNA synthesis using Gibco's "SuperScript Choice System for cDNA Synthesis" kit

5 First Strand cDNA synthesis is performed as follows. Use 5ug of total RNA or 1ug of polyA+ mRNA as starting material. For total RNA, use 2ul of SuperScript RT. For polyA+ mRNA, use 1ul of SuperScript RT. Final volume of first strand synthesis mix is 20ul. RNA must be in a volume no greater than 10ul. Incubate RNA with 1ul of 100pmol T7-T24 oligo for 10 min at 70C. On ice, add 7 ul of: 4ul 5X 1st Strand Buffer, 2ul of 0.1M DTT, and 1 ul of 10mM dNTP mix. Incubate at 37C for 2 min then add SuperScript RT. 10 Incubate at 37C for 1 hour.

For the second strand synthesis, place 1st strand reactions on ice and add: 91ul DEPC H₂O; 30ul 5X 2nd Strand Buffer; 3ul 10mM dNTP mix; 1ul 10U/ul E.coli DNA Ligase; 4ul 10U/ul E.coli DNA Polymerase; and 1ul 2U/ul RNase H. Mix and incubate 2 15 hours at 16C. Add 2ul T4 DNA Polymerase. Incubate 5 min at 16C. Add 10ul of 0.5M EDTA. A further clean-up of DNA is performed using phenol:chloroform:isoamyl Alcohol (25:24:1) purification.

In vitro Transcription (IVT) and labeling with biotin is performed as follows: Pipet 1.5ul of cDNA into a thin-wall PCR tube. Make NTP labeling mix by combining 2ul T7 20 10xATP (75mM) (Ambion); 2ul T7 10xGTP (75mM) (Ambion); 1.5ul T7 10xCTP (75mM) (Ambion); 1.5ul T7 10xUTP (75mM) (Ambion); 3.75ul 10mM Bio-11-UTP (Boehringer-Mannheim/Roche or Enzo); 3.75ul 10mM Bio-16-CTP (Enzo); 2ul 10x T7 transcription buffer (Ambion); and 2ul 10x T7 enzyme mix (Ambion). The final volume is 20ul. Incubate 6 hours at 37°C in a PCR machine. The RNA can be furthered cleaned.

25 Fragmentation is performed as follows. 15 ug of labeled RNA is usually fragmented. Try to minimize the fragmentation reaction volume; a 10 ul volume is recommended but 20 ul is all right. Do not go higher than 20 ul because the magnesium in the fragmentation buffer contributes to precipitation in the hybridization buffer. Fragment RNA by incubation at 94 C for 35 minutes in 1 x Fragmentation buffer (5 x Fragmentation 30 buffer is 200 mM Tris-acetate, pH 8.1; 500 mM KOAc; 150 mM MgOAc). The labeled RNA transcript can be analyzed before and after fragmentation. Samples can be heated to 65°C for 15 minutes and electrophoresed on 1% agarose/TBE gels to get an approximate idea of the transcript size range

For hybridization, 200 μ l (10 μ g cRNA) of a hybridization mix is put on the chip. If multiple hybridizations are to be done (such as cycling through a 5 chip set), then it is recommended that an initial hybridization mix of 300 μ l or more be made. The hybridization mix is: fragment labeled RNA (50ng/ μ l final conc.); 50 pM 948-b control oligo; 1.5 pM BioB; 5 pM BioC; 25 pM BioD; 100 pM CRE; 0.1mg/ml herring sperm DNA; 0.5mg/ml acetylated BSA; and 300 μ l with 1xMES hyb buffer.

Labeling is performed as follows: The hybridization reaction includes non-biotinylated IVT (purified by RNeasy columns); IVT antisense RNA 4 μ g: μ l; random Hexamers (1 μ g/ μ l) 4 μ l and water to 14 μ l. The reaction is incubated at 70°C, 10 min.

Reverse transcription is performed in the following reaction: 5X First Strand (BRL) buffer, 6 μ l; 0.1 M DTT, 3 μ l; 50X dNTP mix, 0.6 μ l; H₂O, 2.4 μ l; Cy3 or Cy5 dUTP (1mM), 3 μ l; SS RT II (BRL), 1 μ l in a final volume of 16 μ l. Add to hybridization reaction. Incubate 30 min., 42°C. Add 1 μ l SSII and incubate another hour. Put on ice. 50X dNTP mix (25mM of cold dATP, dCTP, and dGTP, 10mM of dTTP: 25 μ l each of 100mM dATP, dCTP, and dGTP; 10 μ l of 100mM dTTP to 15 μ l H₂O. dNTPs from Pharmacia)

RNA degradation is performed as follows. Add 86 μ l H₂O, 1.5 μ l 1M NaOH/2mM EDTA and incubate at 65°C, 10 min.. For U-Con 30, 500 μ l TE/sample spin at 7000g for 10 min, save flow through for purification. For Qiagen purification, suspend u-con recovered material in 500 μ l buffer PB and proceed using Qiagen protocol. For DNase digestion, add 1 μ l of 1/100 dil of DNase/30 μ l Rx and incubate at 37°C for 15 min. Incubate at 5 min 95°C to denature the DNase/

For sample preparation, add Cot-1 DNA, 10 μ l; 50X dNTPs, 1 μ l; 20X SSC, 2.3 μ l; Na pyro phosphate, 7.5 μ l; 10mg/ml Herring sperm DNA; 1 μ l of 1/10 dilution to 21.8 final vol. Dry in speed vac. Resuspend in 15 μ l H₂O. Add 0.38 μ l 10% SDS. Heat 95°C, 2 min and slow cool at room temp. for 20 min. Put on slide and hybridize overnight at 64°C. Washing after the hybridization: 3X SSC/0.03% SDS: 2 min., 37.5 mls 20X SSC+0.75mls 10% SDS in 250mls H₂O; 1X SSC: 5 min., 12.5 mls 20X SSC in 250mls H₂O; 0.2X SSC: 5 min., 2.5 mls 20X SSC in 250mls H₂O. Dry slides and scan at appropriate PMT's and channels.

Example 2. A model of angiogenesis is used to determine expression in angiogenesis

In the model of angiogenesis used to determine expression of angiogenesis-associated sequences, human umbilical vein endothelial cells (HUVEC) were obtained, e.g.,

as passage 1 (p1) frozen cells from Cascade Biologics (Oregon) and grown in maintenance medium: Medium 199 (Life Technologies) supplemented with 20% pooled human serum, 100 mg/ml heparin and 75 mg/ml endothelial cell growth supplements (Sigma) and gentamicin (Life Technologies). An *in vitro* cell system model was used in which 2×10^5 HUVECs were cultured in 0.5 ml 3 mgs/ml plasminogen-depleted fibrinogen (Calbiochem, San Diego, CA) that was polymerized by the addition of 1 unit of maintenance medium supplemented with 100 ng/ml VEGF and HGF and 10 ng/ml TGF- α (R&D Systems, Minneapolis, MN) added (growth medium). The growth medium was replaced every 2 days. Samples for RNA were collected, *e.g.*, at 0, 2, 6, 15, 24, 48, and 96 hours of culture. The fibrin clots were placed in Trizol (Life Technologies) and disrupted using a Tissuemizer. Thereafter standard procedures were used for extracting the RNA (*e.g.*, Example 1).

Angiogenesis associated sequences thus identified are shown in Tables 1-8 . As indicated, some of the Accession numbers include expression sequence tags (ESTs). Thus, in one embodiment herein, genes within an expression profile, also termed expression profile genes, include ESTs and are not necessarily full length.

TABLE 1:

Pkey: Unique Eos probeset identifier number
 Accession: Accession number used for previous patent filings
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title

	Pkey	Accession	ExAccn	UnigeneID	UnigeneTitle
5					
10					
15					
20					
25					
30					
35					
40					
45					
50					
55					
60					
65					
70					
75					
	134404	AB000450	AB000450	Hs.82771	vaccinia related kinase 2
	121443	AB002380	AF180681	Hs.6582	Rho guanine exchange factor (GEF) 12
	100082	AB003103	AA130080	Hs.4295	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12
	132817	AB004884	N27852	Hs.57553	tousled-like kinase 2
	130150	AF000573_ma1	BE094848	Hs.15113	homogentisate 1,2-dioxygenase (homogentisate oxidase)
	100104	AF008937	AF008937	Hs.102178	syntaxin 16
	130839	AF009301	AB011169	Hs.20141	similar to S. cerevisiae SSM4
	427064	AF009368	AF029674	Hs.173422	KIAA1605 protein
	100113	D00591	NM_001269	Hs.84746	chromosome condensation 1
	133980	D00760	AA294921	Hs.250811	v-rat simian leukemia viral oncogene homolog B (ras related; GTP binding protein)
	100129	D11139	AA469369	Hs.5831	tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor)
	100154	D14657	H60720	Hs.81892	KIAA0101 gene product
	100169	D14878	AL037228	Hs.82043	D123 gene product
	101956	D17716	NM_002410	Hs.121502	mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-glucosaminyltransferase
	100190	D21090	M91401	Hs.178658	RAD23 (S. cerevisiae) homolog B
	134742	D26135	NM_001346	Hs.89462	diacylglycerol kinase, gamma (90kD)
	100211	D26528	D26528	Hs.123058	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 7 (RNA helicase, 52kD)
	100238	D30742	L24959	Hs.348	calcium/calmodulin-dependent protein kinase IV
	130283	D31762	NM_012288	Hs.153954	TRAM-like protein
	134237	D31765	D31765	Hs.170114	KIAA0061 protein
	100248	D31888	NM_015156	Hs.78398	KIAA0071 protein
	100256	D38128	D25418	Hs.393	prostaglandin I2 (prostacyclin) receptor (IP)
	100262	D38500	D38500	Hs.278468	postmeiotic segregation increased 2-like 4
	134329	D38551	N92036	Hs.81848	RAD21 (S. pombe) homolog
	100281	D42087	AF091035	Hs.184627	KIAA0118 protein
	100294	D49396	AA331881	Hs.75454	peroxiredoxin 3
	100327	D55640	D55640		gb:Human monocyte PABL (pseudautosomal boundary-like sequence) mRNA, clone Mo2.
	100335	D63391	AW247529	Hs.6793	platelet-activating factor acetylhydrolase, isoform Ib, gamma subunit (29kD)
	134495	D63477	D63477	Hs.84087	KIAA0143 protein
	100338	D63483	D86864	Hs.57735	acetyl LDL receptor, SREC
	135152	D64015	M96954	Hs.182741	TIA1 cytotoxic granule-associated RNA-binding protein-like 1
	134269	D79990	NM_014737	Hs.80905	Ras association (RalGDS/AF-6) domain family 2
	100372	D79997	NM_014791	Hs.184339	KIAA0175 gene product
	134304	D80010	BE613486	Hs.81412	lipin 1
	100394	D84276	D84284	Hs.66052	CD38 antigen (p45)
	100405	D86425	AW291587	Hs.82733	nidogen 2
	100418	D86978	D86978	Hs.84790	KIAA0225 protein
	133154	D87012	D87012	Hs.194685	topoisomerase (DNA) III beta
	134347	D87075	AF164142	Hs.82042	solute carrier family 23 (nucleobase transporters), member 1
	128653	D87432	D87432	Hs.10315	solute carrier family 7 (cationic amino acid transporter, y+ system), member 6
	100438	D87448	AA013051	Hs.91417	topoisomerase (DNA) II binding protein
	134593	D87845	NM_000437	Hs.234392	platelet-activating factor acetylhydrolase 2 (40kD)
	100481	HG1098-HT1098	X70377	Hs.121489	cystatin D
	100552	HG2167-HT2237	AA019521	Hs.301946	lysosomal
	100591	HG2415-HT2511	NM_004091	Hs.231444	Homo sapiens, Similar to hypothetical protein PRO1722, clone MGC:15692, mRNA, complete cds
	100652	HG2825-HT2949	BE613608	Hs.142653	ret finger protein
	100662	HG2887-HT3031_r	AI368680	Hs.816	SRY (sex determining region Y)-box 2
	100899	HG4660-HT5073	AL039123	Hs.103042	microtubule-associated protein 1B
	100905	HG4704-HT5146	L12260	Hs.172816	neuregulin 1
	100945	HG884-HT884	AF002225	Hs.180686	ubiquitin protein ligase E3A (human papilloma virus E6-associated protein, Angelman syndrome)
	100950	HG919-HT919	AF128542	Hs.166846	polymerase (DNA directed), epsilon
	100964	J00212_f	J00212		Empirically selected from AFFX single probeset
	135407	J04029	J04029	Hs.99936	keratin 10 (epidermolytic hyperkeratosis; keratosis palmaris et plantaris)
	130149	J04031	AW067805	Hs.172665	methylenetetrahydrofolate dehydrogenase (NADP+ dependent), methylenetetrahydrofolate
	131877	J04088	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)
	101016	J04543	J04543	Hs.78637	annexin A7
	134786	L06139	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous malformations, multiple cutaneous and mucosal)
	134100	L07540	AA460085	Hs.171075	replication factor C (activator 1) 5 (36.5kD)
	134078	L08895	L08895	Hs.78995	MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C)
	101132	L11239	L11239	Hs.36993	gastrulation brain homeo box 1
	134849	L11353	BE409525	Hs.902	neurofibromin 2 (bilateral acoustic neuroma)
	106432	L13773	AK000310	Hs.17138	hypothetical protein FLJ20303

5	101152 L13800	A1984625	Hs.9884	spindle pole body protein
	135397 L14922	L14922	Hs.166563	replication factor C (activator 1) 1 (145kD)
	131687 L15189	BE297635	Hs.3069	heat shock 70kD protein 9B (mortalin-2)
	101168 L15388	NM_005308	Hs.211569	G protein-coupled receptor kinase 5
	421155 L16895	H87879	Hs.102267	lysyl oxidase
	101226 L27476	AF083892	Hs.75608	tight junction protein 2 (zona occludens 2)
	133975 L27624	C18356	Hs.295944	tissue factor pathway inhibitor 2
	134739 L32976	NM_002419	Hs.89449	mitogen-activated protein kinase kinase kinase 11
10	130155 L33404	AA101043	Hs.151254	kallikrein 7 (chymotryptic, stratum comeum)
	440538 L35263	W76332	Hs.79107	mitogen-activated protein kinase 14
	132813 L37347	BE313625	Hs.57435	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2
	101294 L40371	AF168418	Hs.116784	thyroid hormone receptor interactor 4
	101300 L40391	BE535511	Hs.74137	transmembrane trafficking protein
15	101310 L41607	L41607	Hs.934	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme
	130344 L77566	AW250122	Hs.154879	DiGeorge syndrome critical region gene DGS1; likely ortholog of mouse expressed sequence 2
	embryonic lethal			
	101381 M13928	AW675039	Hs.1227	aminolevulinatase, delta-, dehydratase
	101668 M14016	AW005903	Hs.78601	uroporphyrinogen decarboxylase
20	133780 M14219	AA557660	Hs.76152	decorin
	101396 M15796	BE267931	Hs.78996	proliferating cell nuclear antigen
	101447 M21305	M21305		gb:Human alpha satellite and satellite 3 junction DNA sequence.
	101458 M22092	M22092		gb:Human neural cell adhesion molecule (N-CAM) gene, exon SEC and partial cds.
	101470 M22898	NM_000546	Hs.1846	tumor protein p53 (Li-Fraumeni syndrome)
25	134604 M22995	NM_002884	Hs.865	RAP1A, member of RAS oncogene family
	101478 M23379	NM_002890	Hs.758	RAS p21 protein activator (GTPase activating protein) 1
	406698 M24364	X03068	Hs.73931	major histocompatibility complex, class II, DQ beta 1
	133519 M24400	AW583062	Hs.74502	chymotrypsinogen B1
	131185 M25753	BE280074	Hs.23960	cyclin B1
30	134116 M27691	R84694	Hs.79194	cAMP responsive element binding protein 1
	133999 M28213	AA535244	Hs.78305	RAB2, member RAS oncogene family
	130174 M29550	M29551	Hs.151531	protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform (calcineurin A beta)
	129963 M29971	M29971	Hs.1384	O-6-methylguanine-DNA methyltransferase
	132983 M30269	M30269	Hs.62041	nidogen (enactin)
35	133900 M31158	M31158	Hs.77439	protein kinase, cAMP-dependent, regulatory, type II, beta
	101543 M31166	M31166	Hs.2050	pentaxin-related gene, rapidly induced by IL-1 beta
	101545 M31210	BE246154	Hs.154210	endothelial differentiation, sphingolipid G-protein-coupled receptor, 1
	101620 M55420	S55271	Hs.247930	Epsilon, IgE
	134691 M59979	AW382987	Hs.88474	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)
40	133595 M62810	AA393273	Hs.75133	transcription factor 6-like 1 (mitochondrial transcription factor 1-like)
	130425 M63838	AA243383	Hs.155530	interferon, gamma-inducible protein 16
	101700 M64710	D90337	Hs.247916	natriuretic peptide precursor C
	101714 M68874	M68874	Hs.211587	phospholipase A2, group IVA (cytosolic, calcium-dependent)
	134246 M74524	D28459	Hs.80612	ubiquitin-conjugating enzyme E2A (RAD6 homolog)
45	101760 M80254	M80254	Hs.173125	peptidylprolyl isomerase F (cyclophilin F)
	133948 M81780_cds3	X59960	Hs.77813	sphingomyelin phosphodiesterase 1, acid lysosomal (acid sphingomyelinase)
	101791 M83822	M83822	Hs.62354	cell division cycle 4-like
	101812 M86934	BE439894	Hs.78991	DNA segment, numerous copies, expressed probes (GS1 gene)
	101813 M87338	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40kD)
50	133396 M96326_ma1	M96326	Hs.72885	azurocidin 1 (cationic antimicrobial protein 37)
	135152 M96954	M96954	Hs.182741	TIA1 cytotoxic granule-associated RNA-binding protein-like 1
	129026 M98833	AL120297	Hs.108043	Friend leukemia virus integration 1
	101901 S66793	H38026	Hs.308	arrestin 3, retinal (X-arrestin)
	134831 S72370	AA853479	Hs.89890	pyruvate carboxylase
55	134039 S78569	NM_002290	Hs.78672	laminin, alpha 4
	134395 S79873	AA456539	Hs.8262	lysosomal
	101975 S83325	AA079717	Hs.283664	aspartate beta-hydroxylase
	101977 S83364	AF112213	Hs.184062	putative Rab5-interacting protein
	101978 S83365	BE561610	Hs.5809	putative transmembrane protein; homolog of yeast Golgi membrane protein Yif1p (Yip1p-interacting factor)
60	101998 U01212	U01212	Hs.248153	olfactory marker protein
	102003 U01922	U01922	Hs.125565	translocase of inner mitochondrial membrane 8 (yeast) homolog A
	102007 U02556	U02556	Hs.75307	t-complex-associated-testis-expressed 1-like
	102009 U02680	BE245149	Hs.82643	protein tyrosine kinase 9
65	416658 U03272	U03272	Hs.79432	fibrillin 2 (congenital contractural arachnodactyly)
	132951 U04209	AW821182	Hs.61418	microfibrillar-associated protein 1
	135389 U05237	U05237	Hs.99872	fetal Alzheimer antigen
	102048 U07225	U07225	Hs.339	purinergic receptor P2Y, G-protein coupled, 2
	130145 U07620	U34820	Hs.151051	mitogen-activated protein kinase 10
70	303153 U09759	U09759	Hs.246857	mitogen-activated protein kinase 9
	420269 U09820	U72937	Hs.96264	alpha thalassemia/mental retardation syndrome X-linked (RAD54 (S. cerevisiae) homolog)
	102095 U11313	U11313	Hs.75760	sterol carrier protein 2
	102123 U14518	NM_001809	Hs.1594	centromere protein A (17kD)
	102126 U14575	AW950870	Hs.78961	protein phosphatase 1, regulatory (inhibitor) subunit 8
75	102133 U15173	AU076845	Hs.155596	BCL2/adenovirus E1B 19kD-interacting protein 2
	102139 U15932	NM_004419	Hs.2128	dual specificity phosphatase 5
	102162 U18291	AA450274	Hs.1592	CDC16 (cell division cycle 16, S. cerevisiae, homolog)

	102164	U18300	NM_000107	Hs.77602	damage-specific DNA binding protein 2 (48kD)
	427653	U18383	AA159001	Hs.180069	nuclear respiratory factor 1
	131817	U20536	U20536	Hs.3280	caspase 6, apoptosis-related cysteine protease
5	102200	U21551	AA232362	Hs.157205	branched chain aminotransferase 1, cytosolic
	102210	U23028	BE619413	Hs.2437	eukaryotic translation initiation factor 2B, subunit 5 (epsilon, 82kD)
	102214	U23752	U23752	Hs.32964	SRY (sex determining region Y)-box 11
	132811	U25435	U25435	Hs.57419	CCCTC-binding factor (zinc finger protein)
	131319	U25997	NM_003155	Hs.25590	stanniocalcin 1
10	102256	U28251_cds2	U28251	Hs.53237	ESTs, Highly similar to Z169_HUMAN ZINC FINGER PROTEIN 169 [H.sapiens]
	132316	U28831	U28831	Hs.44566	KIAA1641 protein
	102269	U30245	U30245		gb:Human myelomonocytic specific protein (MNDA) gene, 5' flanking sequence and complete exon 1.
	134365	U32315	AA568906	Hs.82240	syntaxin 3A
15	102293	U32439	AF090116	Hs.79348	regulator of G-protein signalling 7
	102298	U32849	AA382169	Hs.54483	N-myc (and STAT) interactor
	102325	U35139	AI815867	Hs.50130	necdin (mouse) homolog
	302344	U36764	BE303044	Hs.192023	eukaryotic translation initiation factor 3, subunit 2 (beta, 36kD)
	102361	U39400	AA223616	Hs.75859	chromosome 11 open reading frame 4
20	102367	U39657	U39656	Hs.118825	mitogen-activated protein kinase kinase 6
	102388	U41344	AA362907	Hs.76494	proline arginine-rich end leucine-rich repeat protein
	102394	U41766	NM_003816	Hs.2442	a disintegrin and metalloproteinase domain 9 (meltrin gamma)
	129829	U41813	AF010258	Hs.127428	homeo box A9
	102251	U41815	NM_004398	Hs.41706	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 10 (RNA helicase)
25	102409	U43286	BE300330	Hs.118725	selenophosphate synthetase 2
	133746	U44378	AW410035	Hs.75862	MAD (mothers against decapentaplegic, Drosophila) homolog 4
	102423	U44754	Z47542	Hs.179312	small nuclear RNA activating complex, polypeptide 1, 43kD
	132828	U47011_cds1	AB014615	Hs.57710	fibroblast growth factor 8 (androgen-induced)
	130441	U47077	U63630	Hs.155637	protein kinase, DNA-activated, catalytic polypeptide
30	102450	U48251	U48251	Hs.75871	protein kinase C binding protein 1
	129350	U50535	U50535	Hs.110630	Human BRCA2 region, mRNA sequence CG006
	102534	U56833	U96759	Hs.198307	von Hippel-Lindau binding protein 1
	130457	U58091	AB014595	Hs.155976	cullin 4B
	135065	U58837	AA019401	Hs.93909	cyclic nucleotide gated channel beta 1
35	102560	U59289	R97457	Hs.63984	cadherin 13, H-cadherin (heart)
	102567	U59863	U63830	Hs.146847	TRAF family member-associated NFKB activator
	134305	U67122	U61397	Hs.81424	ubiquitin-like 1 (sentrin)
	102638	U67319	U67319	Hs.9216	caspase 7, apoptosis-related cysteine protease
	132736	U68019	AW081883	Hs.288261	Homo sapiens cDNA: FLJ23037 fis, clone LNG02036, highly similar to HSU68019 Homo sapiens mad protein homolog (hMAD-3) mRNA
40	133070	U69611	U92649	Hs.64311	a disintegrin and metalloproteinase domain 17 (tumor necrosis factor, alpha, converting enzyme)
	102663	U70322	NM_002270	Hs.168075	karyopherin (importin) beta 2
	134660	U73524	U73524	Hs.87465	ATP/GTP-binding protein
	102735	U79267	AF111106	Hs.3382	protein phosphatase 4, regulatory subunit 1
45	102741	U79291	AW959829	Hs.83572	hypothetical protein MGC14433
	101175	U82671_cds2	U82671	Hs.36980	melanoma antigen, family A, 2
	132164	U84573	AI752235	Hs.41270	procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2
	102823	U90914	D85390	Hs.5057	carboxypeptidase D
	102826	U91316	NM_007274	Hs.8679	cytosolic acyl coenzyme A thioester hydrolase
50	102831	U91932	AA262170	Hs.80917	adaptor-related protein complex 3, sigma 1 subunit
	102846	U96131	BE264974	Hs.6566	thyroid hormone receptor interactor 13
	129777	U97018	U97018	Hs.12451	echinoderm microtubule-associated protein-like
	134161	U97188	AA634543	Hs.79440	IGF-II mRNA-binding protein 3
	134854	V00503	J03464	Hs.179573	collagen, type I, alpha 2
55	302363	X04327	AW163799	Hs.198365	2,3-bisphosphoglycerate mutase
	133708	X06389	AI018666	Hs.75667	synaptophysin
	125701	X07496	T72104	Hs.93194	apolipoprotein A-I
	102915	X07820	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin 2)
	134656	X14787	AI750878	Hs.87409	thrombospondin 1
60	413858	X15525_ma1	NM_001610	Hs.75589	acid phosphatase 2, lysosomal
	102968	X16396	AU076611	Hs.154672	methylene tetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase
	102971	X16609	X16609	Hs.183805	ankyrin 1, erythrocytic
	134037	X53586_ma1	AI808780	Hs.227730	integrin, alpha 6
65	103023	X53793	AW500470	Hs.117950	multifunctional polypeptide similar to SAICAR synthetase and AIR carboxylase
	103037	X54936	BE018302	Hs.2894	placental growth factor, vascular endothelial growth factor-related protein
	130282	X55740	BE245380	Hs.153952	5' nucleotidase (CD73)
	134542	X57025	M14156	Hs.85112	insulin-like growth factor 1 (somatomedin C)
	128568	X60673_ma1	H12912	Hs.274691	adenylate kinase 3
70	103093	X60708	S79876	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine deaminase complexing protein 2)
	133606	X62048	U10564	Hs.75188	wee1+ (S. pombe) homolog
	129063	X63097	X63094	Hs.283822	Rhesus blood group, D antigen
	424460	X63563	BE275979	Hs.296014	polymerase (RNA) II (DNA directed) polypeptide B (140kD)
	133227	X64037	AW977263	Hs.68257	general transcription factor IIF, polypeptide 1 (74kD subunit)
75	103181	X69636	X69636	Hs.334731	Homo sapiens, clone IMAGE:3448306, mRNA, partial cds
	103184	X69878	U43143	Hs.74049	fms-related tyrosine kinase 4
	103194	X70649	NM_004939	Hs.78580	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1

5	103208	X72841	AW411340	Hs.31314	retinoblastoma-binding protein 7
	129698	X74987	BE242144	Hs.12013	ATP-binding cassette, sub-family E (OABP), member 1
	131486	X83107	F06972	Hs.27372	BMX non-receptor tyrosine kinase
	130729	X84194	A1963747	Hs.18573	acylphosphatase 1, erythrocyte (common) type
	103334	X85753	NM_001260	Hs.25283	cyclin-dependent kinase 8
10	132645	X87870	A1654712	Hs.54424	hepatocyte nuclear factor 4, alpha
	135094	X89066	NM_003304	Hs.250687	transient receptor potential channel 1
	103352	X89398_cds2	H09366	Hs.78853	uracil-DNA glycosylase
	103353	X89399	X89399	Hs.119274	RAS p21 protein activator (GTPase activating protein) 3 (Ins(1,3,4,5)P4-binding protein)
	132173	X89426	X89426	Hs.41716	endothelial cell-specific molecule 1
15	103371	X91247	X91247	Hs.13046	thioredoxin reductase 1
	131584	X91648	AA598509	Hs.29117	purine-rich element binding protein A
	103376	X92098	AL036166	Hs.323378	coated vesicle membrane protein
	103378	X92110	AL119690	Hs.153618	HCGVIII-1 protein
	128510	X94703	X94703	Hs.296371	RAB28, member RAS oncogene family
20	103410	X96506	AA158294	Hs.334879	DR1-associated protein 1 (negative cofactor 2 alpha)
	133490	X97230_f	AF022044	Hs.274601	killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 1
	103438	X98263	AW175781	Hs.152720	M-phase phosphoprotein 6
	103440	X98296	X98296	Hs.77578	ubiquitin specific protease 9, X chromosome (Drosophila fat facets related)
	103452	X99584	NM_006936	Hs.85119	SMT3 (suppressor of mif two 3, yeast) homolog 1
25	133536	Y00264	W25797.comp	Hs.177486	amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease)
	135185	Y07566	AW404908	Hs.96038	Ric (Drosophila)-like, expressed in many tissues
	118523	Y07759	Y07759	Hs.170157	myosin VA (heavy polypeptide 12, myoxin)
	134662	Y07827	NM_007048	Hs.284283	butyrophilin, subfamily 3, member A1
	132083	Y07867	BE386490	Hs.279663	Pirin
30	103500	Y09443	AW408009	Hs.22580	alkylglycerone phosphate synthase
	134389	Y09858	Y09858	Hs.82577	spindlin-like
	132084	Y12394	NM_002267	Hs.3886	karyopherin alpha 3 (importin alpha 4)
	103540	Z11559	NM_002197	Hs.154721	aconitase 1, soluble
	133152	Z11695	Z11695	Hs.324473	mitogen-activated protein kinase 1
35	103548	Z15005	Z15005	Hs.75573	centromere protein E (312kD)
	103612	Z46261	BE336654	Hs.70937	H3 histone family, member A
	129092	AA011243_s	D56365	Hs.63525	poly(rC)-binding protein 2
	103692	AA018418	AW137912	Hs.227583	Homo sapiens chromosome X map Xp11.23 L-type calcium channel alpha-1 subunit
	(CACNA1F) gene, complete cds; HSP27 pseudogene, complete sequence; and JM1 protein, JM2 protein, and Hb2E genes, complete cds				
40	103695	AA018758	AW207152	Hs.186600	ESTs
	129796	AA018804	BE218319	Hs.5807	GTPase Rab14
	132258	AA031993	AA306325	Hs.4311	SUMO-1 activating enzyme subunit 2
	132683	AA044217	BE264633	Hs.143638	WD repeat domain 4
	131887	AA046548	W17064	Hs.332848	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1
45	103723	AA057447_s	BE274312	Hs.214783	Homo sapiens cDNA FLJ14041 fis, clone HEMBA1005780
	453368	AA058376	W20296	Hs.288178	Homo sapiens cDNA FLJ11968 fis, clone HEMBB1001133
	133260	AA083572	AA403045	Hs.6906	Homo sapiens cDNA: FLJ23197 fis, clone REC00917
	103765	AA085696	AA085696	Hs.169600	KIAA0826 protein
	103766	AA088744	A1920783	Hs.191435	ESTs
50	103767	AA089688	BE244667	Hs.296155	CGI-100 protein
	132051	AA091284	AA393968	Hs.180145	HSPC030 protein
	103773	AA092700	A1219323	Hs.101077	ESTs, Weakly similar to T22363 hypothetical protein F47G9.4 - Caenorhabditis elegans
	[C.elegans]				
	135289	AA092968	AW372569	Hs.9788	hypothetical protein MGC10924 similar to Nedd4 WW-binding protein 5
55	132729	AA094800	AW970843	Hs.55682	eukaryotic translation initiation factor 3, subunit 7-(zeta, 66/67kD)
	103794	AA100219	AF244135	Hs.30670	hepatocellular carcinoma-associated antigen 66
	131471	AA114885	AA164842	Hs.192619	KIAA1600 protein
	134319	AA129547	BE304999	Hs.75653	fumarate hydratase
	103807	AA133016	AW958264	Hs.103832	similar to yeast Upf3, variant B
60	119159	AA149507	AF142419	Hs.15020	homolog of mouse quaking QKI (KH domain RNA binding protein)
	129863	AA151005	BE379765	Hs.129872	sperm associated antigen 9
	103850	AA187101	AA187101	Hs.213194	hypothetical protein MGC10895
	103855	AA195179_s	W02363	Hs.302267	hypothetical protein FLJ10330
	322026	AA203138	AW024973	Hs.283675	NPD009 protein
65	135300	AA203645	AA142922	Hs.278626	Arg/Abi-interacting protein ArgBP2
	103861	AA206236	AA206236	Hs.4944	hypothetical protein FLJ12783
	130634	AA227621	A1769067	Hs.127824	ESTs, Weakly similar to T28770 hypothetical protein W03D2.1 - Caenorhabditis elegans
	[C.elegans]				
	447735	AA248283	AA775268	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone LNG00943
70	103909	AA249611	AA249611	Hs.47438	SH3 domain binding glutamic acid-rich protein
	131236	AA282640	AF043117	Hs.24594	ubiquitination factor E4B (homologous to yeast UFD2)
	134060	AA287199	D42039	Hs.78871	mesoderm development candidate 2
	129013	AA313990	AA371156	Hs.107942	DKFZP564M112 protein
	129435	AA314256	AF151852	Hs.111449	CGI-94 protein
75	103988	AA314389	AA314389	Hs.42500	ADP-ribosylation factor-like 5
	104000	AA324364	A146527	Hs.80475	polymerase (RNA) II (DNA directed) polypeptide J (13.3kD)
	425284	AA329211_s	AF155568	Hs.155489	NS1-associated protein 1
	128629	AA399187	AL096748	Hs.102708	DKFZP434A043 protein
	133281	AA421079	AK001601	Hs.69594	high-mobility group 20A

	104104	AA422029	AA422029	Hs.143640	ESTs, Weakly similar to hyperpolarization-activated cyclic nucleotide-gated channel hHCN2
	[H.sapiens]				
	108154	AA425230	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain-binding protein
5	132091	AA447052	AW954243	Hs.170218	KIAA0251 protein
	135073	AA452000	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (from clone DKFZp586E1624)
	131367	AA456687	AI750575	Hs.173933	nuclear factor I/A
	129593	AA487015_s	AI338247	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (from clone DKFZp586L0120)
	135266	AB002326	R41179	Hs.97393	KIAA0328 protein
10	133505	C01527	AI630124	Hs.324504	Homo sapiens mRNA; cDNA DKFZp586J0720 (from clone DKFZp586J0720)
	132064	C01714	AA121098	Hs.3838	serum-inducible kinase
	134393	C01811_f	W52642	Hs.8261	hypothetical protein FLJ22393
	131427	C02352_s	AF151879	Hs.26706	CGI-121 protein
	133435	C02375	AI929357	Hs.323966	Homo sapiens clone H63 unknown mRNA
	104282	C14448	C14448	Hs.332338	EST
15	134827	D16611_s	BE314037	Hs.89866	coproporphyrinogen oxidase (coproporphyrin, harderoporphyria)
	130443	D25216	D25216	Hs.155650	KIAA0014 gene product
	131742	D31352	AA961420	Hs.31433	ESTs
	132837	D58024_s	AA370362	Hs.57958	EGF-TM7-latrophilin-related protein
	130377	D80897	NM_014909	Hs.155182	KIAA1036 protein
20	104334	D82614	D82614	Hs.78771	phosphoglycerate kinase 1
	134593	D87845	NM_000437	Hs.234392	platelet-activating factor acetylhydrolase 2 (40kD)
	134731	D89377_i	D89377	Hs.89404	msh (Drosophila) homeo box homolog 2
	129913	H06583	NM_001310	Hs.13313	cAMP responsive element binding protein-like 2
	131670	H40732	H03514	Hs.10130	ESTs
25	104394	H46617	AA129551	Hs.172129	Homo sapiens cDNA: FLJ21409 fis, clone COL03924
	104402	H56731	H56731	Hs.132956	ESTs
	129781	H75570	AA306090	Hs.124707	ESTs
	129077	H78886	N74724	Hs.108479	ESTs
	104417	H81241	AI819448	Hs.320861	Kruppel-like factor 8
30	134927	L36531	L36531	Hs.91296	integrin, alpha 8
	129280	M63154	M63154	Hs.110014	gastric intrinsic factor (vitamin B synthesis)
	134498	M63180	AW246273	Hs.84131	threonyl-tRNA synthetase
	104460	M91504	AW955705	Hs.62604	Homo sapiens, clone IMAGE:4299322, mRNA, partial cds
	104488	N56191	N56191	Hs.106511	protocadherin 17
35	131248	N78483	AI038989	Hs.332633	Bardet-Biedl syndrome 2
	129214	N79268	AL044335	Hs.109526	zinc finger protein 198
	130017	R14652	AK000096	Hs.143198	inhibitor of growth family, member 3
	104530	R20459	AK001676	Hs.12457	hypothetical protein FLJ10814
40	104534	R22303	R22303		gb:yh26b09.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:130841 5', mRNA sequence.
	104544	R33779	AI091173	Hs.222362	ESTs, Weakly similar to p40 [H.sapiens]
	133328	R36553	AW452738	Hs.265327	hypothetical protein DKFZp7611141
	104567	R64534	AA040620	Hs.5672	hypothetical protein AF140225
45	128562	R66475	AA923382	Hs.101490	ESTs
	129575	R70621	F08282	Hs.278428	progesterone induced protein
	130776	R79356	AF167706	Hs.19280	cysteine-rich motor neuron 1
	104599	R84933	AW815036	Hs.151251	ESTs
	104660	RC_AA007160	BE298665	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (from clone DKFZp564D016)
50	104667	RC_AA007234_s	AI239923	Hs.30098	ESTs
	104718	RC_AA018409	AI143020	Hs.36250	ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]
	104764	RC_AA025351	AI039243	Hs.278585	ESTs
	104786	RC_AA027168	AA027167	Hs.10031	KIAA0955 protein
	104787	RC_AA027317	AA027317		gb:ze97d11.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:366933 3'
55	similar to contains Alu repetitive element, mRNA sequence.				
	134079	RC_AA029423	AK001751	Hs.171835	hypothetical protein FLJ10889
	104804	RC_AA031357	AI858702	Hs.31803	ESTs, Weakly similar to N-WASP [H.sapiens]
	104865	RC_AA045136	T79340	Hs.22575	B-cell CLL/lymphoma 6, member B (zinc finger protein)
	130828	RC_AA053400	AW631469	Hs.203213	ESTs
60	104907	RC_AA055829	AA055829	Hs.196701	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION
	WARNING ENTRY [H.sapiens]				
	104943	RC_AA065217	AF072873	Hs.114218	frizzled (Drosophila) homolog 6
	105013	RC_AA116054	H63789	Hs.296288	ESTs, Weakly similar to KIAA0638 protein [H.sapiens]
	105024	RC_AA126311	AA126311	Hs.9879	ESTs
65	132592	RC_AA129390	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone HRC12825
	105038	RC_AA130273	AW503733	Hs.9414	KIAA1488 protein
	105077	RC_AA142919	W55946	Hs.234863	Homo sapiens cDNA FLJ12082 fis, clone HEMBB1002492
	105096	RC_AA150205	AL042506	Hs.21599	Kruppel-like factor 7 (ubiquitous)
	129215	RC_AA176867	AB040930	Hs.126085	KIAA1497 protein
	105169	RC_AA180321	BE245294	Hs.180789	S164 protein
70	132796	RC_AA180487	NM_006283	Hs.173159	transforming, acidic coiled-coil containing protein 1
	130401	RC_AA187634	BE396283	Hs.173987	eukaryotic translation initiation factor 3, subunit 1 (alpha, 35kD)
	105200	RC_AA195399	AA328102	Hs.24641	cytoskeleton associated protein 2
	130114	RC_AA234717	AA233393	Hs.14992	hypothetical protein FLJ11151
	105330	RC_AA234743	AW338625	Hs.22120	ESTs
75	105337	RC_AA234957	AI468789	Hs.23200	myotubularin related protein 1
	129385	RC_AA235604	AA172106	Hs.110950	Rag C protein

	105376	RC_AA236559	AW994032	Hs.8768	hypothetical protein FLJ10849
	105397	RC_AA242868	AA814807	Hs.7395	hypothetical protein FLJ23182
	131982	RC_AA251776	AK000046	Hs.267448	hypothetical protein FLJ20039
5	131991	RC_AA251909	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1 (yeast homolog), beta
	128658	RC_AA252672_s	BE397354	Hs.324830	diphtheria toxin resistance protein required for diphthamide biosynthesis (Saccharomyces)-like 2
	105489	RC_AA256157	AA256157	Hs.24115	Homo sapiens cDNA FLJ14178 fis, clone NT2RP2003339
	105508	RC_AA256680	AA173942	Hs.326416	Homo sapiens mRNA; cDNA DKFZp564H1916 (from clone DKFZp564H1916)
	105539	RC_AA258873	AB040884	Hs.109694	KIAA1451 protein
10	135172	RC_AA262727	AB028956	Hs.12144	KIAA1033 protein
	131569	RC_AA281451	AL389951	Hs.271623	nucleoporin 50kD
	132542	RC_AA281545	AL137751	Hs.263671	Homo sapiens mRNA; cDNA DKFZp434I0812 (from clone DKFZp434I0812); partial cds
	105643	RC_AA282069	BE621719	Hs.173802	KIAA0603 gene product
	105659	RC_AA283044	AA283044	Hs.25625	hypothetical protein FLJ11323
15	105666	RC_AA283930	AA426234	Hs.34906	ESTs, Weakly similar to T17210 hypothetical protein DKFZp434N041.1 [H.sapiens]
	105674	RC_AA284755	AI609530	Hs.279789	histone deacetylase 3
	105709	RC_AA291268	AI928962	Hs.26761	DKFZP586L0724 protein
	105722	RC_AA291927	AI922821	Hs.32433	ESTs
	105765	RC_AA343514	AA299688	Hs.24183	ESTs
20	115951	RC_AA398109	BE546245	Hs.301048	sec13-like protein
	105962	RC_AA405737	AW880358	Hs.339808	hypothetical protein FLJ10120
	105985	RC_AA406610	AA406610		gb:zv15b10.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:753691 3' similar to
	gb:X02067				
	106008	RC_AA411465	AB033888	Hs.8619	SRY (sex determining region Y)-box 18
25	131216	RC_AA416886	AI815486	Hs.243901	Homo sapiens cDNA FLJ20738 fis, clone HEP08257
	134222	RC_AA424013	AW855861	Hs.8025	Homo sapiens clone 23767 and 23782 mRNA sequences
	113689	RC_AA424148	AB037850	Hs.16621	DKFZP434I116 protein
	106141	RC_AA424558	AF031463	Hs.9302	phosducin-like
	130839	RC_AA424961_s	AB011169	Hs.20141	similar to S. cerevisiae SSM4
30	106157	RC_AA425367	W37943	Hs.34892	KIAA1323 protein
	130777	RC_AA425921	AW135049	Hs.285418	Homo sapiens cDNA FLJ10643 fis, clone NT2RP2005753, highly similar to Homo sapiens I-1
	receptor				
	130561	RC_AA426220	AB011095	Hs.16032	KIAA0523 protein
	106196	RC_AA427735	AA525993	Hs.173699	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION
35	WARNING				
	131878	RC_AA430673	AA083764	Hs.6101	hypothetical protein MGC3178
	133200	RC_AA432248	AB037715	Hs.183639	hypothetical protein FLJ10210
	106302	RC_AA435896	AA398859	Hs.18397	hypothetical protein FLJ23221
	106328	RC_AA436705	AL079559	Hs.28020	KIAA0766 gene product
40	450534	RC_AA446561	AI570189	Hs.25132	KIAA0470 gene product
	106423	RC_AA448238	AB020722	Hs.16714	Rho guanine exchange factor (GEF) 15
	133442	RC_AA448688	AL137663	Hs.7378	Homo sapiens mRNA; cDNA DKFZp434G227 (from clone DKFZp434G227)
	439608	RC_AA449756	AW864696	Hs.301732	hypothetical protein MGC5306
	106477	RC_AA450303	R23324	Hs.41693	DnaJ (Hsp40) homolog, subfamily B, member 4
45	106503	RC_AA452411	AB033042	Hs.29679	cofactor required for Sp1 transcriptional activation, subunit 3 (130kD)
	446999	RC_AA454566	AA151520	Hs.334822	hypothetical protein MGC4485
	106543	RC_AA454667	AA676939	Hs.69285	neuropilin 1
	130010	RC_AA456437	AA301116	Hs.142838	nucleolar phosphoprotein Nopp34
	106589	RC_AA456646	AK000933	Hs.28661	Homo sapiens cDNA FLJ10071 fis, clone HEMBA1001702
	106593	RC_AA456826	AW296451	Hs.24605	ESTs
50	106596	RC_AA456981	AA452379	Hs.293552	ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE
	CONTAMINATION				
	134655	RC_AA458959	AF265208	Hs.123090	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily f,
	member 1				
55	106636	RC_AA459950	AW958037	Hs.286	ribosomal protein L4
	106654	RC_AA460449	AW075485	Hs.286049	phosphoserine aminotransferase
	131353	RC_AA463910	AW754182		gb:RC2-CT0321-131199-011-c01 CT0321 Homo sapiens cDNA, mRNA sequence
	106707	RC_AA464603	AK000566	Hs.98135	hypothetical protein FLJ20559
	131710	RC_AA464606	NM_015368	Hs.30985	pannexin 1
60	106717	RC_AA465093	AA600357	Hs.239489	TIA1 cytotoxic granule-associated RNA-binding protein
	131775	RC_AA465692	AB014548	Hs.31921	KIAA0648 protein
	106747	RC_AA476473	NM_007118	Hs.171957	triple functional domain (PTPRF interacting)
	106773	RC_AA478109	AA478109	Hs.188833	ESTs
	106781	RC_AA478474	AA330310	Hs.24181	ESTs
	106817	RC_AA480889	D61216	Hs.18672	ESTs
65	106846	RC_AA485223	AB037744	Hs.34892	KIAA1323 protein
	106848	RC_AA485254	AA449014	Hs.121025	chromosome 11 open reading frame 5
	106856	RC_AA486183	W58353	Hs.285123	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 2005779
	418699	RC_AA496936	BE539639	Hs.173030	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION
	WARNING				
70	107001	RC_AA598589	AI926520	Hs.31016	putative DNA binding protein
	130638	RC_AA598831_f	AW021276	Hs.17121	ESTs
	107054	RC_AA600150	AI076459	Hs.15978	KIAA1272 protein
	107059	RC_AA608545	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E. coli RecA homolog)
	107080	RC_AA609210	AL122043	Hs.19221	hypothetical protein DKFZp566G1424
75	107115	RC_AA610108	BE379623	Hs.27693	peptidylprolyl isomerase (cyclophilin)-like 1
	107130	RC_AA620582	AB033106	Hs.12913	KIAA1280 protein

	107156	RC_AA621239	AA137043	Hs.9663	programmed cell death 6-interacting protein
	107174	RC_AA621714	BE122762	Hs.25338	ESTs
	130621	RC_AA621718	AW513087	Hs.16803	LUC7 (S. cerevisiae)-like
5	107190	RC_D19673	AA836401	Hs.5103	ESTs
	132626	RC_D25755_s	AW504732	Hs.21275	hypothetical protein FLJ11011
	107217	RC_D51095	AL080235	Hs.35861	DKFZP586E1621 protein
	131610	RC_D60272_i	AA357879	Hs.29423	scavenger receptor with C-type lectin
	129604	T08879	AF088886	Hs.11590	cathepsin F
10	107295	T34527	AA186629	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1
	(GalNAc-T1)				
	107299	T40327_s	BE277457	Hs.30661	hypothetical protein MGC4606
	107315	T62771_s	AA316241	Hs.90691	nucleophosmin/nucleoplasmin 3
	107316	T63174_s	T63174	Hs.193700	Homo sapiens mRNA; cDNA DKFZp586i0324 (from clone DKFZp586i0324)
	107328	T83444	AW959891	Hs.76591	KIAA0887 protein
15	107334	T93641	T93597	Hs.187429	ESTs
	134715	U48263	U48263	Hs.89040	prepronociceptin
	128636	U49065	U49065	Hs.102865	interleukin 1 receptor-like 2
	129938	U79300	AW003668	Hs.135587	Human clone 23629 mRNA sequence
	107375	U88573	BE011845	Hs.251064	high-mobility group (nonhistone chromosomal) protein 14
20	130074	U93867	AL038596	Hs.250745	polymerase (RNA) III (DNA directed) (62kD)
	107387	W01094	D86983	Hs.118893	Melanoma associated gene
	132036	W01568	AL157433	Hs.37706	hypothetical protein DKFZp434E2220
	107426	W26853	W26853	Hs.291003	hypothetical protein MGC4707
	113857	W27179	AW243158	Hs.5297	DKFZP564A2416 protein
25	135388	W27965	W27965	Hs.99865	epimorphin
	130419	W36280_s	AF037448	Hs.155489	NS1-associated protein 1
	107469	W47063	W47063	Hs.94668	ESTs
	132616	W79060	BE262677	Hs.283558	hypothetical protein PRO1855
	107506	W88550	AB028981	Hs.8021	KIAA1058 protein
30	132358	X60486	NM_003542	Hs.46423	H4 histone family, member G
	107522	X78931_s	X78931	Hs.99971	zinc finger protein 272
	125827	Z14077_s	NM_003403	Hs.97496	YY1 transcription factor
	107582	RC_AA002147	AA002147	Hs.59952	EST
35	107609	RC_AA004711	R75654	Hs.164797	hypothetical protein FLJ13693
	107661	RC_AA010383	AA010383	Hs.60389	ESTs
	107714	RC_AA015761	AA015761	Hs.60642	ESTs
	107775	RC_AA018772	AW008846	Hs.60857	ESTs
	107832	RC_AA021473_r	AA021473		gb:ze66c11.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:363956 3', mRNA sequence.
40	107859	RC_AA024835	AW732573	Hs.47584	potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3
	124337	RC_AA025858	N23541	Hs.281561	Homo sapiens cDNA: FLJ23582 fis, clone LNG13759
	107914	RC_AA027229	AA027229	Hs.61329	ESTs, Weakly similar to T16370 hypothetical protein F45E12.5 - Caenorhabditis elegans
	[C.elegans]				
45	107935	RC_AA029428	AA029428	Hs.61555	ESTs
	116262	RC_AA035143	AI936442	Hs.59838	hypothetical protein FLJ10808
	131461	RC_AA035237	AA992841	Hs.27263	KIAA1458 protein
	108007	RC_AA039347	AA039347	Hs.61916	EST
	108029	RC_AA040740	AA040740	Hs.62007	ESTs
50	108040	RC_AA041551	AL121031	Hs.159971	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1
	108084	RC_AA045513	AA058944	Hs.116602	Homo sapiens, clone IMAGE:4154008, mRNA, partial cds
	108088	RC_AA045745	AA045745	Hs.62886	ESTs
	108168	RC_AA055348	AI453137	Hs.63176	ESTs
55	130719	RC_AA056582_s	AA679262	Hs.14235	hypothetical protein FLJ20008; KIAA1839 protein
	108189	RC_AA056697	AW376061	Hs.63335	ESTs, Moderately similar to A46010 X-linked retinopathy protein [H.sapiens]
	108190	RC_AA056746	AA056746	Hs.63338	EST
	108203	RC_AA057678	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone COL06049
	108216	RC_AA058681	AA524743	Hs.44883	ESTs
60	108217	RC_AA058686	AA058686	Hs.62588	ESTs
	108245	RC_AA062840	BE410285	Hs.89545	proteasome (prosome, macropain) subunit, beta type, 4
	108277	RC_AA064859	AA064859		gb:zm50f03.s1 Stratagene fibroblast (937212) Homo sapiens cDNA clone IMAGE:529085 3', mRNA
	108280	RC_AA065069	AA065069		gb:zm12e11.s1 Stratagene pancreas (937208) Homo sapiens cDNA clone 3', mRNA sequence
65	108309	RC_AA069923	AA069818		gb:zm67e03.r1 Stratagene neuroepithelium (937231) Homo sapiens cDNA clone 5' similar to
	133739	RC_AA070799_s	BE536554	Hs.278270	inactive progesterone receptor, 23 kD
	108340	RC_AA070815	AA069820	Hs.180909	peroxiredoxin 1
	108403	RC_AA075374	AA075374		gb:zm87a01.s1 Stratagene ovarian cancer (937219) Homo sapiens cDNA clone IMAGE:544872
	3', mRNA sequence.				
70	108427	RC_AA076382	AA076382		gb:zm91g08.s1 Stratagene ovarian cancer (937219) Homo sapiens cDNA clone IMAGE:545342
	3', mRNA sequence.				
	108435	RC_AA078787	T82427	Hs.194101	Homo sapiens cDNA: FLJ20869 fis, clone ADKA02377
	108439	RC_AA078986	AA078986		gb:zm92h01.s1 Stratagene ovarian cancer (937219) Homo sapiens cDNA clone IMAGE:545425
	3', mRNA sequence.				
75	108465	RC_AA079393	AA079393	Hs.3462	cytochrome c oxidase subunit VIIc
	108469	RC_AA079487	AA079487		gb:zm97f08.s1 Stratagene colon HT29 (937221) Homo sapiens cDNA clone 3', mRNA sequence

5	108500	RC_AA083207	AA083207	Hs.68270	EST
	108501	RC_AA083256	AA083256		gb:zn08g12.s1 Stratagene hNT neuron (937233) Homo sapiens cDNA clone 3' similar to
	gb:M33308				
	108533	RC_AA084415	AA084415		gb:zn06g09.s1 Stratagene hNT neuron (937233) Homo sapiens cDNA clone IMAGE:546688 3',
	mRNA				
10	108562	RC_AA085274	AA100796		gb:zm26c06.s1 Stratagene pancreas (937208) Homo sapiens cDNA clone 3' similar to
	gb:X15341				
	108589	RC_AA088678	AI732404	Hs.68846	ESTs
	130890	RC_AA100925	AI907537	Hs.76698	stress-associated endoplasmic reticulum protein 1; ribosome associated membrane protein 4
	134585	RC_AA101255	D14041	Hs.278573	H-2K binding factor-2
15	130385	RC_AA126474	AW067800	Hs.155223	stanniocalcin 2
	108749	RC_AA127017	AA127017	Hs.71052	ESTs
	108807	RC_AA129988	AI652236	Hs.49376	hypothetical protein FLJ20644
	108808	RC_AA130240	AA045088	Hs.62738	ESTs
	108833	RC_AA131866	AF188527	Hs.61661	ESTs, Weakly similar to AF174605 1 F-box protein Fbx25 [H.sapiens]
20	107290	RC_AA132039	W27740	Hs.323780	ESTs
	108846	RC_AA132983	AL117452	Hs.44155	DKFZP586G1517 protein
	108857	RC_AA133250	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), actin binding protein
	131474	RC_AA133583_s	L46353	Hs.2726	high-mobility group (nonhistone chromosomal) protein isoform I-C
	108894	RC_AA135941	AK001431	Hs.5105	hypothetical protein FLJ10569
25	108941	RC_AA148650	AA148650		gb:zo09e06.s1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone
	IMAGE:567202 3',				
	108968	RC_AA151110	AI304870	Hs.188680	ESTs
	108996	RC_AA155754	AW995610	Hs.332436	EST
	109001	RC_AA156125	AI056548	Hs.72116	hypothetical protein FLJ20992 similar to hedgehog-interacting protein
30	131183	RC_AA156289	AI611807	Hs.285107	hypothetical protein FLJ13397
	109019	RC_AA156997	AA156755	Hs.72150	ESTs
	109022	RC_AA157291	AA157291	Hs.21479	ubiquitin 1
	109023	RC_AA157293	AA157293	Hs.72168	ESTs
	109068	RC_AA164293_f	AA164293	Hs.72545	ESTs
35	109072	RC_AA164676	AI732585	Hs.22394	hypothetical protein FLJ10893
	129021	RC_AA167375	AL044675	Hs.173081	KIAA0530 protein
	130346	RC_AA167550	H05769	Hs.188757	Homo sapiens, clone MGC:5564, mRNA, complete cds
	109146	RC_AA176589	AA176589	Hs.142078	EST
	109172	RC_AA180448	AA180448	Hs.144300	EST
40	131080	RC_AA187144_s	NM_001955	Hs.2271	endothelin 1
	129208	RC_AA189170_f	AI587376	Hs.109441	MSTP033 protein
	109222	RC_AA192757	AA192833	Hs.333512	similar to rat myomegalin
	109300	RC_AA205650	AA418276	Hs.170142	ESTs
	109481	RC_AA233342	AA878923	Hs.289069	hypothetical protein FLJ21016
45	109485	RC_AA233472	BE619092	Hs.28465	Homo sapiens cDNA: FLJ21869 fis, clone HEP02442
	109516	RC_AA234110	AI471639	Hs.71913	ESTs
	109537	RC_D80981	AI858695	Hs.34898	ESTs
	109556	RC_F01660	AI925294	Hs.87385	ESTs
	109577	RC_F02206	F02206	Hs.296639	Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
50	109578	RC_F02208	F02208	Hs.27214	ESTs
	109595	RC_F02544	AA078629	Hs.27301	ESTs
	109625	RC_F03918	H29490	Hs.22697	ESTs
	131983	RC_F04258_s	AF119665	Hs.184011	pyrophosphatase (inorganic)
	109648	RC_F04600	H17800	Hs.7154	ESTs
55	109671	RC_F08998	R59210	Hs.26634	ESTs
	109699	RC_F09605	H18013	Hs.167483	ESTs
	109820	RC_F11115	AW016809	Hs.323795	ESTs
	109933	RC_H06371	R52417	Hs.20945	Homo sapiens clone 24993 mRNA sequence
	110014	RC_H10995	AL109666	Hs.7242	Homo sapiens mRNA full length insert cDNA clone EUROIIMAGE 35907
60	110039	RC_H11938	H11938	Hs.21907	histone acetyltransferase
	110099	RC_H16568	R44557	Hs.23748	ESTs
	110107	RC_H16772	AW151660	Hs.31444	ESTs
	110155	RC_H18951	AI559626	Hs.93522	Homo sapiens mRNA for KIAA1647 protein, partial cds
	110197	RC_H20859	AW090386	Hs.112278	arrestin, beta 1
65	110223	RC_H23747	H19836	Hs.31697	ESTs
	110306	RC_H38087	H38087	Hs.105509	CTL2 gene
	110335	RC_H40331	H65490	Hs.18845	ESTs
	110342	RC_H40567	H40961	Hs.33008	ESTs
	110395	RC_H46966	AA025116	Hs.33333	ESTs
70	110511	RC_H56640_j	H56640	Hs.221460	ESTs
	110523	RC_H57154	AI040384	Hs.19102	ESTs, Weakly similar to organic anion transporter 1 [H.sapiens]
	110715	RC_H96712	H96712	Hs.269029	ESTs
	110754	RC_N20814	AW302200	Hs.6336	KIAA0672 gene product
	130132	RC_N25249	U55936	Hs.184376	synaptosomal-associated protein, 23kD
75	131135	RC_N27100	NM_016569	Hs.267182	TBX3-iso protein
	134263	RC_N39616	AW973443	Hs.8086	RNA (guanine-7-) methyltransferase
	110938	RC_N48982	N48982	Hs.38034	Homo sapiens cDNA FLJ12924 fis, clone NT2RP2004709
	110983	RC_N51957	NM_015367	Hs.10267	MIL1 protein
	115062	RC_N52271	AA253314	Hs.154103	LIM protein (similar to rat protein kinase C-binding enigma)
	111081	RC_N59435	AI146349	Hs.271614	CGI-112 protein

5	111128 RC_N64139	AW505364	Hs.19074	LATS (large tumor suppressor, Drosophila) homolog 2
	135244 RC_N66981	AI834273	Hs.9711	novel protein
	111216 RC_N68640	AW139408	Hs.152940	ESTs
	437562 RC_N69352	AB001636	Hs.5683	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 15
	131002 RC_N95226	AL050295	Hs.22039	KIAA0758 protein
	111399 RC_R00138	AW270776	Hs.18857	ESTs
	111514 RC_R07998	R07998		gb:ylf6g11.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:127076 3'
	similar to			
10	130182 RC_R08929	BE267033	Hs.192853	ubiquitin-conjugating enzyme E2G 2 (homologous to yeast UBC7)
	111574 RC_R10307	AI024145	Hs.188526	ESTs
	111804 RC_R33354	AA482478	Hs.181785	ESTs
	111831 RC_R36083	R36095	Hs.268695	ESTs
	129675 RC_R37938_f	NM_015556	Hs.172180	KIAA0440 protein
	111904 RC_R39330	Z41572		gb:HSCZYB122 normalized infant brain cDNA Homo sapiens cDNA clone c-zyb12, mRNA
15	sequence			
	133868 RC_R40816_s	AB012193	Hs.183874	cullin 4A
	112033 RC_R43162_s	R49031	Hs.22627	ESTs
	130987 RC_R45698	BE613269	Hs.21893	hypothetical protein DKFZp761N0624
20	112300 RC_R54554	H24334	Hs.26125	ESTs
	112513 RC_R68425	R68425	Hs.13809	hypothetical protein FLJ10648
	112514 RC_R68568	R68568	Hs.183373	src homology 3 domain-containing protein HIP-55
	112522 RC_R68763	R68857	Hs.265499	ESTs
	112540 RC_R70467	R69751		gb:yl40a10.s1 Soares placenta Nb2HP Homo sapiens cDNA clone 3', mRNA sequence
25	130346 RC_R73565	H05769	Hs.188757	Homo sapiens, clone MGC:5564, mRNA, complete cds
	129534 RC_R73640	AK002126	Hs.11260	hypothetical protein FLJ11264
	112597 RC_R78376	R78376	Hs.29733	EST
	112732 RC_R92453	R92453	Hs.34590	ESTs
	131458 RC_T03865	BE297567	Hs.27047	hypothetical protein FLJ20392
30	112888 RC_T03872	AW195317	Hs.107716	hypothetical protein FLJ22344
	131863 RC_T10072	AI656378	Hs.33461	ESTs
	112911 RC_T10080	AW732747	Hs.13493	like mouse brain protein E46
	132215 RC_T10132	AL035703	Hs.4236	KIAA0478 gene product
	112931 RC_T15343	T02966	Hs.167428	ESTs
35	112984 RC_T23457	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 precursor, intestinal [H.sapiens]
	112998 RC_T23555	H11257	Hs.22968	Homo sapiens clone IMAGE:451939, mRNA sequence
	133376 RC_T23670	BE618768	Hs.7232	acetyl-Coenzyme A carboxylase alpha
	113026 RC_T23948	AA376654	Hs.183684	eukaryotic translation initiation factor 4 gamma, 2
	113070 RC_T33464	AB032977	Hs.6298	KIAA1151 protein
40	128970 RC_T34413	AI375672	Hs.165028	ESTs
	113074 RC_T34611	AK001335	Hs.31137	protein tyrosine phosphatase, receptor type, E
	113095 RC_T40920	AA828380	Hs.126733	ESTs
	113179 RC_T55182	BE622021	Hs.152571	ESTs, Highly similar to IGF-II mRNA-binding protein 2 [H.sapiens]
	113337 RC_T77453	T77453	Hs.302234	ESTs
45	113421 RC_T84039	AI769400	Hs.189729	ESTs
	113454 RC_T86458	AI022166	Hs.16188	ESTs
	113481 RC_T87693	T87693	Hs.204327	EST
	131441 RC_T89350_s	AA302862	Hs.90063	neurocalcin delta
50	113557 RC_T90945	H66470	Hs.16004	ESTs
	113559 RC_T90987	T79763	Hs.14514	ESTs
	113589 RC_T91863	AI078554	Hs.15682	ESTs
	113591 RC_T91881	T91881	Hs.200597	KIAA0563 gene product
	113619 RC_T93783_s	R08665	Hs.17244	hypothetical protein FLJ13605
	113683 RC_T96687	AB035335	Hs.144519	T-cell leukemia/lymphoma 6
55	113692 RC_T96944	AL360143	Hs.17936	DKFZP434H132 protein
	113702 RC_T97307	T97307		gb:ye53h05.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121497 3', mRNA
	113717 RC_T97764	T99513	Hs.187447	ESTs
	113824 RC_W48817	AI631964	Hs.34447	ESTs
60	113840 RC_W58343	R72137	Hs.7949	DKFZP586B2420 protein
	113844 RC_W59949	AI369275	Hs.243010	Homo sapiens cDNA FLJ14445 fis, clone HEMBB1001294, highly similar to GTP-BINDING PROTEIN TC10
	113902 RC_W74644	AA340111	Hs.100009	acyl-Coenzyme A oxidase 1, palmitoyl
	113904 RC_W74761	AF125044	Hs.19196	ubiquitin-conjugating enzyme HBUCE1
65	113905 RC_W74802	R81733	Hs.33106	ESTs
	113931 RC_W81205	BE255499	Hs.3496	hypothetical protein MGC15749
	113932 RC_W81237	AA256444	Hs.126485	hypothetical protein FLJ12604; KIAA1692 protein
	131965 RC_W90146_f	W79283	Hs.35962	ESTs
	114035 RC_W92798	W92798	Hs.269181	ESTs
70	114106 RC_Z38412	AW602528		gb:RC5-BT0562-260100-011-A02 BT0562 Homo sapiens cDNA, mRNA sequence
	133593 RC_Z38709	AI416988	Hs.238272	inositol 1,4,5-triphosphate receptor, type 2
	114161 RC_Z38904	BE548222	Hs.299883	hypothetical protein FLJ23399
	424949 RC_Z39103	AF052212	Hs.153934	core-binding factor, runt domain, alpha subunit 2; translocated to, 2
	129059 RC_Z39930_f	AW069534	Hs.279583	CGI-81 protein
75	128937 RC_Z39939	AA251380	Hs.10726	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION
	WARNING			
	130983 RC_Z40012_i	AI479813	Hs.278411	NCK-associated protein 1

	114277	RC_Z40377_s	AI052229	Hs.25373	ESTs, Weakly similar to T20410 hypothetical protein E02A10.2 - <i>Caenorhabditis elegans</i>
	114304	RC_Z40820	AI934204	Hs.16129	ESTs
5	114364	RC_Z41680	AL117427	Hs.172778	Homo sapiens mRNA; cDNA DKFZp566P013 (from clone DKFZp566P013)
	132900	RC_AA005112	AA777749	Hs.5978	LIM domain only 7
	129034	RC_AA005432	AA481157	Hs.108110	DKFZP547E2110 protein
	131881	RC_AA010163	AW361018	Hs.3383	upstream regulatory element binding protein 1
	452461	RC_AA026356	N78223	Hs.108106	transcription factor
10	114465	RC_AA026901	BE621056	Hs.131731	hypothetical protein FLJ11099
	131376	RC_AA036867	AK001644	Hs.26156	hypothetical protein FLJ10782
	101567	RC_AA044644	M33552	Hs.56729	lysosomal
	431555	RC_AA046426	AI815470	Hs.260024	Cdc42 effector protein 3
	132944	RC_AA054515	T96641	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone LNG00943
15	114618	RC_AA084162	AW979261	Hs.291993	ESTs
	130274	RC_AA085749	AA128376	Hs.153884	ATP binding protein associated with cell differentiation
	110330	RC_AA098874	AI288666	Hs.16621	DKFZP434I116 protein
	114648	RC_AA101056	AA101056		gb:zn25b03.s1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone
	IMAGE:548429 3'				
20	114658	RC_AA102746	AA102383	Hs.249190	tumor necrosis factor receptor superfamily, member 10a
	132456	RC_AA114250_s	AB011084	Hs.48924	KIAA0512 gene product; ALEX2
	131319	RC_AA126561_s	NM_003155	Hs.25590	stanniocalcin 1
	132225	RC_AA128980_j	AA128980		gb:zo09a11.s1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone
	IMAGE:567164 3'				
25	132669	RC_AA129757	W38586	Hs.293981	guanine nucleotide binding protein (G protein), gamma 3, linked
	114709	RC_AA129921	AA397651	Hs.301959	proline synthetase co-transcribed (bacterial homolog)
	131973	RC_AA133331	AB018284	Hs.158688	KIAA0741 gene product
	114750	RC_AA135958	AA887211	Hs.129467	ESTs
	115714	RC_AA136524_s	T19228	Hs.172572	hypothetical protein FLJ20093
30	114763	RC_AA147044	AA810755	Hs.88977	hypothetical protein dJ511E16.2
	114767	RC_AA148885	AI859865	Hs.154443	minichromosome maintenance deficient (S. cerevisiae) 4
	114774	RC_AA150043	AV656017	Hs.184325	CGI-76 protein
	129388	RC_AA151621	AA662477	Hs.110964	hypothetical protein FLJ23471
	129183	RC_AA155743	BE561824	Hs.273369	uncharacterized hematopoietic stem/progenitor cells protein MDS027
35	128869	RC_AA156335	AA768242	Hs.80618	hypothetical protein
	130207	RC_AA156336	AF044209	Hs.144904	nuclear receptor co-repressor 1
	114798	RC_AA159181	AA159181	Hs.54900	serologically defined colon cancer antigen 1
	114800	RC_AA159825	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypothetical protein T03F6.2 - <i>Caenorhabditis elegans</i>
	[C.elegans]				
40	114828	RC_AA234185	AA252937	Hs.283522	Homo sapiens mRNA; cDNA DKFZp434J1912 (from clone DKFZp434J1912)
	114846	RC_AA234929	BE018682	Hs.166196	ATPase, Class I, type 8B, member 1
	114848	RC_AA234935	BE614347	Hs.169615	hypothetical protein FLJ20989
	114902	RC_AA236359	AW275480	Hs.39504	hypothetical protein MGC4308
	132271	RC_AA236466	AB030034	Hs.115175	sterile-alpha motif and leucine zipper containing kinase AZK
45	114907	RC_AA236535	N29390	Hs.13804	hypothetical protein dJ462O23.2
	135159	RC_AA236935_s	U43374	Hs.95631	Human normal keratinocyte mRNA
	132204	RC_AA236942	AA235827	Hs.42265	ESTs
	114928	RC_AA237018	AA237018	Hs.94869	ESTs
	132481	RC_AA237025	W93378	Hs.49614	ESTs
50	114932	RC_AA242751	AA971436	Hs.16218	KIAA0903 protein
	314162	RC_AA242760	BE041820	Hs.38516	Homo sapiens, clone MGC:15887, mRNA, complete cds
	131006	RC_AA242763	AF064104	Hs.22116	CDC14 (cell division cycle 14, S. cerevisiae) homolog B
	114935	RC_AA242809	H23329	Hs.290880	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION
	WARNING				
55	132454	RC_AA243133	BE296227	Hs.250822	serine/threonine kinase 15
	437754	RC_AA243495	R60366	Hs.5822	Homo sapiens cDNA: FLJ22120 fis, clone HEP18874
	114957	RC_AA243706	AW170425	Hs.87680	ESTs
	114974	RC_AA250848	AW966931	Hs.179662	nucleosome assembly protein 1-like 1
	114977	RC_AA250868	AW296978	Hs.87787	ESTs
60	114995	RC_AA251152	AA769266	Hs.193657	ESTs
	115005	RC_AA251544_s	AI760825	Hs.111339	ESTs
	417177	RC_AA251792	NM_004458	Hs.81452	fatty-acid-Coenzyme A ligase, long-chain 4
	131889	RC_AA252063	NM_002589	Hs.34073	BH-protocadherin (brain-heart)
	115026	RC_AA252144	AA251972	Hs.188718	ESTs
	115045	RC_AA252524	AW014549	Hs.58373	ESTs
65	115068	RC_AA253461	AW512260	Hs.87767	ESTs
	133138	RC_AA255522	AV657594	Hs.181161	Homo sapiens cDNA FLJ14643 fis, clone NT2RP2001597, weakly similar to RYANODINE
	RECEPTOR,				
70	115114	RC_AA256468	AA527548	Hs.7527	small fragment nuclease
	129584	RC_AA256528	AV656017	Hs.184325	CGI-76 protein
	115137	RC_AA257976	AW968304	Hs.56156	ESTs
	134312	RC_AA258296	AB011151	Hs.334659	hypothetical protein MGC14139
	115166	RC_AA258409	AF095727	Hs.287832	myelin protein zero-like 1
	115167	RC_AA258421	AA749209	Hs.43728	hypothetical protein
75	129807	RC_AA262077	Y11192	Hs.5299	aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase)
	115239	RC_AA278650	BE251328	Hs.73291	hypothetical protein FLJ10881
	115243	RC_AA278766	AA806600	Hs.116665	KIAA1842 protein

	100850	RC_AA279667_s	AA836472	Hs.297939	cathepsin B
	126884	RC_AA280791	U49436	Hs.286236	KIAA1856 protein
	115322	RC_AA280819	L08895	Hs.78995	MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2C)
5	133626	RC_AA280828	AW836130	Hs.75277	hypothetical protein FLJ13910
	115372	RC_AA282195	AW014385	Hs.88678	ESTs, Weakly similar to Unknown [H.sapiens]
	132825	RC_AA283127_s	U82671	Hs.57698	Empirically selected from AFFX single probeset
	130269	RC_AA284694	F05422	Hs.168352	nucleoporin-like protein 1
	129192	RC_AA291137	AA286914	Hs.183299	ESTs
10	452598	RC_AA291708	AI831594	Hs.68647	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION
	WARNING				
	132131	RC_AA293495	AF069291	Hs.40539	chromosome 8 open reading frame 1
	115536	RC_AA347193	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), actin binding protein
	132411	RC_AA398474_s	AA059412	Hs.47986	hypothetical protein MGC10940
15	115575	RC_AA398512	AA393254	Hs.43619	ESTs
	115601	RC_AA400277	AA148984	Hs.48849	ESTs, Weakly similar to ALU4_HUMAN ALU SUBFAMILY SB2 SEQUENCE CONTAMINATION
	WARNING				
	103928	RC_AA400896	D14540	Hs.199160	myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog)
	125819	RC_AA404494	AA044840	Hs.251871	CTP synthase
20	115683	RC_AA410345	AF255910	Hs.54650	junctional adhesion molecule 2
	115715	RC_AA416733	BE395161	Hs.1390	proteasome (prosome, macropain) subunit, beta type, 2
	132952	RC_AA425154	AI658580	Hs.61426	Homo sapiens mesenchymal stem cell protein DSC96 mRNA, partial cds
	115819	RC_AA426573	AA486620	Hs.41135	endomucin-2
	132525	RC_AA431418	AW292809	Hs.50727	N-acetylglucosaminidase, alpha- (Sanfilippo disease IIIB)
25	115895	RC_AA436182	AB033035	Hs.51965	KIAA1209 protein
	132333	RC_AA437099	AA192669	Hs.45032	ESTs
	115962	RC_AA446585	AI636361	Hs.179520	hypothetical protein MGC10702
	115967	RC_AA446887	AI745379	Hs.42911	ESTs
	115974	RC_AA447224	BE513442	Hs.238944	hypothetical protein FLJ10631
30	115985	RC_AA447709	AA447709	Hs.268115	ESTs, Weakly similar to T08599 probable transcription factor CA150 [H.sapiens]
	129254	RC_AA453624	AA252468	Hs.1098	DKFZp434J1813 protein
	133071	RC_AA455044	BE384932	Hs.64313	ESTs, Weakly similar to AF257182 1 G-protein-coupled receptor 48 [H.sapiens]
	116095	RC_AA456045	AA043429	Hs.62618	ESTs
	122691	RC_AA460454_s	R19768	Hs.172788	ALEX3 protein
35	116210	RC_AA476494	BE622792	Hs.172788	ALEX3 protein
	116213	RC_AA476738	AA292105	Hs.326740	hypothetical protein MGC10947
	134585	RC_AA481422	D14041	Hs.278573	H-2K binding factor-2
	134790	RC_AA482269	BE002798	Hs.287850	integral membrane protein 1
	116265	RC_AA482595	BE297412	Hs.55189	hypothetical protein
40	129334	RC_AA485084_s	AW157022	Hs.4947	hypothetical protein FLJ22584
	116274	RC_AA485431_s	AI129767	Hs.182874	guanine nucleotide binding protein (G protein) alpha 12
	303150	RC_AA489057	AA887146	Hs.8217	stromal antigen 2
	129945	RC_AA489638	BE514376	Hs.165998	PAI-1 mRNA-binding protein
	116331	RC_AA491000	NA1300	Hs.71616	Homo sapiens mRNA; cDNA DKFZp586N1720 (from clone DKFZp586N1720)
45	116333	RC_AA491250	AF155827	Hs.203963	hypothetical protein FLJ10339
	132994	RC_AA505133	AA112748	Hs.279905	clone HQ0310 PRO0310p1
	134577	RC_AA598447	BE244323	Hs.85951	exportin, tRNA (nuclear export receptor for tRNAs)
	116391	RC_AA599243	T86558	Hs.75113	general transcription factor IIIA
	116394	RC_AA599574_s	NM_006033	Hs.65370	lipase, endothelial
50	134531	RC_AA600153	AI742845	Hs.110713	DEK oncogene (DNA binding)
	116417	RC_AA609309	AW499664	Hs.12484	Human clone 23826 mRNA sequence
	116429	RC_AA609710	AF191018	Hs.279923	putative nucleotide binding protein, estradiol-induced
	116439	RC_AA610068	AA251594	Hs.43913	PIBF1 gene product
	116459	RC_AA621399	R80137	Hs.302738	Homo sapiens cDNA: FLJ21425 fis, clone COL04162
55	427505	RC_AA621752	AA361562	Hs.178761	26S proteasome-associated pad1 homolog
	132699	RC_C21523	AW449822	Hs.55200	ESTs
	116541	RC_D12160	D12160	Hs.249212	polymerase (RNA) III (DNA directed) (155kD)
	132557	RC_D19708	AA114926	Hs.5122	ESTs
	112259	RC_D25801	AA337548	Hs.333402	hypothetical protein MGC12760
60	116571	RC_D45652	D45652		gb:HUMGS02848 Human adult lung 3' directed Mbol cDNA Homo sapiens cDNA 3', mRNA sequence.
	129815	RC_D60208_f	BE565817	Hs.26498	hypothetical protein FLJ21657
	421919	RC_D80504_s	AJ224901	Hs.109526	zinc finger protein 198
	116643	RC_F03010	AI367044	Hs.153638	myeloid/lymphoid or mixed-lineage leukemia 2
65	116661	RC_F04247	R61504		gb:yh16a03.s1 Soares infant brain 1NIB Homo sapiens cDNA clone 3' similar to contains Alu repetitive
	116715	RC_F10966	AL117440	Hs.170263	tumor protein p53-binding protein, 1
	116729	RC_F13700	BE549407	Hs.115823	ribonuclease P, 40kD subunit
	318709	RC_H05063	R52576	Hs.285280	Homo sapiens cDNA: FLJ22096 fis, clone HEP16953
70	134760	RC_H16758	NM_000121	Hs.89548	erythropoietin receptor
	116773	RC_H17315_s	AI823410	Hs.169149	karyopherin alpha 1 (importin alpha 5)
	106425	RC_H22556	H24201	Hs.247423	adducin 2 (beta)
	116780	RC_H22566	H22566	Hs.30098	ESTs
	131978	RC_H48459_s	AA355925	Hs.36232	KIAA0186 gene product
	116819	RC_H53073	H53073	Hs.93698	EST
75	111428	RC_H56559_s	AL031428	Hs.174174	KIAA0601 protein
	133175	RC_H57957_s	AW955632	Hs.66666	ESTs, Weakly similar to S19560 proline-rich protein MP4 - mouse [M.musculus]

5	116844	RC_H64938_s	H64938	Hs.337434	ESTs, Weakly similar to A46010 X-linked retinopathy protein [H.sapiens]
	116845	RC_H64973	AA649530		gb:ns44f05.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone, mRNA sequence
	116892	RC_H69535	A1573283	Hs.38458	ESTs
	116925	RC_H73110	H73110	Hs.260603	ESTs, Moderately similar to A47582 B-cell growth factor precursor [H.sapiens]
	116981	RC_H81783	N29218	Hs.40290	ESTs
10	131768	RC_H86259	AC005757	Hs.31809	hypothetical protein
	117031	RC_H88353	H88353		gb:yy21a02.s1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:252842 3' similar to contains L1
	117034	RC_H88639	U72209	Hs.180324	YY1-associated factor 2
	132542	RC_H88675	AL137751	Hs.263671	Homo sapiens mRNA; cDNA DKFZp434I0812 (from clone DKFZp434I0812); partial cds
	134403	RC_H93708_s	AA334551	Hs.82767	sperm specific antigen 2
15	117280	RC_N22107	M18217	Hs.172129	Homo sapiens cDNA: FLJ21409 fis, clone COL03924
	117344	RC_N24046	R19085	Hs.210706	Homo sapiens cDNA FLJ13182 fis, clone NT2RP3004070
	117422	RC_N27028	A1355562	Hs.43880	ESTs, Weakly similar to A46010 X-linked retinopathy protein [H.sapiens]
	117475	RC_N30205	N30205	Hs.93740	ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]
	117487	RC_N30621	N30621	Hs.44203	ESTs
20	130207	RC_N33258	AF044209	Hs.144904	nuclear receptor co-repressor 1
	117549	RC_N33390	N33390	Hs.44483	EST
	117683	RC_N40180	N40180		gb:yy44d02.s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone
	117710	RC_N45198	N45198	Hs.47248	ESTs, Highly similar to similar to Cdc14B1 phosphatase [H.sapiens]
	104514	RC_N45979_s	AF164622	Hs.182982	golgin-67
25	117791	RC_N48325	N48325	Hs.93956	EST
	117822	RC_N48913	AA706282	Hs.93963	ESTs
	129647	RC_N49394	AB018259	Hs.118140	KIAA0716 gene product
	117895	RC_N50656	AW450348	Hs.93996	ESTs, Highly similar to SORL_HUMAN SORTILIN-RELATED RECEPTOR PRECURSOR [H.sapiens]
	131557	RC_N50721	AA317439	Hs.28707	signal sequence receptor, gamma (translocon-associated protein gamma)
30	133057	RC_N53143	AA465131	Hs.64001	Homo sapiens clone 25218 mRNA sequence
	118103	RC_N55326	AA401733	Hs.184134	ESTs
	118111	RC_N55493	N55493		gb:yy50c02.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:246146 3', mRNA
	118129	RC_N57493	N57493		gb:yy54c08.s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone
	IMAGE:277358 3', mRNA				
35	118278	RC_N62955	N62955	Hs.316433	Homo sapiens cDNA FLJ11375 fis, clone HEMBA1000411, weakly similar to ANKYRIN
	118329	RC_N63520	N63520		gb:yy62f01.s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:278137 3', mRNA
	118336	RC_N63604	BE327311	Hs.47166	HT021
	132457	RC_N64166	AB017365	Hs.173859	frizzled (Drosophila) homolog 7
	118363	RC_N64168	A1183838	Hs.48938	hypothetical protein FLJ21802
40	118364	RC_N64191	N46114	Hs.29169	hypothetical protein FLJ22623
	118475	RC_N66845	N66845		gb:za46c11.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:295604 3' similar to
	118491	RC_N67135	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone HEP09071
	118500	RC_N67295	W32889	Hs.154329	ESTs
	101663	RC_N68399	NM_003528	Hs.2178	H2B histone family, member Q
45	118584	RC_N68963	AW136928		gb:UI-H-B11-adp-d-08-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone 3', mRNA sequence
	421983	RC_N69331	A1252640	Hs.110364	peptidylprolyl isomerase C (cyclophilin C)
	118661	RC_N70777	AL137554	Hs.49927	protein kinase NYD-SP15
	118684	RC_N71364_s	N71313	Hs.163986	Homo sapiens cDNA: FLJ22765 fis, clone KAIA1180
	118689	RC_N71545_s	AW390601	Hs.184544	Homo sapiens, clone IMAGE:3355383, mRNA, partial cds
55	118690	RC_N71571	N71571	Hs.269142	ESTs
	118766	RC_N74456	N74456	Hs.50499	EST
	118793	RC_N75594	N75594	Hs.285921	ESTs, Moderately similar to T47135 hypothetical protein DKFZp761L0812.1 [H.sapiens]
	118817	RC_N79035	A1668658	Hs.50797	ESTs
	118844	RC_N80279	AL035364	Hs.50891	hypothetical protein
60	118919	RC_N91797	AW452696	Hs.130760	myosin phosphatase, target subunit 2
	129558	RC_N92454	AW580922	Hs.180446	karyopherin (importin) beta 1
	132692	RC_N94581	AW191962	Hs.249239	collagen, type VIII, alpha 2
	118996	RC_N94746	N94746	Hs.274248	hypothetical protein FLJ20758
	119021	RC_N98238	N98238	Hs.55185	ESTs
65	119039	RC_R02384	A1160570	Hs.252097	pregnancy specific beta-1-glycoprotein 6
	119063	RC_R16833	R16833	Hs.53106	ESTs, Moderately similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION
	WARNING				
	118523	RC_R41828_s	Y07759	Hs.170157	myosin VA (heavy polypeptide 12, myoxin)
	119111	RC_R43203	T02865	Hs.328321	EST
70	133970	RC_R46395	AA214228	Hs.127751	hypothetical protein
	119146	RC_R58863	R58863	Hs.91815	ESTs
	120296	RC_R78248	AW995911	Hs.299883	hypothetical protein FLJ23399
	119239	RC_T11483	T11483		gb:CHR90049 Chromosome 9 exon Homo sapiens cDNA clone 111-1 5' and 3', mRNA sequence.
	119281	RC_T16896	A1692322	Hs.65373	ESTs, Weakly similar to T02345 hypothetical protein KIAA0324 [H.sapiens]
75	119298	RC_T23820	NM_001241	Hs.155478	cyclin T2
	126502	RC_T30222	T10077	Hs.13453	hypothetical protein FLJ14753
	135073	RC_W15275_s	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (from clone DKFZp586E1624)

	119558	RC_W38194	W38194		Empirically selected from AFFX single probeset
	132736	RC_W42414_s	AW081883	Hs.288261	Homo sapiens cDNA: FLJ23037 fis, clone LNG02036, highly similar to HSU68019 Homo sapiens mad protein
5	132173	RC_W46577_s	X89426	Hs.41716	endothelial cell-specific molecule 1
	134873	RC_W49632_s	AA884471	Hs.90449	Human clone 23908 mRNA sequence
	119650	RC_W57613	R82342	Hs.79856	ESTs, Weakly similar to S65657 alpha-1C-adrenergic receptor splice form 2 [H.sapiens]
	119654	RC_W57759	W57759		gb:zd20g11.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:341252 3' similar to
10	119683	RC_W61118	W65379	Hs.57835	ESTs
	119694	RC_W65344	AA041350	Hs.57847	ESTs, Moderately similar to ICE4_HUMAN CASPASE-4 PRECURSOR [H.sapiens]
	119718	RC_W69216	W69216	Hs.92848	ESTs
	133010	RC_W69379	AI287518	Hs.62669	Homo sapiens mRNA; cDNA DKFZp586D0923 (from clone DKFZp586D0923)
	119938	RC_W86728	AW014862	Hs.58885	ESTs
15	120128	RC_Z38499	BE379320	Hs.91448	MKP-1 like protein tyrosine phosphatase
	120130	RC_Z38630	AA045767	Hs.5300	bladder cancer associated protein
	120148	RC_Z39494	F02806	Hs.65765	ESTs
	120155	RC_Z39623	Z39623	Hs.65783	ESTs
	131486	RC_Z40071_s	F06972	Hs.27372	BMX non-receptor tyrosine kinase
20	120183	RC_Z40174	AW082866	Hs.65882	ESTs
	120184	RC_Z40182	Z40182	Hs.65885	EST
	120211	RC_Z40904	Z40904	Hs.66012	EST
	120245	RC_AA166965	AW959615	Hs.111045	ESTs
	120247	RC_AA167500	AA167500	Hs.103939	EST
25	120254	RC_AA169599_s	W90403	Hs.111054	ESTs
	120259	RC_AA171724	AW014786	Hs.192742	hypothetical protein FLJ12785
	120260	RC_AA171739	AK000061	Hs.101590	hypothetical protein
	120275	RC_AA177105	AA177105	Hs.78457	solute carrier family 25 (mitochondrial carrier; ornithine transporter) member 15
	120284	RC_AA182626	AA179656		gb:zp54e11.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone 3' similar to contains
30	114056	RC_AA186324	AA188175	Hs.82506	KIAA1254 protein
	129507	RC_AA192099	AJ236885	Hs.112180	zinc finger protein 148 (pHZ-52)
	120302	RC_AA192173	AA837098	Hs.269933	ESTs
	120303	RC_AA192415	AI216292	Hs.96184	ESTs
35	120305	RC_AA192553	AW295096	Hs.101337	uncoupling protein 3 (mitochondrial, proton carrier)
	120319	RC_AA194851	T57776	Hs.191094	ESTs
	133389	RC_AA195520_s	AA195764	Hs.72639	ESTs
	120326	RC_AA196300	AA196300	Hs.21145	hypothetical protein RG083M05.2
	134272	RC_AA196517	X76040	Hs.278614	protease, serine, 15
40	133145	RC_AA196549	H94227	Hs.6592	Homo sapiens, clone IMAGE:2961368, mRNA, partial cds
	120327	RC_AA196721	AK000292	Hs.278732	hypothetical protein FLJ20285
	106686	RC_AA196729_i	N66397	Hs.334825	Homo sapiens cDNA FLJ14752 fis, clone NT2RP3003071
	120328	RC_AA196979	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapiens]
	120340	RC_AA206828	AA206828		gb:zq80b08.s1 Stratagene hNT neuron (937233) Homo sapiens cDNA clone IMAGE:647895 3' similar to
45	134292	RC_AA207123	AI906291	Hs.81234	immunoglobulin superfamily, member 3
	131522	RC_AA214539_i	AI380040	Hs.239489	TIA1 cytotoxic granule-associated RNA-binding protein
	129051	RC_AA226914_s	AA227068	Hs.108301	nuclear receptor subfamily 2, group C, member 1
	120375	RC_AA227260	AF028706	Hs.111227	Zic family member 3 (odd-paired Drosophila homolog, heterotaxy 1)
50	120376	RC_AA227469	AA227469		gb:zr18a07.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone IMAGE:663732 3', mRNA sequence.
	120390	RC_AA233122	AA837093	Hs.111460	calcium/calmodulin-dependent protein kinase (CaM kinase) II delta
	303876	RC_AA233334_s	U64820	Hs.66521	Machado-Joseph disease (spinocerebellar ataxia 3, olivopontocerebellar ataxia 3, autosomal dominant, ataxin 3)
55	132038	RC_AA233347	AI825842	Hs.3776	zinc finger protein 216
	104463	RC_AA233519	T85825	Hs.246885	hypothetical protein FLJ20783
	125750	RC_AA233714	AA018515	Hs.264482	Homo sapiens mRNA; cDNA DKFZp761A0411 (from clone DKFZp761A0411)
	120396	RC_AA233796	AA134006	Hs.79306	eukaryotic translation initiation factor 4E
	120409	RC_AA235050_f	AA235050		gb:zs38e04.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:687486 3' similar to gb:107077
60	120414	RC_AA235704	AW137156	Hs.181202	hypothetical protein FLJ10038
	120420	RC_AA236031	AI128114	Hs.112885	spinal cord-derived growth factor-B
	120422	RC_AA236352	AL133097	Hs.301717	hypothetical protein DKFZp434N1928
	132221	RC_AA236390_s	W94915	Hs.42419	ESTs
65	120423	RC_AA236453	AA236453	Hs.18978	Homo sapiens cDNA: FLJ22822 fis, clone KAIA3968
	120435	RC_AA243370	AA243370	Hs.96450	EST
	120453	RC_AA250947	AA250947	Hs.170263	tumor protein p53-binding protein, 1
	120455	RC_AA251083	AA251720	Hs.104347	ESTs, Weakly similar to ALUC_HUMAN !!!! ALU CLASS C WARNING ENTRY !!! [H.sapiens]
	120456	RC_AA251113	AA488750	Hs.88414	BTB and CNC homology 1, basic leucine zipper transcription factor 2
70	120473	RC_AA251973	AA251973	Hs.269988	ESTs
	128922	RC_AA252023	AI244901	Hs.9589	ubiquitin 1
	120477	RC_AA252414	AA252414	Hs.43141	DKFZP727C091 protein
	120479	RC_AA252650	AF006689	Hs.110299	mitogen-activated protein kinase kinase 7
	120488	RC_AA255523	AW952916	Hs.63510	KIAA0141 gene product
75	120510	RC_AA258128	AI796395	Hs.111377	ESTs
	120527	RC_AA262105	AA262105	Hs.4094	Homo sapiens cDNA FLJ14208 fis, clone NT2RP3003264
	120528	RC_AA262107	AI923511	Hs.104413	ESTs

	120529	RC_AA262235	AI434823	Hs.104415	ESTs
	120541	RC_AA278298	W07318	Hs.240	M-phase phosphoprotein 1
	131445	RC_AA278529_i	NM_014264	Hs.172052	serine/threonine kinase 18
5	120544	RC_AA278721	BE548277	Hs.103104	ESTs
	120562	RC_AA280036	BE244580	Hs.302267	hypothetical protein FLJ10330
	120569	RC_AA280648	AA807544	Hs.24970	ESTs, Weakly similar to B34323 GTP-binding protein Rab2 [H.sapiens]
	120571	RC_AA280738	AB037744	Hs.34892	KIAA1323 protein
	120572	RC_AA280794	H39599	Hs.294008	ESTs
10	129434	RC_AA280837	AW967495	Hs.186644	ESTs
	130529	RC_AA280886	AA178953		gb:z39e03.s1 Stratagene muscle 937209 Homo sapiens cDNA clone 3' similar to contains Alu repetitive
	120575	RC_AA280934	AW978022	Hs.238911	hypothetical protein DKFZp762E1511; KIAA1816 protein
	132635	RC_AA281535	AB020686	Hs.54037	ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative function)
15	120591	RC_AA281797_s	AF078847	Hs.191356	general transcription factor IIH, polypeptide 2 (44kD subunit)
	120593	RC_AA282047	AA748355	Hs.193522	ESTs
	430275	RC_AA283002	Z11773	Hs.237786	zinc finger protein 187
	117729	RC_AA283709	AA306166	Hs.7145	calpain 7
	120609	RC_AA283902	AW978721	Hs.266076	ESTs, Weakly similar to A46010 X-linked retinopathy protein [H.sapiens]
20	132754	RC_AA284108	AI752244	Hs.75309	eukaryotic translation elongation factor 2
	130315	RC_AA284109	AI241084	Hs.154353	nonselective sodium potassium/proton exchanger
	132614	RC_AA284371	AA284371	Hs.118064	similar to rat nuclear ubiquitous casein kinase 2
	447503	RC_AA284744_f	AA115496	Hs.336898	Homo sapiens, Similar to RIKEN cDNA 1810038N03 gene, clone MGC:9890, mRNA, complete cds
25	135376	RC_AA284784	BE617856	Hs.99756	mitochondrial ribosome recycling factor
	120621	RC_AA284840	AW961294	Hs.143818	hypothetical protein FLJ23459
	107868	RC_AA286844	AA286844	Hs.61260	hypothetical protein FLJ13164
	129868	RC_AA287032	AW172431	Hs.13012	ESTs
	120644	RC_AA287038	AI869129	Hs.96616	ESTs
30	120660	RC_AA287546	AA286785	Hs.99677	ESTs
	135370	RC_AA287553_s	BE622187	Hs.99670	ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]
	120661	RC_AA287556	AA287556	Hs.263412	ESTs, Weakly similar to ALUB_HUMAN !!! ALU CLASS B WARNING ENTRY !!! [H.sapiens]
	129116	RC_AA287564	AB019494	Hs.225767	IDN3 protein
	131567	RC_AA291015_s	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisiae, homolog)-like 1
35	120699	RC_AA291716	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribosomal protein L13a, cytosolic [H.sapiens]
	100690	RC_AA291749_s	AA383256	Hs.1657	estrogen receptor 1
	120726	RC_AA293656	AA293655	Hs.97293	ESTs
	120737	RC_AA302430	AL049176	Hs.82223	chordin-like
	120745	RC_AA302809	AA302809		gb:EST10426 Adipose tissue, white I Homo sapiens cDNA 3' end, mRNA sequence.
40	135192	RC_AA302820_s	U83993	Hs.321709	purinergic receptor P2X, ligand-gated ion channel, 4
	120750	RC_AA310499	AI191410	Hs.96693	ESTs, Moderately similar to 2109260A B cell growth factor [H.sapiens]
	120761	RC_AA321890	AA321890	Hs.1265	branched chain keto acid dehydrogenase E1, beta polypeptide (maple syrup urine disease)
	120768	RC_AA340589	AA340589	Hs.104560	EST
	120769	RC_AA340622	AI769467	Hs.96769	ESTs
45	135232	RC_AA342457_i	AL038812	Hs.96800	ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE
	CONTAMINATION				
	133439	RC_AA342828_s	Z23091	Hs.73734	glycoprotein V (platelet)
	120793	RC_AA342864	AA342864	Hs.96812	ESTs
	120796	RC_AA342973	AI247356	Hs.96820	ESTs
50	120809	RC_AA346495	AA346495		gb:EST52657 Fetal heart II Homo sapiens cDNA 3' end similar to EST containing O family repeat, mRNA sequence.
	132459	RC_AA347573	AL120071	Hs.48998	fibronectin leucine rich transmembrane protein 2
	120825	RC_AA347614	AI280215	Hs.96885	ESTs
	120827	RC_AA347717	AA382525	Hs.132967	Human EST clone 122887 mariner transposon Hsmar1 sequence
55	120839	RC_AA348913	AA348913		gb:EST55442 Infant adrenal gland II Homo sapiens cDNA 3' end similar to EST containing Alu repeat, mRNA sequence.
	120850	RC_AA349647	AA349647	Hs.96927	Homo sapiens cDNA FLJ12573 fis, clone NT2RM4000979
	120852	RC_AA349773	AA349773	Hs.191564	ESTs
	128852	RC_AA350541_s	R40622	Hs.106601	ESTs
60	135240	RC_AA357159_i	AA357159	Hs.96986	EST
	120870	RC_AA357172_i	AA357172	Hs.292581	ESTs, Moderately similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING
	134637	RC_AA369856_s	U87309	Hs.180941	vacuolar protein sorting 41 (yeast homolog)
	120894	RC_AA370132	AA370132	Hs.97063	ESTs
65	131854	RC_AA370472_s	AF229839	Hs.173202	I-kappa-B-interacting Ras-like protein 1
	120897	RC_AA370867	AA370867	Hs.97079	ESTs, Moderately similar to AF174605 1 F-box protein Fbx25 [H.sapiens]
	120915	RC_AA377296	AL135556	Hs.97104	ESTs
	120935	RC_AA383902	AL048409	Hs.97177	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING
	120936	RC_AA385934	AA385934	Hs.97184	EST, Highly similar to (define not available 7499603) [C.elegans]
70	120937	RC_AA386255	AA386255	Hs.97186	EST
	120938	RC_AA386260	AA386260	Hs.104632	EST
	129722	RC_AA386266	R20855	Hs.5422	glycoprotein M6B
	120960	RC_AA398014	AA398014	Hs.104684	EST
	120985	RC_AA398222	AI219896	Hs.97592	ESTs
75	120988	RC_AA398235	AA398235	Hs.97631	ESTs

	121008	RC_AA398348	AA398348	Hs.301720	Human DNA sequence from clone RP11-251J8 on chromosome 13 Contains ESTs, STSs, GSSs and a CpG
5	121029	RC_AA398482	AA398482	Hs.97641	EST
	121032	RC_AA398504	AA393037	Hs.161798	ESTs
	121033	RC_AA398505	AA398505	Hs.97360	ESTs
	121034	RC_AA398507	AL389951	Hs.271623	nucleoporin 50kD
	121035	RC_AA398523	AA398523	Hs.210579	ESTs
	121058	RC_AA398625	AA398625	Hs.97391	ESTs
10	121060	RC_AA398632	AA398632	Hs.97395	ESTs
	121061	RC_AA398633	AA393288	Hs.97396	ESTs
	121091	RC_AA398894	AA398894	Hs.97657	ESTs, Moderately similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE
	121092	RC_AA398895	AA398895	Hs.97658	EST
15	121094	RC_AA398900	AA402505		gb:zt62h10.r1 Soares_testis_NHT Homo sapiens cDNA clone 5', mRNA sequence
	121096	RC_AA398904	AA398904	Hs.332690	ESTs
	121115	RC_AA399122	AA398187	Hs.104682	ESTs, Weakly similar to mitochondrial citrate transport protein [H.sapiens]
	121121	RC_AA399371	AA399371	Hs.189095	similar to SALL1 (sal (Drosophila)-like
	121122	RC_AA399373	AI126713	Hs.192233	ESTs, Highly similar to T00337 hypothetical protein KIAA0568 [H.sapiens]
20	121125	RC_AA399441	AL042981	Hs.251278	KIAA1201 protein
	121151	RC_AA399636	AA399636	Hs.143629	ESTs
	121153	RC_AA399640	AA399640	Hs.97694	ESTs
	121163	RC_AA399680	AI676062	Hs.111902	ESTs
	121176	RC_AA400080	AL121523	Hs.97774	ESTs
25	121192	RC_AA400262	AA400262	Hs.190093	ESTs
	121223	RC_AA400725	AI002110	Hs.97169	ESTs, Weakly similar to dJ667H12.2.1 [H.sapiens]
	121227	RC_AA400748	AA400748	Hs.97823	Homo sapiens mRNA; cDNA DKFZp434D024 (from clone DKFZp434D024)
	121231	RC_AA400780	AA814948	Hs.96343	ESTs, Weakly similar to ALUC_HUMAN !!!! ALU CLASS C WARNING ENTRY !!! [H.sapiens]
	121278	RC_AA401631	AA037121	Hs.98518	Homo sapiens cDNA FLJ11490 fis, clone HEMBA1001918
30	121279	RC_AA401688	AA292873	Hs.177996	ESTs
	121282	RC_AA401695	AA401695	Hs.97334	ESTs
	121299	RC_AA402227	AA402227	Hs.22826	tropomodulin 3 (ubiquitous)
	121301	RC_AA402329	NM_006202	Hs.89901	phosphodiesterase 4A, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E2)
	121302	RC_AA402398	AA402587	Hs.325520	LAT1-3TM protein
35	121304	RC_AA402449	AA293863	Hs.97316	EST
	121305	RC_AA402468	AA402468	Hs.291557	ESTs
	134721	RC_AA403268_s	AK000112	Hs.89306	hypothetical protein FLJ20105
	121323	RC_AA403314	AA291411	Hs.97247	ESTs
	121324	RC_AA404229	AA404229	Hs.97842	EST
40	129047	RC_AA404260	AI768623	Hs.108264	ESTs
	131074	RC_AA404271	U16125	Hs.181581	glutamate receptor, ionotropic, kainate 1
	121344	RC_AA405026	AA405026	Hs.193754	ESTs
	121348	RC_AA405182	AA405182	Hs.97973	ESTs
	121350	RC_AA405237	AA405237		gb:zt06e10.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712362 3' similar to contains Alu
45	121400	RC_AA406061	AA406061	Hs.98001	EST
	121402	RC_AA406063	AA406063	Hs.98003	ESTs
	121403	RC_AA406070	AA406070	Hs.98004	EST
	121408	RC_AA406137	AA406137	Hs.98019	EST
50	121431	RC_AA406335	AA035279	Hs.176731	ESTs
	132936	RC_AA411801	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear translocator 2
	121471	RC_AA411804	AA411804	Hs.261575	ESTs
	121474	RC_AA411833	AA402335	Hs.188760	ESTs, Highly similar to Trad [H.sapiens]
	121526	RC_AA412219	AW665325	Hs.98120	ESTs
55	121530	RC_AA412259	AA778658	Hs.98122	ESTs
	121558	RC_AA412497	AA412497		gb:zt95g12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730150 3' similar to contains L1.L3 L1
	121559	RC_AA412498	AI192044	Hs.104778	ESTs
	121584	RC_AA416586	AI024471	Hs.98232	ESTs
60	121609	RC_AA416867	AA416867	Hs.98185	EST
	121612	RC_AA416874	AA416874	Hs.98168	ESTs
	121737	RC_AA421133	AA421133	Hs.104671	erythrocyte transmembrane protein
	121740	RC_AA421138	AA421138	Hs.98334	EST
	129194	RC_AA422079	AA150797	Hs.109276	latexin protein
65	121784	RC_AA423837	T90789	Hs.94308	RAB35, member RAS oncogene family
	121802	RC_AA424328	AI251870	Hs.188898	ESTs
	121803	RC_AA424339	AI338371	Hs.157173	ESTs
	135286	RC_AA424469_s	AW023482	Hs.97849	ESTs
	121806	RC_AA424502	AA424313	Hs.98402	ESTs
70	129517	RC_AA425004	AW972853	Hs.112237	ESTs
	121845	RC_AA425734	AI732692	Hs.165066	ESTs, Moderately similar to ALU2_HUMAN ALU SUBFAMILY SB SEQUENCE
	121853	RC_AA425887	AA425887	Hs.98502	hypothetical protein FLJ14303
	121891	RC_AA426456	AA426456	Hs.98469	ESTs
75	121895	RC_AA427396	AA427396		gb:zw33a02.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:771050 3' similar to contains
	121899	RC_AA427555	R55341	Hs.50421	KIAA0203 gene product

	121917	RC_AA428218	AA406397	Hs.98038	ESTs
	121918	RC_AA428242	BE274689	Hs.184175	chromosome 2 open reading frame 3
	121919	RC_AA428281	AA428281	Hs.98560	EST
5	121941	RC_AA428865	AA428865	Hs.98563	ESTs
	121942	RC_AA428994	AW452701	Hs.293237	ESTs
	121970	RC_AA429666	AA429666	Hs.98617	EST
	121993	RC_AA430181	AW297880	Hs.98661	ESTs
	134660	RC_AA430184_s	U73524	Hs.87465	ATP/GTP-binding protein
10	126753	RC_AA431288_s	AA306478	Hs.95327	CD3D antigen, delta polypeptide (TIT3 complex)
	122022	RC_AA431293	AA431293	Hs.98716	ESTs, Moderately similar to T42650 hypothetical protein DKFZp434D0215.1 [H.sapiens]
	122050	RC_AA431478	AI453076	Hs.166109	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2
	122051	RC_AA431492	AA431492	Hs.98742	EST
	122055	RC_AA431732	AA431732	Hs.98747	EST
15	122105	RC_AA432278	AW241685	Hs.98699	ESTs
	122125	RC_AA434411	AK000492	Hs.98806	hypothetical protein
	135235	RC_AA435512_i	AW298244	Hs.293507	ESTs
	122162	RC_AA435698	AA628233	Hs.79946	cytochrome P450, subfamily XIX (aromatization of androgens)
	129406	RC_AA435711	AB018255	Hs.111138	KIAA0712 gene product
20	318801	RC_AA435815_s	U40763	Hs.77965	peptidyl-prolyl isomerase G (cyclophilin G)
	122186	RC_AA435842	AA398811	Hs.104673	ESTs
	122235	RC_AA436475	AA436475	Hs.112227	membrane-associated nucleic acid binding protein
	129131	RC_AA436489	AB026436	Hs.177534	dual specificity phosphatase 10
	134664	RC_AA442060	AA256106	Hs.87507	ESTs
25	122310	RC_AA442079	AW192803	Hs.98974	ESTs, Weakly similar to S65824 reverse transcriptase homolog [H.sapiens]
	122334	RC_AA443151	BE465894	Hs.98365	ESTs, Weakly similar to LB4D_HUMAN NADP-DEPENDENT LEUKOTRIENE B4 12-
	122382	RC_AA446133	AA446440	Hs.98643	ESTs
	122425	RC_AA447145	AB007859	Hs.100955	KIAA0399 protein
	122431	RC_AA447398	AA447398	Hs.99104	ESTs
30	122450	RC_AA447643	AA447643	Hs.112095	hypothetical protein DKFZp434F1819
	302653	RC_AA447742_s	AJ404468	Hs.284259	dynein, axonemal, heavy polypeptide 9
	122477	RC_AA448226	AA448226	Hs.324123	ESTs
	122500	RC_AA448825	AA448825	Hs.99190	ESTs
	122522	RC_AA449444	AA299607	Hs.98969	ESTs
35	122536	RC_AA450087	AF060877	Hs.99236	regulator of G-protein signalling 20
	122538	RC_AA450211	AA450211	Hs.99239	ESTs
	122540	RC_AA450244	AA476741	Hs.98279	ESTs, Weakly similar to A43932 mucin 2 precursor, intestinal [H.sapiens]
	122560	RC_AA452123	AW392342	Hs.283077	centrosomal P4.1-associated protein; uncharacterized bone marrow protein BM032
	421919	RC_AA452155	AJ224901	Hs.109526	zinc finger protein 198
40	122562	RC_AA452156	AA452156		gb:zx29c03.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:787876 3', mRNA
	122585	RC_AA453036	AI681654	Hs.170737	hypothetical protein FLJ23251
	122608	RC_AA453526	AA453525	Hs.143077	ESTs
	122635	RC_AA454085	AA454085		gb:zx33a08.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:788246 3' similar to
45	122636	RC_AA454103	AW651706	Hs.99519	hypothetical protein FLJ14007
	122653	RC_AA454642	AW009166	Hs.99376	ESTs
	122660	RC_AA454935	AI816827	Hs.180069	nuclear respiratory factor 1
	122703	RC_AA456323	AA456323	Hs.269369	ESTs
50	122724	RC_AA457395	AA457395	Hs.99457	ESTs
	122749	RC_AA458850	AA458850	Hs.293372	ESTs, Weakly similar to B34087 hypothetical protein [H.sapiens]
	122772	RC_AA459662	AW117452	Hs.99489	ESTs
	131098	RC_AA459668	U66669	Hs.236642	3-hydroxyisobutyryl-Coenzyme A hydrolase
	129045	RC_AA459679_s	AI082883	Hs.30732	hypothetical protein FLJ13409; KIAA1711 protein
55	122777	RC_AA459702	AK001022	Hs.214397	hypothetical protein FLJ10160 similar to insulin related protein 2
	135362	RC_AA460017_f	AA978128	Hs.99513	ESTs, Weakly similar to T17454 diaphanous-related formin - mouse [M.musculus]
	122798	RC_AA460324	AW366286	Hs.145696	splicing factor (CC1.3)
	122837	RC_AA461509	AA461509	Hs.293565	ESTs, Weakly similar to putative p150 [H.sapiens]
	122860	RC_AA464414_i	AA464414		gb:zx78g01.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:809904 3', mRNA sequence.
60	122861	RC_AA464428	AA335721	Hs.119394	ESTs
	122910	RC_AA470084	AA470084	Hs.98358	ESTs
	132899	RC_AA476606_s	AA476606	Hs.59666	SMAD in the antisense orientation
	122967	RC_AA478521	AA806187	Hs.289101	glucose regulated protein, 58kD
65	129560	RC_AA478523	AA317841	Hs.7845	hypothetical protein MGC2752
	123009	RC_AA479949	AA535244	Hs.78305	RAB2, member RAS oncogene family
	128917	RC_AA481252	AI365215	Hs.206097	oncogene TC21
	123081	RC_AA485351	AI815486	Hs.243901	Homo sapiens cDNA FLJ20738 fis, clone HEP08257
	123133	RC_AA487264	AA487264	Hs.154974	Homo sapiens mRNA; cDNA DKFZp667N064 (from clone DKFZp667N064)
	123184	RC_AA489072	BE247767	Hs.18166	KIAA0870 protein
70	129671	RC_AA489630	NM_014700	Hs.119004	KIAA0665 gene product
	123233	RC_AA490225	AW974175	Hs.188751	ESTs, Weakly similar to MAPB_HUMAN MICROTUBULE-ASSOCIATED PROTEIN 1B [H.sapiens]
	123234	RC_AA490227	NM_001938	Hs.16697	down-regulator of transcription 1, TBP-binding (negative cofactor 2)
	123236	RC_AA490255	AW968504	Hs.123073	CDC2-related protein kinase 7
75	123255	RC_AA490890	AA830335	Hs.105273	ESTs
	129503	RC_AA490916_s	AW768399	Hs.112157	ESTs

	131043	RC_AA490925	AF084535	Hs.22464	epilepsy, progressive myoclonus type 2, Lafora disease (laforin)
	123259	RC_AA490955	AI744152	Hs.283374	ESTs, Weakly similar to CA15_HUMAN COLLAGEN ALPHA 1(V) CHAIN PRECURSOR [H.sapiens]
5	123284	RC_AA495812	AA488988	Hs.293796	ESTs
	123286	RC_AA495824	AA495824	Hs.188822	ESTs, Weakly similar to A46010 X-linked retinopathy protein [H.sapiens]
	123315	RC_AA496369	AA496369		gb:zv37d10.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:755827 3' similar to contains
	129179	RC_AA504125_s	AW969025	Hs.109154	ESTs
10	131612	RC_AA521473	AU076668	Hs.334884	SEC10 (S. cerevisiae)-like 1
	123421	RC_AA598440	AA598440	Hs.291154	EST, Weakly similar to I38022 hypothetical protein [H.sapiens]
	123449	RC_AA598899_i	AL049325	Hs.112493	Homo sapiens mRNA; cDNA DKFZp564D036 (from clone DKFZp564D036)
	129021	RC_AA599244	AL044675	Hs.173081	KIAA0530 protein
	132830	RC_AA599694_s	NM_014777	Hs.57730	KIAA0133 gene product
15	123497	RC_AA600037	AA765256	Hs.135191	ESTs, Weakly similar to unnamed protein product [H.sapiens]
	123604	RC_AA609135	AA609135	Hs.293076	ESTs
	129539	RC_AA609582	T47614	Hs.323022	ESTs, Highly similar to p60 katanin [H.sapiens]
	123712	RC_AA609684	AA609684	Hs.112748	Homo sapiens cDNA: FLJ21543 fis, clone COL06171
	123731	RC_AA609839	AA609839		gb:ae62f01.s1 Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:951481 3' similar to
20	130725	RC_AA609862	T98807	Hs.80248	RNA-binding protein gene with multiple splicing
	123800	RC_AA620423	AA620423	Hs.112862	EST
	123841	RC_AA620747	AA620747	Hs.112896	ESTs
	123929	RC_AA621364	AA621364	Hs.112981	ESTs
25	123978	RC_C20653	T89832	Hs.170278	ESTs
	133184	RC_D20085	AA001021	Hs.6685	thyroid hormone receptor interactor 8
	132835	RC_D20749	Z83844	Hs.5790	hypothetical protein dJ37E16.5
	132406	RC_D51285_s	AL133731	Hs.4774	Homo sapiens mRNA; cDNA DKFZp761C1712 (from clone DKFZp761C1712)
	128695	RC_D59972_i	NM_003478	Hs.101299	cullin 5
30	124028	RC_F04112_f	F04112		gb:HSC2JH062 normalized infant brain cDNA Homo sapiens cDNA clone c-2jh06 3', mRNA sequence.
	124057	RC_F13604	AA902384	Hs.73853	bone morphogenetic protein 2
	134899	RC_H01662	AI609045	Hs.321775	hypothetical protein DKFZp434D1428
	130973	RC_H05135_i	AI638418	Hs.78580	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1
35	124106	RC_H12245	H12245		gb:ym17a12.r1 Soares infant brain 1NIB Homo sapiens cDNA clone 3', mRNA sequence
	124136	RC_H22842	H22842	Hs.101770	EST
	124165	RC_H30894	H30039	Hs.107674	ESTs
	131229	RC_H43442_s	NM_015340	Hs.2450	leucyl-tRNA synthetase, mitochondrial
	124178	RC_H45996	BE463721	Hs.97101	putative G protein-coupled receptor
40	129948	RC_H69281_i	AI537162	Hs.263988	ESTs
	134374	RC_H69485_f	N22687	Hs.8236	ESTs
	124254	RC_H69899	H69899		gb:yu70c12.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:239158 3' similar to
	129056	RC_H70627_s	AI769958	Hs.108336	ESTs, Weakly similar to ALUE_HUMAN !!!! ALU CLASS E WARNING ENTRY !!! [H.sapiens]
45	100919	RC_H73050_s	X54534	Hs.278994	Rhesus blood group, CcEe antigens
	130724	RC_H73260	AK001507	Hs.306084	Homo sapiens clone FLB6914 PRO1821 mRNA, complete cds
	100716	RC_H77531_s	X89887	Hs.172350	HIR (histone cell cycle regulation defective, S. cerevisiae) homolog A
	124274	RC_H80552	H80552	Hs.102249	EST
	129078	RC_H80737_s	AI351010	Hs.102267	lysosomal
50	124828	RC_H93412	AW952124	Hs.13094	presenilins associated rhomboid-like protein
	124315	RC_H94892_s	NM_005402	Hs.288757	v-rat simian leukemia viral oncogene homolog A (ras related)
	100747	RC_H95643_s	X04588	Hs.85844	neurotrophic tyrosine kinase, receptor, type 1
	124324	RC_H96552	H96552	Hs.159472	Homo sapiens cDNA: FLJ22224 fis, clone HRC01703
	452933	RC_H97146	AW391423	Hs.288555	Homo sapiens cDNA: FLJ22425 fis, clone HRC08686
55	132231	RC_H99131_s	AA662910	Hs.42635	hypothetical protein DKFZp434K2435
	129170	RC_H99462_s	AW250380	Hs.109059	mitochondrial ribosomal protein L12
	133143	RC_H99837_s	AA094538	Hs.272808	putative transcription regulation nuclear protein; KIAA1689 protein
	132963	RC_N22140	AA099693	Hs.34851	epsilon-tubulin
	135297	RC_N22197	AL118782	Hs.300208	Sec23-interacting protein p125
60	134347	RC_N23756_s	AF164142	Hs.82042	solute carrier family 23 (nucleobase transporters), member 1
	130365	RC_N24134	W56119	Hs.155103	eukaryotic translation initiation factor 1A, Y chromosome
	421642	RC_N24195	AF172066	Hs.106346	retinoic acid repressible protein
	439311	RC_N26739	BE270668	Hs.151945	mitochondrial ribosomal protein L43
	124383	RC_N27098	N27098	Hs.102463	EST
65	124387	RC_N27637	N27637	Hs.109019	ESTs
	129341	RC_N33090	AI193519	Hs.226396	hypothetical protein FLJ11126
	129081	RC_N35957	AI364933	Hs.168913	serine/threonine kinase 24 (Ste20, yeast homolog)
	102827	RC_N38959_f	BE244588	Hs.6456	chaperonin containing TCP1, subunit 2 (beta)
	124433	RC_N39069	AA280319	Hs.288840	PRO1575 protein
70	124441	RC_N46441	AW450481	Hs.161333	ESTs
	132338	RC_N48270_f	AA353868	Hs.182982	golgin-67
	131403	RC_N48365_s	AI473114	Hs.26455	ESTs
	124466	RC_N51316	R10084	Hs.113319	kinesin heavy chain member 2
	132210	RC_N51499_s	NM_007203	Hs.42322	A kinase (PRKA) anchor protein 2
75	124483	RC_N53976	AI821780	Hs.179864	ESTs
	124484	RC_N54157	H66118	Hs.285520	ESTs, Weakly similar to 2109260A B cell growth factor [H.sapiens]
	124485	RC_N54300	AB040933	Hs.15420	KIAA1500 protein

	124494	RC_N54831	N54831	Hs.271381	ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]
	129200	RC_N59849	N59849	Hs.13565	Sam68-like phosphotyrosine protein, T-STAR
	124527	RC_N62132	N79264	Hs.269104	ESTs
5	124532	RC_N62375	N62375	Hs.102731	EST
	133213	RC_N63138	AA903424	Hs.6786	ESTs
	124539	RC_N63172	D54120	Hs.146409	cell division cycle 42 (GTP-binding protein, 25kD)
	133651	RC_N63772	AI301740	Hs.173381	dihydropyrimidinase-like 2
	129196	RC_N63787	BE296313	Hs.265592	ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]
10	124575	RC_N68168	N68168		gb:za11c01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone 3', mRNA sequence
	124576	RC_N68201	N68201	Hs.269124	ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]
	124577	RC_N68300	N68300		gb:za12g07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:292380 3', mRNA
	124578	RC_N68321	N68321	Hs.231500	EST
15	124593	RC_N69575	N69575	Hs.102788	ESTs
	128501	RC_N75007	AL133572	Hs.199009	protein containing CXXC domain 2
	105691	RC_N75542	AI680737	Hs.289068	Homo sapiens cDNA FLJ11918 fis, clone HEMBB1000272
	128473	RC_N90066	T78277	Hs.100293	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-CGI-47 protein
	128639	RC_N91246	AW582962	Hs.102897	regulator of nonsense transcripts 2; DKFZP434D222 protein
20	124652	RC_N92751	W19407	Hs.3862	KIAA0318 protein
	133137	RC_N93214_s	AB002316	Hs.65746	Homo sapiens cDNA FLJ10495 fis, clone NT2RP2000297, moderately similar to ZINC FINGER
	124671	RC_N99148	AK001357	Hs.102951	ESTs, Weakly similar to T27173 hypothetical protein Y54G11A.9 - Caenorhabditis elegans
	133054	RC_R07876	AA464836	Hs.291079	ESTs, Weakly similar to T27173 hypothetical protein Y54G11A.9 - Caenorhabditis elegans
25	130410	RC_R10865_f	J00077	Hs.155421	alpha-fetoprotein
	124720	RC_R11056	R05283		gb:ye91c08.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:125102 3' similar to
	124722	RC_R11488	T97733	Hs.185685	ESTs
30	129961	RC_R22947	R23053		gb:yh31a05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone 5' similar to contains L1
	132965	RC_R26589_f	AI248173	Hs.191460	Hs.52763 anaphase-promoting complex subunit 7
	133740	RC_R37588_s	AW162919	Hs.170160	hypothetical protein MGC12936
	133074	RC_R37613	AL134275	Hs.6434	RAB2, member RAS oncogene family-like
	124757	RC_R38398	H11368	Hs.141055	hypothetical protein DKFZp761F2014
35	124762	RC_R39179_f	AA553722	Hs.92096	Homo sapiens clone 23758 mRNA sequence
	124773	RC_R40923	R45154	Hs.106604	ESTs, Moderately similar to A46010 X-linked retinopathy protein [H.sapiens]
	135266	RC_R41179	R41179	Hs.97393	ESTs
	131375	RC_R41294_s	AW293165	Hs.143134	KIAA0328 protein
40	133753	RC_R42307_f	NM_004427	Hs.165263	ESTs
	128540	RC_R43189_f	AW297929	Hs.328317	early development regulator 2 (homolog of polyhomeotic 2)
	124785	RC_R43306	W38537	Hs.280740	EST
	124792	RC_R44357	R44357	Hs.48712	hypothetical protein MGC3040
	124793	RC_R44519	R44519		hypothetical protein FLJ20736
45	124799	RC_R45088	R45088		gb:yg24h04.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:33350 3', mRNA sequence.
	124812	RC_R47948_i	R47948	Hs.188732	gb:yg38g04.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:34896 3', mRNA sequence.
	124821	RC_R51524	H87832	Hs.7388	ESTs
50	127274	RC_R54950	AW966158	Hs.58582	kelch (Drosophila)-like 3
	124835	RC_R55241	R55241	Hs.101214	Homo sapiens cDNA FLJ12789 fis, clone NT2RP2001947
	124845	RC_R59585	R59585	Hs.101255	EST
	124847	RC_R60044	W07701	Hs.304177	ESTs
55	440630	RC_R60872	BE561430	Hs.239388	Homo sapiens clone FLB8503 PRO2286 mRNA, complete cds
	124861	RC_R66690	R67567	Hs.107110	Human DNA sequence from clone RP1-304B14 on chromosome 6. Contains a gene for a novel protein and a part of a gene for a novel protein with two isoforms. Contains ESTs, STSs, GSSs and a CpG island
	130141	RC_R67266_s	NM_004455	Hs.150956	ESTs
	124879	RC_R73588	R73588	Hs.101533	exostoses (multiple)-like 1
	124892	RC_R79403	AI970003	Hs.23756	ESTs
60	124906	RC_R87647	H75964	Hs.107815	hypothetical protein similar to swine acylneuraminase lyase
	124922	RC_R93622	R93622	Hs.12163	ESTs
	124940	RC_R99599_s	AF068846	Hs.103804	eukaryotic translation initiation factor 2, subunit 2 (beta, 38kD)
	124941	RC_R99612	AI766661	Hs.27774	heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)
	124943	RC_T02888	AW963279	Hs.123373	ESTs, Highly similar to AF161349 1 HSPC086 [H.sapiens]
65	124947	RC_T03170	T03170	Hs.100165	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION
	124954	RC_T10465	AW964237	Hs.6728	ESTs
	132924	RC_T15418_f	U55184	Hs.154145	KIAA1548 protein
	133113	RC_T15597_f	BE383768	Hs.65238	hypothetical protein FLJ11585
70	132975	RC_T15652_i	R43504	Hs.6181	95 kDa retinoblastoma protein binding protein; KIAA0661 gene product
	133235	RC_T16898_s	AW960782	Hs.6856	ESTs
	131082	RC_T26644_i	AI091121	Hs.246218	ash2 (absent, small, or homeotic, Drosophila, homolog)-like
	124980	RC_T40841	T40841	Hs.98681	Homo sapiens cDNA: FLJ21781 fis, clone HEP00223
	124984	RC_T47566_i	BE313210	Hs.223241	ESTs
75	124991	RC_T50116	T50116		eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)
	129475	RC_T50145_s	NM_004477	Hs.203772	gb:yb77c10.s1 Stratagene ovary (937217) Homo sapiens cDNA clone IMAGE:77202 3' similar to similar to SP:VE22_LAMBD P03756 EA22 GENE, mRNA sequence.
					F5HD region gene 1

	125000	RC_T58615	T58615	Hs.110640	ESTs
	132932	RC_T59940_f	AW118826	Hs.6093	Homo sapiens cDNA: FLJ22783 fis, clone KAIA1993
	129534	RC_T63595	AK002126	Hs.11260	hypothetical protein FLJ11264
5	125008	RC_T64891	T91251		gb:yd60a10.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone 3', mRNA sequence
	125009	RC_T64924	T64924	Hs.303046	ESTs
	132940	RC_T64933_r	T79136	Hs.127243	Homo sapiens mRNA for KIAA1724 protein, partial cds
	125017	RC_T68875	T68875		gb:yc30f05.s1 Stratagene liver (937224) Homo sapiens cDNA clone IMAGE:82209 3', mRNA sequence.
10	125018	RC_T69027	T69027	Hs.57475	sex comb on midleg homolog 1
	125020	RC_T69924	T69981		gb:yc19d03.r1 Stratagene lung (937210) Homo sapiens cDNA clone 5', mRNA sequence
	129891	RC_T70353	AI084813	Hs.13197	ESTs
	134204	RC_T79780_s	AI873257	Hs.7994	hypothetical protein FLJ20551
	125050	RC_T79951	AW970209	Hs.111805	ESTs
15	125052	RC_T80174_s	T85104	Hs.222779	ESTs, Moderately similar to similar to NEDD-4 [H.sapiens]
	125054	RC_T80622	T80622	Hs.268601	ESTs, Weakly similar to envelope [H.sapiens]
	125063	RC_T85352	T85352		gb:yd82d01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:114721 3'
					similar to contains Alu repetitive element; contains L1 repetitive element ;, mRNA sequence.
	125064	RC_T85373	T85373		gb:yd82f07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:114757 3'
20					similar to contains Alu repetitive element; contains MER3 repetitive element ;, mRNA sequence.
	125066	RC_T86284	T86284		gb:yd77b07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone 3' similar to contains
					Alu repetitive element; mRNA sequence
	112264	RC_T89579_s	AL045364	Hs.79353	transcription factor Dp-1
	125080	RC_T90360	T90360	Hs.268620	ESTs, Highly similar to ALU6_HUMAN ALU SUBFAMILY SP SEQUENCE CONTAMINATION
25					WARNING ENTRY [H.sapiens]
	125097	RC_T94328_i	AW576389	Hs.335774	EST, Moderately similar to S65657 alpha-1C-adrenergic receptor splice form 2 [H.sapiens]
	125104	RC_T95590	T95590		gb:ye40a03.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone 3' similar to
					gb M10817 IGURRAA Iguana Iguana 5S (rRNA);, mRNA sequence
30	135107	RC_T97257_f	T97257	Hs.337531	ESTs, Moderately similar to I38022 hypothetical protein [H.sapiens]
	129550	RC_T97599_i	AA845462	Hs.124024	deltex (Drosophila) homolog 1
	125118	RC_T97620	R10606		gb:y35f11.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:128877 3'
					similar to contains Alu repetitive element; mRNA sequence.
	125120	RC_T97775	T97775	Hs.100717	EST
35	134160	RC_T98152	T98152	Hs.79432	fibrillin 2 (congenital contractural arachnodactyly)
	125136	RC_W31479	AW962364	Hs.129051	ESTs
	125144	RC_W37999	AB037742	Hs.24336	KIAA1321 protein
	125150	RC_W38240	W38240		Empirically selected from AFFX single probeset
	104180	RC_W40150	AA247778	Hs.119155	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 814975
	131987	RC_W45435	AW453069	Hs.3657	activity-dependent neuroprotective protein
40	125178	RC_W58202	W93127	Hs.31845	ESTs
	125180	RC_W58344	W58469	Hs.103120	ESTs
	125182	RC_W58650	AA451755	Hs.263560	ESTs
	130588	RC_W68736	AL030996	Hs.16411	hypothetical protein LOC57187
	125197	RC_W69106	AF086270	Hs.278554	heterochromatin-like protein 1
45	133497	RC_W69111	BE617303	Hs.74266	hypothetical protein MGC4251
	100562	RC_W69385_s	NM_006185	Hs.301512	nuclear mitotic apparatus protein 1
	125639	RC_W69399_s	Z97630	Hs.226117	H1 histone family, member 0
	129232	RC_W69459	R98881	Hs.109655	sex comb on midleg (Drosophila)-like 1
	101495	RC_W72424	W72424	Hs.112405	S100 calcium-binding protein A9 (calgranulin B)
50	125209	RC_W72724	W72724	Hs.103174	ESTs, Weakly similar to TSP2_HUMAN THROMBOSPONDIN 2 PRECURSOR [H.sapiens]
	125212	RC_W72834	AA746225	Hs.103173	ESTs
	129132	RC_W73955	BE383436	Hs.108847	hypothetical protein MGC2749
	125223	RC_W74701	AI916269	Hs.109057	ESTs, Weakly similar to ALU5_HUMAN ALU SUBFAMILY SC SEQUENCE CONTAMINATION
					WARNING ENTRY [H.sapiens]
55	125225	RC_W76540	W74169	Hs.16492	DKFZP564G2022 protein
	125228	RC_W79397	AA033982	Hs.110059	ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]
	132393	RC_W85888	AL135094	Hs.47334	hypothetical protein FLJ14495
	125238	RC_W86038	N99713	Hs.109514	ESTs
	125247	RC_W86881	AA694191	Hs.163914	ESTs
60	129296	RC_W87804	AI051967	Hs.110122	ESTs
	125263	RC_W88942	AA098878		gb:zn45g10.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone 5', mRNA sequence
	125266	RC_W90022	W90022	Hs.186809	ESTs, Highly similar to LCT2_HUMAN LEUKOCYTE CELL-DERIVED CHEMOTAXIN 2
					PRECURSOR [H.sapiens]
	131321	RC_W92272	U91543	Hs.25601	chromodomain helicase DNA binding protein 3
65	131601	RC_W92764_s	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced protein 6
	131677	RC_W93040	H05317	Hs.283549	ESTs
	120837	RC_W93092	BE149656	Hs.306621	Homo sapiens cDNA FLJ11963 fis, clone HEMBB1001051
	125277	RC_W93227	W93227	Hs.103245	EST
	125278	RC_W93523	AI218439	Hs.129998	enhancer of polycomb 1
70	125280	RC_W93659	AI123705	Hs.106932	ESTs
	131856	RC_W94003_s	W93949	Hs.33245	ESTs
	131844	RC_W94401_s	AI419294	Hs.324342	ESTs
	125284	RC_W94688	NM_002666	Hs.103253	perlepin
	313447	RC_W94787_s	AW016321	Hs.82306	destrin (actin depolymerizing factor)
75	130799	RC_Z38294_s	AB028945	Hs.12696	cortactin SH3 domain-binding protein
	125289	RC_Z38311	T34530	Hs.4210	Homo sapiens cDNA FLJ13069 fis, clone NT2RP3001752
	128874	RC_Z38465_s	H06245	Hs.106801	ESTs, Weakly similar to PC4259 ferritin associated protein [H.sapiens]

5	130966	RC_Z38525_s	AW971018	Hs.21659	ESTs
	128875	RC_Z38538_f	AB040923	Hs.106808	kelch (Drosophila)-like 1
	133200	RC_Z38551_s	AB037715	Hs.183639	hypothetical protein FLJ10210
	130158	RC_Z38783_s	AB032947	Hs.151301	Ca2+-dependent activator protein for secretion
	125295	RC_Z39113	AB022317	Hs.25887	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4F
	125298	RC_Z39255_f	AW972542	Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone HEP01068
	125300	RC_Z39591	Z39591	Hs.101376	EST
10	323122	RC_Z39783_s	BE622770	Hs.264915	Homo sapiens cDNA FLJ12908 fis, clone NT2RP2004399
	311463	RC_Z39920	R55344	Hs.22142	cytochrome b5 reductase b5R.2
	130882	RC_Z40166_f	AA497044	Hs.20887	hypothetical protein FLJ10392
	128888	RC_Z40388_s	AI760853	Hs.241558	ariadne (Drosophila) homolog 2
	125310	RC_Z40646	R59161	Hs.124953	ESTs
15	125315	RC_Z41697	R38110	Hs.106296	ESTs
	125317	RC_Z99349	Z99348	Hs.112461	ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]
	135096	RC_Z99394_s	AA081258	Hs.132390	zinc finger protein 36 (KOX 18)
	104786	RC_AA027168	AA027167	Hs.10031	KIAA0955 protein
	132837	D58024_s	AA370362	Hs.57958	EGF-TM7-latrophilin-related protein
20	120456	RC_AA251113	AA488750	Hs.88414	BTB and CNC homology 1, basic leucine zipper transcription factor 2
	132459	RC_AA347573	AL120071	Hs.48998	fibronectin leucine rich transmembrane protein 2
	101545	M31210	BE246154	Hs.154210	endothelial differentiation, sphingolipid G-protein-coupled receptor, 1
	133505	C01527	AI630124	Hs.324504	Homo sapiens mRNA; cDNA DKFZp586J0720 (from clone DKFZp586J0720)
	132360	RC_N62948_s	AW893660	Hs.46440	solute carrier family 21 (organic anion transporter), member 3
25	132738	RC_W42674	AK000738	Hs.264636	hypothetical protein FLJ20731
	119586	RC_W43000_s	AF088033	Hs.159225	ESTs
	129914	RC_N31750_s	NM_012421	Hs.13321	rearranged L-myc fusion sequence
	130839	AF009301	AB011169	Hs.20141	similar to S. cerevisiae SSM4
	132813	L37347	BE313625	Hs.57435	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2
30	134342	M99564	NM_000275	Hs.82027	oculocutaneous albinism II (pink-eye dilution (murine) homolog)
	131878	RC_AA430673	AA083764	Hs.6101	hypothetical protein MGC3178
	105426	RC_AA251297	W20027	Hs.23439	ESTs
	132968	RC_AA620722	AF234532	Hs.61638	myosin X
	132173	RC_W46577_s	X89426	Hs.41716	endothelial cell-specific molecule 1
35	113932	RC_W81237	AA256444	Hs.126485	hypothetical protein FLJ12604; KIAA1692 protein
	114452	RC_AA020825	AI369275	Hs.243010	Homo sapiens cDNA FLJ14445 fis, clone HEMBB1001294, highly similar to GTP-BINDING PROTEIN TC10
	115243	RC_AA278766	AA806600	Hs.116665	KIAA1842 protein
	134403	RC_H93708_s	AA334551	Hs.82767	sperm specific antigen 2
40	129647	RC_N49394	AB018259	Hs.118140	KIAA0716 gene product
	111428	RC_H56559_s	AL031428	Hs.174174	KIAA0601 protein
	115967	RC_AA446887	AI745379	Hs.42911	ESTs
	120726	RC_AA293656	AA293655	Hs.97293	ESTs
	114995	RC_AA251152	AA769266	Hs.193657	ESTs
45	303876	RC_AA233334_s	U64820	Hs.66521	Machado-Joseph disease (spinocerebellar ataxia 3, olivopontocerebellar ataxia 3, autosomal dominant, ataxin 3)
	311463	RC_Z39920	R55344	Hs.22142	cytochrome b5 reductase b5R.2
	120302	RC_AA192173	AA837098	Hs.269933	ESTs
	133071	RC_AA455044	BE384932	Hs.64313	ESTs, Weakly similar to AF257182 1 G-protein-coupled receptor 48 [H.sapiens]
50	121032	RC_AA398504	AA393037	Hs.161798	ESTs
	129829	U41813	AF010258	Hs.127428	homeo box A9
	120245	RC_AA166965	AW959615	Hs.111045	ESTs
	120985	RC_AA398222	AI219896	Hs.97592	ESTs
	114184	RC_Z39095	R56434	Hs.21062	ESTs
55	447503	RC_AA284744_f	AA115496	Hs.336898	Homo sapiens, Similar to RIKEN cDNA 1810038N03 gene, clone MGC:9890, mRNA, complete cds
	132837	RC_AA428201	AA370362	Hs.57958	EGF-TM7-latrophilin-related protein
	121034	RC_AA398507	AL389951	Hs.271623	nucleoporin 50kD
	119718	RC_W69216	W69216	Hs.92848	ESTs
60	120455	RC_AA251083	AA251720	Hs.104347	ESTs, Weakly similar to ALUC_HUMAN !!!! ALU CLASS C WARNING ENTRY !!! [H.sapiens]
	125280	RC_W93659	AI123705	Hs.106932	ESTs
	132155	RC_AA227903	AK001607	Hs.41127	hypothetical protein FLJ13220
	120609	RC_AA283902	AW978721	Hs.266076	ESTs, Weakly similar to A46010 X-linked retinopathy protein [H.sapiens]
	121278	RC_AA401631	AA037121	Hs.98518	Homo sapiens cDNA FLJ11490 fis, clone HEMBA1001918
65	109023	RC_AA157293	AA157293	Hs.72168	ESTs
	129815	RC_D60208_f	BE565817	Hs.26498	hypothetical protein FLJ21657
	108061	RC_AA043979	AA043979	Hs.62651	EST
	113287	RC_T66847	T66847	Hs.194040	ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]
	114082	RC_Z38239	AK001612	Hs.26962	Homo sapiens cDNA FLJ10750 fis, clone NT2RP3001929
70	116334	RC_AA491457	AL038450	Hs.48948	ESTs
	131486	RC_Z40071_s	F06972	Hs.27372	BMX non-receptor tyrosine kinase
	107860	RC_AA024961	AA024961	Hs.50730	ESTs
	131263	RC_AA443826	AU077002	Hs.24950	regulator of G-protein signalling 5
	132207	RC_AA443294	BE206939	Hs.42287	E2F transcription factor 6
75	129183	RC_AA155743	BE561824	Hs.273369	uncharacterized hematopoietic stem/progenitor cells protein MDS027
	408431	RC_T23708	AI338631	Hs.43266	Homo sapiens cDNA: FLJ22536 fis, clone HRC13155
	120575	RC_AA280934	AW978022	Hs.238911	hypothetical protein DKFZp762E1511; KIAA1816 protein

	132121	RC_AA443284_s	NM_004529	Hs.404	myeloid/lymphoid or mixed-lineage leukemia (trithorax (<i>Drosophila</i>) homolog); translocated to, 3
	117657	RC_N39074	N39074	Hs.44933	ESTs
	134922	RC_W04507_s	A1718295	Hs.91161	prefoldin 4
5	118523	RC_R41828_s	Y07759	Hs.170157	myosin VA (heavy polypeptide 12, myosin)
	116845	RC_H64973	AA649530		gb:ns44f05.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone, mRNA sequence
	115291	RC_AA279943	BE545072	Hs.122579	hypothetical protein FLJ10461
	120326	RC_AA196300	AA196300	Hs.21145	hypothetical protein RG083M05.2
	130174	M29550	M29551	Hs.151531	protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform (calcineurin A beta)
10	129131	RC_AA436489	AB026436	Hs.177534	dual specificity phosphatase 10
	129868	RC_AA287032	AW172431	Hs.13012	ESTs
	118661	RC_N70777	AL137554	Hs.49927	protein kinase NYD-SP15
	129829	RC_AA496921	AF010258	Hs.127428	homeo box A9
	115985	RC_AA447709	AA447709	Hs.268115	ESTs, Weakly similar to T08599 probable transcription factor CA150 [H.sapiens]
15	134637	RC_AA369856_s	U87309	Hs.180941	vacuolar protein sorting 41 (yeast homolog)
	132714	RC_AA252598	W39388	Hs.55336	Homo sapiens, clone MGC:17421, mRNA, complete cds
	129771	RC_H73237	AL096748	Hs.102708	DKFZP434A043 protein
	123360	RC_AA504784	AA532718	Hs.178604	ESTs
	132902	RC_AA490969	AI936442	Hs.59838	hypothetical protein FLJ10808
20	113716	RC_T97750	AA001356	Hs.18159	ESTs
	113825	RC_W48860	AW014486	Hs.22509	ESTs
	130367	RC_Z38501	AL135301	Hs.8768	hypothetical protein FLJ10849
	120541	RC_AA278298	W07318	Hs.240	M-phase phosphoprotein 1
	116727	RC_F13684	R76472	Hs.65646	ESTs
25	118219	RC_N62231	AA862391	Hs.48494	ESTs, Moderately similar to A46010 X-linked retinopathy protein [H.sapiens]
	119767	RC_W72562	W72562	Hs.58119	ESTs
	128917	RC_AA481252	AI365215	Hs.206097	oncogene TC21
	451553	RC_AA020928	AA018454	Hs.269211	ESTs
	132716	RC_AA251288	BE379595	Hs.283738	casein kinase 1, alpha 1
30	118525	RC_N67861	N67861	Hs.49390	ESTs
	114618	RC_AA084162	AW979261	Hs.291993	ESTs
	119743	RC_W70242	AA947552	Hs.58086	ESTs
	108154	RC_AA425151_s	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain-binding protein
	122798	RC_AA460324	AW366286	Hs.145696	splicing factor (CC1.3)
35	133746	U44378	AW410035	Hs.75862	MAD (mothers against decapentaplegic, <i>Drosophila</i>) homolog 4
	119822	RC_W74471	AF086409	Hs.301327	ESTs
	122186	RC_AA435842	AA398811	Hs.104673	ESTs
	114941	RC_AA243017	AA236512	Hs.87331	ESTs
	118053	RC_N53367	N53391	Hs.47629	ESTs
40	123234	RC_AA490227	NM_001938	Hs.16697	down-regulator of transcription 1, TBP-binding (negative cofactor 2)
	129280	M63154	M63154	Hs.110014	gastric intrinsic factor (vitamin B synthesis)
	118995	RC_N94591	N94591	Hs.323056	ESTs
	116750	RC_H05960	AA760689	Hs.92418	ESTs
	129026	M98833	AL120297	Hs.108043	Friend leukemia virus integration 1
45	105127	RC_AA158132	AA045648	Hs.301957	nudix (nucleoside diphosphate linked moiety X)-type motif 5
	114513	RC_AA044825	AA044873	Hs.103446	ESTs
	411856	RC_T35697	H67899	Hs.4190	Homo sapiens cDNA: FLJ23269 fis, clone COL09533
	132036	W01568	AL157433	Hs.37706	hypothetical protein DKFZp434E2220
	130091	RC_W88999	W88999		gb:zh70h03.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone 3', mRNA sequence
50	414108	U09564	AI267592	Hs.75761	SFRS protein kinase 1
	119881	RC_W81456	W81486	Hs.58648	ESTs
	117770	RC_N47953	AW957372	Hs.46791	ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]
	119850	RC_W80447	AI247568	Hs.58452	ESTs
55	115439	RC_AA284561	AI567972	Hs.193090	ESTs, Highly similar to AF161437 1 HSPC319 [H.sapiens]
	123107	RC_AA486071	AA225048	Hs.104207	ESTs
	406698	M24364	X03068	Hs.73931	major histocompatibility complex, class II, DQ beta 1
	121231	RC_AA400780	AA814948	Hs.96343	ESTs, Weakly similar to ALUC_HUMAN !!!! ALU CLASS C WARNING ENTRY !!! [H.sapiens]
	132074	AB002366	AA478486	Hs.3852	KIAA0368 protein
60	413670	AB000115	AB000115	Hs.75470	hypothetical protein, expressed in osteoblast
	125277	RC_W93227	W93227	Hs.103245	EST
	114056	RC_AA186324	AA188175	Hs.82506	KIAA1254 protein
	121153	RC_AA399640	AA399640	Hs.97694	ESTs
	121609	RC_AA416867	AA416867	Hs.98185	EST
65	120661	RC_AA287556	AA287556	Hs.263412	ESTs, Weakly similar to ALUB_HUMAN !!!! ALU CLASS B WARNING ENTRY !!! [H.sapiens]
	120850	RC_AA349647	AA349647	Hs.96927	Homo sapiens cDNA FLJ12573 fis, clone NT2RM000979
	124947	RC_T03170	T03170	Hs.100165	ESTs
	130529	RC_AA280886	AA178953		gb:zp39e03.s1 Stratagene muscle 937209 Homo sapiens cDNA clone 3' similar to contains Alu
	117683	RC_N40180	N40180		gb:yy44d02.s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone
70	IMAGE:276387	3' similar to contains L1.11	L1 repetitive element		sequence.
	120745	RC_AA302809	AA302809		gb:EST10426 Adipose tissue, white I Homo sapiens cDNA 3' end, mRNA sequence.
	120936	RC_AA385934	AA385934	Hs.97184	EST, Highly similar to (define not available 7499603) [C.elegans]
	112597	RC_R78376	R78376	Hs.29733	EST
	120183	RC_Z40174	AW082866	Hs.65882	ESTs
75	120644	RC_AA287038	AI869129	Hs.96616	ESTs

	119023	RC_N98488	N98488		gb:zb82h01.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone
		IMAGE:310129 3', mRNA sequence.			
	107582	RC_AA002147	AA002147	Hs.59952	EST
5	118249	RC_N62580	N62580	Hs.322925	EST, Weakly similar to putative p150 [H.sapiens]
	115022	RC_AA252029	AA252029	Hs.87935	ESTs
	117710	RC_N45198	N45198	Hs.47248	ESTs, Highly similar to similar to Cdc14B1 phosphatase [H.sapiens]
	115341	RC_AA281452	AA281452	Hs.88840	EST, Weakly similar to granule cell marker protein [M.musculus]
	118896	RC_N90680	N90680	Hs.54642	methionine adenosyltransferase II, beta
10	121121	RC_AA399371	AA399371	Hs.189095	similar to SALL1 (sal (Drosophila)-like
	118329	RC_N63520	N63520		gb:yy62f01.s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:278137
		3', mRNA sequence.			
	119496	RC_W35416	W35416	Hs.156861	ESTs, Moderately similar to A46010 X-linked retinopathy protein [H.sapiens]
	118111	RC_N55493	N55493		gb:yy50c02.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:246146 3',
		mRNA sequence.			
15	119062	RC_R16698	AW444881	Hs.77829	ESTs
	116710	RC_F10577_f	F10577	Hs.306088	v-crk avian sarcoma virus CT10 oncogene homolog
	119261	RC_T15956	T15956	Hs.65289	EST
	122723	RC_AA457380	AA457380		gb:aa86b10.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838171 3'
		similar to contains L1.b3 L1 repetitive element ;, mRNA sequence.			
20	117732	RC_N46452	N46452		gb:yy76h09.s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone
		IMAGE:279521 3' similar to contains L1.t2 L1 repetitive element ;, mRNA sequence.			
	104787	RC_AA027317	AA027317		gb:ze97d11.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:366933 3'
		similar to contains Alu repetitive element ;, mRNA sequence.			
25	100071	A28102	A28102		Human GABAA receptor alpha-3 subunit
	115819	RC_AA426573	AA486620	Hs.41135	endomucin-2
	130882	RC_Z40166_f	AA497044	Hs.20887	hypothetical protein FLJ10392
	125225	RC_W76540	W74169	Hs.16492	DKFZP564G2022 protein
	108339	RC_AA070801	AW151340	Hs.51615	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION
		WARNING ENTRY [H.sapiens]			
30	100338	D63483	D86864	Hs.57735	acetyl LDL receptor; SREC
	121636	RC_AA417027	AA379203	Hs.306654	Homo sapiens cDNA FLJ13574 fis, clone PLACE1008625
	103875	RC_AA418387	T26379	Hs.48802	Homo sapiens clone 23632 mRNA sequence
	118716	RC_N73460	AI658908	Hs.118722	fucosyltransferase 8 (alpha (1,6) fucosyltransferase)
35	119763	RC_W72450	R54146	Hs.10450	Homo sapiens cDNA: FLJ22063 fis, clone HEP10326
	121917	RC_AA428218	AA406397	Hs.98038	ESTs
	132806	M91488	AI699432	Hs.278619	hypothetical protein FLJ10099
	130949	Y10659	AV656840	Hs.285115	interleukin 13 receptor, alpha 1
	108806	RC_AA129933	AF070578	Hs.71168	Homo sapiens clone 24674 mRNA sequence
40	133276	RC_AA490478	AW978439	Hs.69504	ESTs
	134760	RC_H16758	NM_000121	Hs.89548	erythropoietin receptor
	132867	AA121287	AF226667	Hs.58553	CTP synthase II
	132051	AA091284	AA393968	Hs.180145	HSPC030 protein
	114208	RC_Z39301	AL049466	Hs.7859	ESTs
45	104094	AA418187	AA418187	Hs.330515	ESTs
	128718	AA426361	NM_002959	Hs.281706	sortilin 1
	302032	RC_N20407	NM_001992	Hs.128087	coagulation factor II (thrombin) receptor
	115501	RC_AA291553	AA291553	Hs.190086	ESTs
	101997	U01160	AU076536	Hs.50984	sarcoma amplified sequence
50	103708	AA037206	AA430591	Hs.72071	hypothetical protein FLJ20038
	101899	S59184	S59184	Hs.79350	RYK receptor-like tyrosine kinase
	115839	RC_AA429038	BE300266	Hs.28935	transducin-like enhancer of split 1, homolog of Drosophila E(sp1)
	409459	D50678	D86407	Hs.54481	low density lipoprotein receptor-related protein 8, apolipoprotein e receptor
	103563	Z22534	L02911	Hs.150402	Activin A receptor, type I (ACVR1) (ALK-2)
55	123233	RC_AA490225	AW974175	Hs.188751	ESTs, Weakly similar to MAPB_HUMAN MICROTUBULE-ASSOCIATED PROTEIN 1B
		[H.sapiens]			
	121305	RC_AA402468	AA402468	Hs.291557	ESTs
	114798	RC_AA159181	AA159181	Hs.54900	serologically defined colon cancer antigen 1
	133145	RC_AA196549	H94227	Hs.6592	Homo sapiens, clone IMAGE:2961368, mRNA, partial cds
60	131567	RC_AA291015_s	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisiae, homolog)-like 1
	112300	RC_R54554	H24334	Hs.26125	ESTs
	129507	RC_AA192099	AJ236885	Hs.112180	zinc finger protein 148 (pH2-52)
	121033	RC_AA398505	AA398505	Hs.97360	ESTs
	121151	RC_AA399636	AA399636	Hs.143629	ESTs
65	121402	RC_AA406063	AA406063	Hs.98003	ESTs
	123203	RC_AA489671	AA352335	Hs.65641	hypothetical protein FLJ20073
	132271	RC_AA236466	AB030034	Hs.115175	sterile-alpha motif and leucine zipper containing kinase AZK
	125197	RC_W69106	AF086270	Hs.278554	heterochromatin-like protein 1
	114935	RC_AA242809	H23329	Hs.290880	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION
		WARNING ENTRY [H.sapiens]			
70	125279	RC_W93640	AW401809	Hs.4779	KIAA1150 protein
	108778	RC_AA128548	AF133123	Hs.90847	general transcription factor IIIC, polypeptide 3 (102kD)
	108087	RC_AA045709	AA045708	Hs.40545	ESTs
	132466	RC_N66810_s	AI597655	Hs.49265	ESTs
75	133328	R36553	AW452738	Hs.265327	hypothetical protein DKFZp7611141
	124057	RC_F13604	AA902384	Hs.73853	bone morphogenetic protein 2
	124800	RC_R45115	AW864086	Hs.138617	thyroid hormone receptor interactor 12

	121029	RC_AA398482	AA398482	Hs.97641	EST
	120663	RC_AA287627	AA827798	Hs.105089	ESTs
	102133	U15173	AU076845	Hs.155596	BCL2/adenovirus E1B 19kD-interacting protein 2
5	108246	RC_AA062855	AA23132	Hs.146343	ESTs
	125226	RC_W78134	AA782536	Hs.122647	N-myristoyltransferase 2
	120260	RC_AA171739	AK000061	Hs.101590	hypothetical protein
	124906	RC_R87647	H75964	Hs.107815	ESTs
	109406	RC_AA226877	AA199883	Hs.67624	ESTs
	109271	RC_AA195668	AW137422	Hs.86022	ESTs
10	125052	RC_T80174_s	T85104	Hs.222779	ESTs, Moderately similar to similar to NEDD-4 [H.sapiens]
	109101	RC_AA167708	AW608930	Hs.52184	hypothetical protein FLJ20618
	115241	RC_AA278723	AA648278	Hs.193859	ESTs
	117163	RC_H97909	N36861	Hs.42344	ESTs
	113530	RC_T90313	T90313	Hs.16732	ESTs
15	120375	RC_AA227260	AF028706	Hs.111227	Zic family member 3 (odd-paired Drosophila homolog, heterotaxy 1)
	129435	AA314256	AF151852	Hs.111449	CGI-94 protein
	114864	RC_AA235256	AA135332	Hs.71608	ESTs
	103988	AA314389	AA314389	Hs.42500	ADP-ribosylation factor-like 5
	131006	RC_AA242763	AF064104	Hs.22116	CDC14 (cell division cycle 14, S. cerevisiae) homolog B
20	106781	RC_AA478474	AA330310	Hs.24181	ESTs
	106141	RC_AA424558	AF031463	Hs.9302	phosducin-like
	116213	RC_AA476738	AA292105	Hs.326740	hypothetical protein MGC10947
	135266	AB002326	R41179	Hs.97393	KIAA0328 protein
	135058	RC_AA430152	AI379720	Hs.93814	hypothetical protein
25	119908	RC_W85844	AA524470	Hs.58753	ESTs
	103695	AA018758	AW207152	Hs.186600	ESTs
	103978	AA307443	NM_016940	Hs.34136	chromosome 21 open reading frame 6
	109485	RC_AA233472	BE619092	Hs.28465	Homo sapiens cDNA: FLJ21869 fis, clone HEP02442
	129574	AA458603	AA026815	Hs.11463	UMP-CMP kinase
30	115347	RC_AA281528	AA356792	Hs.334824	hypothetical protein FLJ14825
	120765	RC_AA338735	AW961026	Hs.96752	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION
	WARNING ENTRY [H.sapiens]				
	121059	RC_AA398628	AA393283		gb:zt74e03.r1 Soares_testis_NHT Homo sapiens cDNA clone 5', mRNA sequence
35	131887	AA046548	W17064	Hs.332848	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1
	112064	RC_R43812	AL049390	Hs.22689	Homo sapiens mRNA; cDNA DKFZp586O1318 (from clone DKFZp586O1318)
	115606	RC_AA400465	AI025829	Hs.86320	ESTs
	131750	RC_H94855_s	NM_004349	Hs.31551	core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related
40	102123	U14518	NM_001809	Hs.1594	centromere protein A (17kD)
	129847	RC_W46767	N64025	Hs.296178	hypothetical protein FLJ22637
	133809	RC_AA235275	AV649326	Hs.76359	catalase
	132210	RC_N51499_s	NM_007203	Hs.42322	A kinase (PRKA) anchor protein 2
	122356	RC_AA443794	AA443794	Hs.98390	ESTs
	114958	RC_AA243708	N20912	Hs.42369	ESTs
45	103951	AA287840	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (from clone DKFZp761J1112)
	134703	RC_AA280704	AF117065	Hs.88764	male-specific lethal-3 (Drosophila)-like 1
	128727	AA287864	AI223335	Hs.50651	Janus kinase 1 (a protein tyrosine kinase)
	105743	RC_AA293300_s	BE246502	Hs.9598	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic
50	domain, (semaphorin) 4B				
	103744	AA076003	AA079267		gb:zm97e10.s1 Stratagene colon HT29 (937221) Homo sapiens cDNA clone 3', mRNA sequence
	114348	N80402	AL050321	Hs.301532	CRP2 binding protein
	114009	RC_W90067	AI248544	Hs.103000	KIAA0831 protein
55	134704	RC_AA280849	AA837124	Hs.88780	ESTs
	128629	AA399187	AL096748	Hs.102708	DKFZP434A043 protein
	104410	H65925	AI807519	Hs.104520	Homo sapiens cDNA FLJ13694 fis, clone PLACE2000115
	110200	RC_H21075	H21075	Hs.31802	ESTs, Highly similar to A59266 unconventional myosin-15 [H.sapiens]
	124483	RC_N53976	AI821780	Hs.179864	ESTs
60	101391	M14648	NM_002210	Hs.295726	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)
	109657	RC_F04826	R60900	Hs.26814	ESTs
	117140	RC_H96813	H96813	Hs.42241	ESTs
	132937	RC_AA233706_f	AW952912	Hs.300383	hypothetical protein MGC3032
	129799	R36410	AW967473	Hs.239114	mannosidase, alpha, class 1A, member 2
	105077	RC_AA142919	W55946	Hs.234863	Homo sapiens cDNA FLJ12082 fis, clone HEMBB1002492
65	100850	RC_N58561_s	AA836472	Hs.297939	cathepsin B
	131043	RC_AA490925	AF084535	Hs.22464	epilepsy, progressive myoclonus type 2, Lafora disease (laforin)
	118417	RC_N66048_f	AF080229		gb:Human endogenous retrovirus K clone 10.1 polymerase mRNA, partial cds
	129254	RC_AA243695	AA252468	Hs.1098	DKFZp434J1813 protein
	119149	RC_R58910	BE304701	Hs.65732	ESTs
70	133996	AA091367	AA380267	Hs.78277	DKFZP434F2021 protein
	110223	RC_H23747	H19836	Hs.31697	ESTs
	117626	RC_N36090	AK001757	Hs.281348	hypothetical protein FLJ10895
	135286	RC_AA424469_s	AW023482	Hs.97849	ESTs
	122967	RC_AA478521	AA806187	Hs.289101	glucose regulated protein, 58kD
75	131236	AA282640	AF043117	Hs.24594	ubiquitination factor E4B (homologous to yeast UFD2)
	128568	AA463380	H12912	Hs.274691	adenylate kinase 3

	112888	RC_T03872	AW195317	Hs.107716	hypothetical protein FLJ22344
	115192	RC_AA261920	AA741024	Hs.88378	ESTs
	118688	RC_N71484	AK000708	Hs.169764	hypothetical protein FLJ20701
5	122264	RC_AA436837	AA436837		gb:zv57g07.s1 Soares_testis_NHT Homo sapiens cDNA clone 3', mRNA sequence
	128981	AA135452	AA927177	Hs.86041	CGG triplet repeat binding protein 1
	131042	RC_R42457	A1826288	Hs.171637	hypothetical protein MGC2628
	103704	AA028171	AA028171	Hs.151258	hypothetical protein FLJ21062
	121341	AA233107	AF035528	Hs.153863	MAD (mothers against decapentaplegic, Drosophila) homolog 6
10	106593	RC_AA456826	AW296451	Hs.24605	ESTs
	115195	RC_AA262156	AW968619	Hs.155849	ESTs
	115425	RC_AA284071	AA811895	Hs.180680	ESTs, Weakly similar to I54374 gene NF2 protein [H.sapiens]
	117258	RC_N21299	AF086041	Hs.42975	ESTs
	120209	RC_Z40892	F02951		gb:HSC1HB082 normalized infant brain cDNA Homo sapiens cDNA clone c-1hb08 3', mRNA sequence
15	134082	L16991	L16991	Hs.79006	deoxythymidylate kinase (thymidylate kinase)
	104774	RC_AA026066	AW959755	Hs.288896	Homo sapiens cDNA FLJ12977 fis, clone NT2RP2006261
	115625	RC_AA401630	AA059459	Hs.62592	ESTs
	104469	N28707	N28707	Hs.154304	Homo sapiens chromosome 19, BAC 282485 (CIT-B-344H19)
20	107401	W20054	N91453	Hs.102987	ESTs
	111686	RC_R21510	R22039	Hs.23217	ESTs
	115300	RC_AA280026	AA280095	Hs.88689	ESTs
	115378	RC_AA282292	AA282292	Hs.279841	hypothetical protein FLJ10335
	132224	RC_H97819	N41549	Hs.285410	ESTs
25	113791	M95767	A1269096	Hs.135578	chitinase, di-N-acetyl-
	129144	AA004987	AL137275	Hs.20137	hypothetical protein DKFZp434P0116
	104448	L44574	NM_007331	Hs.110457	Wolf-Hirschhorn syndrome candidate 1
	132084	RC_T26981_s	NM_002267	Hs.3886	karyopherin alpha 3 (importin alpha 4)
	111831	RC_R36083	R36095	Hs.268695	ESTs
30	114765	RC_AA252163	AA463550	Hs.337532	ESTs, Weakly similar to A47582 B-cell growth factor precursor [H.sapiens]
	115029	RC_AA252219	AL137939	Hs.40096	ESTs
	100457	H81492	BE246400	Hs.285176	acetyl-Coenzyme A transporter
	104536	R24011	R24024	Hs.158101	Homo sapiens cDNA FLJ14673 fis, clone NT2RP2003714, moderately similar to ZINC FINGER
	PROTEIN 91				
35	116167	RC_AA461562	A1091731	Hs.87293	hypothetical protein FLJ20045
	103889	AA236771	R85350	Hs.101368	ESTs
	131978	RC_H48459_s	AA355925	Hs.36232	KIAA0186 gene product
	118843	RC_N80181	N80181	Hs.221498	ESTs
	120837	RC_W93092	BE149656	Hs.306621	Homo sapiens cDNA FLJ11963 fis, clone HEMBB1001051
40	133647	D21852	NM_015361	Hs.268053	KIAA0029 protein
	129521	U41815	AF071076	Hs.112255	nucleoporin 98kD
	103746	AA081876	AA075000		gb:zm83c07.s1 Stratagene ovarian cancer (937219) Homo sapiens cDNA clone 3', mRNA sequence
	132019	RC_AA134965_i	H56995	Hs.37372	Homo sapiens DNA binding peptide mRNA, partial cds
45	132310	RC_AA284107	AA173223	Hs.289044	Homo sapiens cDNA FLJ12048 fis, clone HEMBB1001990
	117367	RC_N24954	A1041793	Hs.42502	ESTs
	103743	AA075998	AA075998		gb:zm89b09.r1 Stratagene ovarian cancer (937219) Homo sapiens cDNA clone 5' similar to
	gb:M15887 ACYL-COA-BINDING PROTEIN (HUMAN);, mRNA sequence				
	103761	AA085138	AA765163		gb:nz79b10.s1 NCL CGAP_GCB1 Homo sapiens cDNA clone 3' similar to gb:M34539 FK506-
	BINDING PROTEIN (HUMAN);, mRNA sequence				
50	130237	L39060	AA913909	Hs.153088	TATA box binding protein (TBP)-associated factor, RNA polymerase I, A, 48kD
	128752	RC_N72879	AA504428	Hs.10487	Homo sapiens, clone IMAGE:3954132, mRNA, partial cds
	135162	AA045930	A187925	Hs.95667	F-box protein 30
	131386	AA096412	BE219898	Hs.173135	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2
55	129021	RC_AA599244	AL044675	Hs.173081	KIAA0530 protein
	424274	AA293634	W73933	Hs.283738	casein kinase 1, alpha 1
	129913	H06583	NM_001310	Hs.13313	cAMP responsive element binding protein-like 2
	131888	U79298	AW294659	Hs.34054	Homo sapiens cDNA: FLJ22488 fis, clone HRC10948, highly similar to HSU79298 Human clone
	23803 mRNA				
60	118612	RC_N69466	AB037788	Hs.224961	cleavage and polyadenylation specific factor 2, 100kD subunit
	322026	AA203138	AW024973	Hs.283675	NPD009 protein
	110892	RC_N38882	AL035301	Hs.97375	H.sapiens gene from PAC 106H8
	111429	RC_R01245	A1038052	Hs.19162	ESTs, Weakly similar to I54374 gene NF2 protein [H.sapiens]
	113334	RC_T76962	AW974666	Hs.293024	ESTs
65	104091	AA417310	BE465093	Hs.106101	hypothetical protein FLJ22557
	105246	RC_AA226879	AA226879		gb:zr19c09.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone
	IMAGE:663856 3' similar to contains Alu repetitive element, mRNA sequence.				
	113300	RC_T67448	T67448	Hs.13101	ESTs
	117147	RC_H97225_s	AW901347	Hs.38592	hypothetical protein FLJ23342
70	121349	RC_AA405205	AA405205	Hs.97960	ESTs, Weakly similar to T51146 ring-box protein 1 [H.sapiens]
	100294	D49396	AA331881	Hs.75454	peroxiredoxin 3
	133999	M28213	AA535244	Hs.78305	RAB2, member RAS oncogene family
	133259	AA278548	BE379646	Hs.6904	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 2004403
	129423	AA371418	AA204686	Hs.234149	hypothetical protein FLJ20647
	131098	RC_AA459668	U66669	Hs.236642	3-hydroxyisobutyryl-Coenzyme A hydrolase
75	135272	AA399391	A1828337	Hs.97591	ESTs
	129155	AA046865	A1952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (from clone DKFZp434P228)

	311291	AA056319	AA782601	Hs.319817	ESTs
	120750	RC_AA310499	AI191410	Hs.96693	ESTs, Moderately similar to 2109260A B cell growth factor [H.sapiens]
	101002	J04058	AV655843	Hs.169919	electron-transfer-flavoprotein, alpha polypeptide (glutaric aciduria II)
5	133012	AA099241	AA847843	Hs.62711	Homo sapiens, clone IMAGE:3351295, mRNA
	103879	AA228148_s	BE543269	Hs.50252	mitochondrial ribosomal protein L32
	131281	RC_AA443212	AA251716	Hs.25227	ESTs
	115109	RC_AA256383	AJ249977	Hs.88049	protein kinase, AMP-activated, gamma 3 non-catalytic subunit
	118502	RC_N67317	AL157488	Hs.50150	Homo sapiens mRNA; cDNA DKFZp564B182 (from clone DKFZp564B182)
10	134100	L07540	AA460085	Hs.171075	replication factor C (activator 1) 5 (36.5kD)
	131869	AA484944	AW968547	Hs.33540	ESTs, Weakly similar to dJ309K20.4 [H.sapiens]
	115396	RC_AA282985	AA810854	Hs.89081	ESTs
	103860	AA203742	AW976877	Hs.38057	ESTs
	135089	N75611_s	AI918035	Hs.301198	roundabout (axon guidance receptor, Drosophila) homolog 1
15	129938	U79300	AW003668	Hs.135587	Human clone 23629 mRNA sequence
	107508	W90095	N74925	Hs.38761	Homo sapiens cDNA: FLJ21564 fis, clone COL06452
	103685	AA005190	AA158008	Hs.292444	ESTs
	125170	AA203147	AL020996	Hs.8518	selenoprotein N
	129179	RC_AA504125_s	AW969025	Hs.109154	ESTs
	116262	AA477046	AI936442	Hs.59838	hypothetical protein FLJ10808
20	123009	RC_AA479949	AA535244	Hs.78305	RAB2, member RAS oncogene family
	131004	D29833	D29833	Hs.2207	salivary proline-rich protein
	103317	X83441	X83441	Hs.166091	ligase IV, DNA, ATP-dependent
	132814	RC_C15251_f	D60730	Hs.57471	ESTs
25	103992	U77718	BE018142	Hs.300954	Huntingtin interacting protein K
	109258	X59710	AL044818	Hs.84928	nuclear transcription factor Y, beta
	110754	RC_N20814	AW302200	Hs.6336	KIAA0672 gene product
	132727	AA136382_s	N27495	Hs.5565	hypothetical protein FLJ22626
	100341	D63506	AF032922	Hs.8813	syntaxin binding protein 3
30	134664	AA256106	AA256106	Hs.87507	ESTs
	103826	AA165564	AW162998	Hs.24684	KIAA1376 protein
	111678	RC_R20628	R38487	Hs.169927	ESTs
	101341	L76159	NM_004477	Hs.203772	FSHD region gene 1
	115455	RC_AA285068	AA876002	Hs.120551	toll-like receptor 10
35	111192	RC_AA477748	AW021988	Hs.109438	Homo sapiens clone 24775 mRNA sequence
	129385	RC_AA235604	AA172106	Hs.110950	Rag C protein
	125050	RC_T79951	AW970209	Hs.111805	ESTs
	122105	RC_AA432278	AW241685	Hs.98699	ESTs
	121324	RC_AA404229	AA404229	Hs.97842	EST
40	120938	RC_AA386260	AA386260	Hs.104632	EST
	115001	RC_AA251376	AA251376		gb:zs10a06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684754 3', mRNA sequence.
	124799	RC_R45088	R45088		gb:yg38g04.s1 Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:34896 3', mRNA sequence.
45	122724	RC_AA457395	AA457395	Hs.99457	ESTs
	117791	RC_N48325	N48325	Hs.93956	EST
	121895	RC_AA427396	AA427396		gb:zw33a02.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:771050 3'
					similar to contains Alu repetitive element; contains MER12.12 MER12 repetitive element ; mRNA sequence.
	108244	RC_AA062839	AA062839		gb:zm05c09.s1 Stratagene corneal stroma (937222) Homo sapiens cDNA clone IMAGE:513232
50	117852	RC_N49408	AW877787	Hs.136102	KIAA0853 protein
	109298	RC_AA205432	R77854	Hs.250693	Krueppel-related zinc finger protein
	122432	RC_AA447400	AA447400	Hs.187684	ESTs, Weakly similar to B34087 hypothetical protein [H.sapiens]
	124627	RC_N74625	N74625		gb:za55c03.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:296452 3'
55					similar to gb:M14338 VITAMIN K-DEPENDENT PROTEIN S PRECURSOR (HUMAN); contains OFR.b3 OFR repetitive element ; mRNA sequence.
	115141	RC_AA258071	AA465131	Hs.64001	Homo sapiens clone 25218 mRNA sequence
	128636	U49065	U49065	Hs.102865	interleukin 1 receptor-like 2
	115373	RC_AA282197	AA664862	Hs.181022	CGI-07 protein
	114651	RC_AA101400	AA101400	Hs.189960	ESTs
60	132796	RC_AA180487	NM_006283	Hs.173159	transforming, acidic coiled-coil containing protein 1
	103749	RC_N35583	AL135301	Hs.8768	hypothetical protein FLJ10849
	107328	T83444	AW959891	Hs.76591	KIAA0887 protein
	115349	RC_AA281563	AF121176	Hs.12797	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 16
	111490	RC_R06862	R06862		gb:yf11e09.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:126568 3'
65					similar to contains L1 repetitive element ; mRNA sequence.
	103763	AA085354	AA085291		gb:zn01g06.s1 Stratagene colon HT29 (937221) Homo sapiens cDNA clone 3' similar to
					contains Alu repetitive element ; mRNA sequence
	118791	RC_N75520	N75520	Hs.261003	ESTs, Moderately similar to B34087 hypothetical protein [H.sapiens]
	116644	RC_F03032	F03032	Hs.290278	ESTs, Weakly similar to B34087 hypothetical protein [H.sapiens]
70	116823	RC_H56485	AW204742	Hs.143542	ESTs, Highly similar to CSA_HUMAN COCKAYNE SYNDROME WD-REPEAT PROTEIN CSA [H.sapiens]
	108940	RC_AA148603	AA148603		gb:zo09e04.s1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone
					IMAGE:567198 3', mRNA sequence.
	112218	RC_R50057	R50057	Hs.272251	Homo sapiens mRNA; cDNA DKFZp586M1418 (from clone DKFZp586M1418)
	116557	RC_D20572_I	D20572	Hs.90171	EST
75	133649	U25849	U25849	Hs.75393	acid phosphatase 1, soluble
	131745	RC_C20746	AI828559	Hs.31447	ESTs, Moderately similar to A46010 X-linked retinopathy protein [H.sapiens]

	116801	RC_H43879	H43879		gb:yo69h09.s1 Soares breast 3NbHBst Homo sapiens cDNA clone IMAGE:183233 3', mRNA sequence.
	115006	RC_AA251548	AA251548	Hs.87886	EST
	123424	RC_AA598500	H29882	Hs.162614	ESTs
5	120831	RC_AA347919	AA347919	Hs.96889	EST
	103691	AA018298	AA018298	Hs.103332	ESTs
	121555	RC_AA412491	AF025771	Hs.50123	zinc finger protein 189
	111193	RC_N67946	N67946	Hs.117569	ESTs
10	132061	RC_AA058946	AB020700	Hs.3830	KIAA0893 protein
	134575	RC_AA194568_i	AA194568	Hs.85938	EST
	115050	RC_AA252794	AA252794	Hs.88009	ESTs
	420208	U31799	BE276055	Hs.95972	silver (mouse homolog) like
	133735	AC002045_xpt1	R66740	Hs.110613	KIAA0220 protein
	128546	Z21305	NM_003478	Hs.101299	cullin 5
15	111946	RC_R40697	R40697	Hs.76666	C9orf10 protein
	124879	RC_R73588	R73588	Hs.101533	ESTs
	115683	AA410345	AF255910	Hs.54650	junctional adhesion molecule 2
	103692	AA018418	AW137912	Hs.227583	Homo sapiens chromosome X map Xp11.23 L-type calcium channel alpha-1 subunit
20	(CACNA1F) gene, complete cds; HSP27				pseudogene, complete sequence; and JM1 protein, JM2 protein, and Hb2E genes, complete cds
	103767	AA089688	BE244667	Hs.296155	CGI-100 protein
	125266	W90022	W90022	Hs.186809	ESTs, Highly similar to LCT2_HUMAN LEUKOCYTE CELL-DERIVED CHEMOTAXIN 2
	PRECURSOR [H.sapiens]				
	135235	AA435512	AW298244	Hs.293507	ESTs
	134497	RC_AA404494	BE258532	Hs.251871	CTP synthase
25	426754	RC_AA278529_i	NM_014264	Hs.172052	serine/threonine kinase 18
	412177	RC_AA342828_s	Z23091	Hs.73734	glycoprotein V (platelet)
	132000	RC_AA044644	AW247017	Hs.36978	melanoma antigen, family A, 3
	124738	RC_AA044644	T07568	Hs.137158	ESTs
30	324000	RC_AA196729_i	AA604749	Hs.190213	ESTs
	106896	RC_AA196729_i	AW073202	Hs.334825	Homo sapiens cDNA FLJ14752 fis, clone NT2RP3003071
	132000	RC_AA025858	AW247017	Hs.36978	melanoma antigen, family A, 3
	129577	RC_AA025858	N75346	Hs.82906	CDC20 (cell division cycle 20, S. cerevisiae, homolog)
	107091	RC_AA233519	AI949109	Hs.246885	hypothetical protein FLJ20783
35	130296	RC_N52271	D31139	Hs.154103	LIM protein (similar to rat protein kinase C-binding enigma)
	102855	RC_N68399	NM_003528	Hs.2178	H2B histone family, member Q
	113689	RC_AA098874	AB037850	Hs.16621	DKFZP434I116 protein
	100939	RC_AA279667_s	L04288	Hs.297939	cathepsin B
	130430	RC_H22556	W27893	Hs.150580	putative translation initiation factor
40	106734	RC_N45979_s	BE296690	Hs.288173	Homo sapiens cDNA: FLJ21747 fis, clone COLF5160, highly similar to AF182198 Homo sapiens intersectin 2 long isoform (ITSN2) mRNA
	135148	RC_AA431288_s	AA306478	Hs.95327	CD3D antigen, delta polypeptide (TIT3 complex)
	134221	RC_AA609862	BE280456	Hs.80248	RNA-binding protein gene with multiple splicing
	105376	RC_N35583	AW994032	Hs.8768	hypothetical protein FLJ10849
45	124541	U77718	AF112222	Hs.44499	pinin, desmosome associated protein
	134546	AA203147	AL020996	Hs.8518	selenoprotein N
	134000	RC_W93092	AW175787	Hs.334841	selenium binding protein 1
	125656	RC_W93092	AW516428	Hs.78687	neutral sphingomyelinase (N-SMase) activation associated factor
	100939	RC_N58561_s	L04288	Hs.297939	cathepsin B
50	125656	RC_W93092	AW516428	Hs.78687	neutral sphingomyelinase (N-SMase) activation associated factor
	101779	RC_W69385_s	BE543412	Hs.250505	retinoic acid receptor, alpha
	332489	RC_R22947	R23053	NA	Hu01 Chip Redos
	133000	RC_N38959_f	AL042444	Hs.62402	p21/Cdc42/Rac1-activated kinase 1 (yeast Ste20-related)
	125905	RC_N38959_f	AI678638	Hs.6456	chaperonin containing TCP1, subunit 2 (beta)
55	129000	RC_H73050_s	AA744902	Hs.107767	hypothetical protein PRO1489
	100920	RC_H73050_s	X54534	Hs.278994	Rhesus blood group, CcEe antigens

TABLE 1A

Table 1A shows the accession numbers for those pkeys lacking unigenelD's for Tables 1. The pkeys in Table 7 lacking unigenelD's are represented within Tables 1-6A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

5			
10	Pkey:	Unique Eos probeset identifier number	
	CAT number:	Gene cluster number	
	Accession:	Genbank accession numbers	
15	Pkey	CAT Number	Accession
	108469	116761_1	AA079487 AA128547 AA128291 AA079587 AA079600
	124106	125446_1	H12245 AA094769 R14576
	108501	13684_-12	AA083256
20	108562	36375_1	AA100796 AF020589 AA074629 AA075946 AA100849 AA085347 AA126309 AA079311 AA079323 AA085274
	125008	1802095_1	T91251 T64891 T85665
	125020	116017_1	T69981 T69924 AA078476
	125066	1814993_1	T86284 T81933
	116661	1532859_1	R61504 F04247
25	125104	413347_1	T95590 AA703278 H62764
	124575	1666649_1	N68168 N69188 N90450
	125263	1547_2	AA098878 W88942
	116845	393481_1	AA649530 AA659316 H64973
30	118417	37186_1	AF080229 AF080231 AF080230 AF080232 AF080233 AF080234 BE550633 AI636743 AW614951 BE467547 AI680833
			AI633818 N29986 U87592 U87593 U87590 U87591 S46404 U87587 AA463992 AW206802 AI970376 AI583718 AI672574
			N25695 AW665466 AI818326 AA126128 AI480345 AW013827 AA248638 AI214968 AA204735 AA207155 AA206262 AA204833
			AW003247 AW496808 AI080480 AI631703 AI651023 AI867418 AW818140 AA502500 AI206199 AI671282 AI352545 BE501030
			AI652535 BE465762 AA206331 AW451866 AA471088 AA206342 AA204834 AA206100 AW021661 AA332922 N66048
			AA703396 H92278 AW139734 H92683 U87589 U87595 H69001 U87594 BE466420 AI624817 BE466611 AI206344 AA574397
35			AA348354 AI493192
	118584	532052_1	AW136928 AI685655 BE218584 BE465078 N68963 AA975338 BE147199 N76377
	103743	112194_1	AA075998 AA075999 AA070986 AA070896 AA129207 AA078942 AA070783 AA078941
	103744	114161_1	AA079267 AA076003
	103746	113452_1	AA075000 AA081876
40	103761	114208_1	AA765163 AW298222 AA126126 AA085138 AA076068
	103763	48290_6	AA085291 AA085354
	120209	1531817_1	F02951 Z40892 F04711
	120284	158963_1	AA179656 AA182626 AA182603
45	112540	1605263_1	R69751 R70467 H69771 H80879 H80878
	111904	1719336_1	Z41572 R39330
	121059	273450_1	AA393283 AA398628
	121094	275729_1	AA402505 AA398900
	114106	1182096_1	AW602528 BE073859 Z38412
	130091	23961_-3	W88999
50	122264	296527_1	AA436837 AA442594
	108280	110682_1	AA065069 AA085108
	129961	1706092_1	R23053 R79884 R76271
	130529	158447_1	AA178953 AA192740
	108309	111495_1	AA069818 AA069971 AA069923 AA069908
55	107832	genbank_AA021473	AA021473
	123731	genbank_AA609839	AA609839
	116571	genbank_D45652	D45652
	132225	genbank_AA128980	AA128980
	125017	genbank_T68875	T68875
60	125063	genbank_T85352	T85352
	125064	genbank_T85373	T85373
	100964	entrez_J00212 J00212	
	125118	149288_1	R10606 T97620 AA576309
	102269	entrez_U30245U30245	
65	125150	NOT_FOUND_entrez_W38240	W38240
	116801	genbank_H43879	H43879
	118111	genbank_N55493	N55493
	118129	genbank_N57493	N57493
	118329	genbank_N63520	N63520
70	118475	genbank_N66845	N66845
	111490	genbank_R06862	R06862
	111514	genbank_R07998	R07998
	104534	R22303_at	R22303
	120340	genbank_AA206828	AA206828

	120376	genbank_AA227469	AA227469
	104787	genbank_AA027317	AA027317
	120409	genbank_AA235050	AA235050
	120745	genbank_AA302809	AA302809
5	120809	genbank_AA346495	AA346495
	120839	genbank_AA348913	AA348913
	113702	genbank_T97307	T97307
	115001	genbank_AA251376	AA251376
10	122562	genbank_AA452156	AA452156
	122635	genbank_AA454085	AA454085
	108244	genbank_AA062839	AA062839
	108277	genbank_AA064859	AA064859
	122723	genbank_AA457380	AA457380
15	124028	genbank_F04112	F04112
	108403	genbank_AA075374	AA075374
	122860	genbank_AA464414	AA464414
	108427	genbank_AA076382	AA076382
	108439	genbank_AA078986	AA078986
20	131353	231290_1	AW411259 H23555 AW015049 AI684275 AW015886 AW068953 AW014085 AI027260 R52686 AA918278 AI129462
	AA969360		
			N34869 AI948416 AA534205 AA702483 AA705292
	108533	genbank_AA084415	AA084415
	117031	genbank_H88353	H88353
	124254	genbank_H69899	H69899
25	101447	entrez_M21305	M21305
	101458	entrez_M22092	M22092
	124577	genbank_N68300	N68300
	108940	genbank_AA148603	AA148603
	108941	genbank_AA148650	AA148650
30	124627	genbank_N74625	N74625
	124720	144582_1	R05283 R11056
	124793	genbank_R44519	R44519
	124799	genbank_R45088	R45088
35	117683	genbank_N40180	N40180
	117732	genbank_N46452	N46452
	124991	genbank_T50116	T50116
	119023	genbank_N98488	N98488
	119239	95573_2	T11483 T11472
40	119558	NOT_FOUND_entrez_W38194	W38194
	119654	genbank_W57759	W57759
	105246	genbank_AA226879	AA226879
	121350	genbank_AA405237	AA405237
	121558	genbank_AA412497	AA412497
45	105985	genbank_AA406610	AA406610
	100071	entrez_A28102A28102	
	114648	genbank_AA101056	AA101056
	121895	genbank_AA427396	AA427396
	100327	entrez_D55640D55640	
	123315	714071_1	AA496369 AA496646

TABLE 2:

5	Pkey: Unique Eos probeset identifier number Accession: Accession number used for previous patent filings ExAccn: Exemplar Accession number, Genbank accession number UnigeneID: Unigene number Unigene Title: Unigene gene title				
10	Pkey	Accession	ExAccn	UnigeneID	UnigeneTitle
15	100420	100420	D86983	Hs.118893	Melanoma associated gene
	100484	100484	NM_005402	Hs.288757	v-rat simian leukemia viral oncogene hom
	100991	100991	J03836	Hs.82085	serine (or cysteine) proteinase inhibito
	101168	101168	NM_005308	Hs.211569	G protein-coupled receptor kinase 5
	101261	101261	D30857	Hs.82353	protein C receptor, endothelial (EPCR)
20	101447	101447	M21305		gb:Human alpha satellite and satellite 3
	101543	101543	M31166	Hs.2050	pentaxin-related gene, rapidly induced b
	101560	101560	AW958272	Hs.347326	intercellular adhesion molecule 2
	101714	101714	M68874	Hs.211587	phospholipase A2, group IVA (cytosolic,
	101838	101838	BE243845	Hs.75511	connective tissue growth factor
25	102012	102012	BE259035	Hs.118400	singed (Drosophila)-like (sea urchin fas
	102164	102164	NM_000107	Hs.77602	damage-specific DNA binding protein 2 (4
	102283	102283	AW161552	Hs.83381	guanine nucleotide binding protein 11
	102564	102564	U59423	Hs.79067	MAD (mothers against decapentaplegic, Dr
	102759	102759	NM_005100	Hs.788	A kinase (PRKA) anchor protein (gravin)
30	102804	102804	NM_002318	Hs.83354	lysyl oxidase-like 2
	102898	102898	NM_002205	Hs.149609	Integrin, alpha 5 (fibronectin receptor,
	103036	103036	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial
	103095	103095	NM_005424	Hs.78824	tyrosine kinase with immunoglobulin and
	103166	103166	AA159248	Hs.180909	peroxiredoxin 1
35	103280	103280	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula
	103850	103850	AA187101	Hs.213194	hypothetical protein MGC10895
	104592	104592	AW630488	Hs.25338	protease, serine, 23
	104786	104786	AA027167	Hs.10031	KIAA0955 protein
	104865	104865	T79340	Hs.22575	B-cell CLL/lymphoma 6, member B (zinc fi
40	104952	104952	AW076098	Hs.345588	desmoplakin (DPI, DP11)
	105178	105178	AA313825	Hs.21941	AD036 protein
	105330	105330	AW338625	Hs.22120	ESTs
	105729	105729	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds
	105977	105977	AK001972	Hs.30822	hypothetical protein FLJ11110
45	106031	106031	X64116	Hs.171844	Homo sapiens cDNA: FLJ22296 fis, clone H
	106155	106155	AA425414	Hs.33287	nuclear factor I/B
	106423	106423	AB020722	Hs.16714	Rho guanine exchange factor (GEF) 15
	107174	107174	BE122762	Hs.25338	ESTs
	107295	107295	AA186629	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp
50	108756	108756	AA127221	Hs.117037	ESTs
	108888	108888	AA135606	Hs.189384	gb:z10a05.s1 Soares_pregnant_uterus_NbH
	109166	109166	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines
	109768	109768	F06838	Hs.14763	ESTs
	110906	110906	AA035211	Hs.17404	ESTs
55	111006	111006	BE387014	Hs.166146	Homer, neuronal immediate early gene, 3
	111133	111133	AW580939	Hs.97199	complement component C1q receptor
	113073	113073	N39342	Hs.103042	microtubule-associated protein 1B
	113923	113923	AW953484	Hs.3849	hypothetical protein FLJ22041 similar to
	115061	115061	AI751438	Hs.41271	Homo sapiens mRNA full length insert cDN
60	115145	115145	AA740907	Hs.88297	ESTs
	115947	115947	R47479	Hs.94761	KIAA1691 protein
	116339	116339	AK000290	Hs.44033	dipeptidyl peptidase 8
	116589	116589	AI557212	Hs.17132	ESTs, Moderately similar to I54374 gene
	117023	117023	AW070211	Hs.102415	Homo sapiens mRNA; cDNA DKFZp586N0121 (f
65	117563	117563	AF055634	Hs.44553	unc5 (C.elegans homolog) c
	118475	118475	N66845		gb:za46c11.s1 Soares fetal liver spleen
	119073	119073	BE245360	Hs.279477	ESTs
	119174	119174	R71234		gb:yi54c08.s1 Soares placenta Nb2HP Homo
	119416	119416	T97186		gb:ye50h09.s1 Soares fetal liver spleen
70	121335	121335	AA404418		gb:zw37e02.s1 Soares_total_fetus_Nb2HF8_
	123160	123160	AA488687	Hs.284235	ESTs, Weakly similar to I38022 hypotheti
	123523	123523	AA608588		gb:ae54e06.s1 Stratagene lung carcinoma
	123964	123964	C13961		gb:C13961 Clontech human aorta polyA+ mR
	124315	124315	NM_005402	Hs.288757	v-rat simian leukemia viral oncogene hom
75	124669	124669	AI571594	Hs.102943	hypothetical protein MGC12916
	124875	124875	AI887664	Hs.285814	sprouty (Drosophila) homolog 4
	125103	125103	AA570056	Hs.122730	ESTs, Moderately similar to KIAA1215 pro
	125565	125565	R20840		gb:y905c08.r1 Soares infant brain 1N1B H

	126511	126511	T92143	Hs.57958	EGF-TM7-latrophilin-related protein
	126649	126649	AA001860	Hs.279531	ESTs
	449602	449602	AA001860	Hs.279531	ESTs
5	127402	127402	AA358869	Hs.227949	SEC13 (S. cerevisiae)-like 1
	128992	128992	H04150	Hs.107708	ESTs
	129188	129188	NM_001078	Hs.109225	vascular cell adhesion molecule 1
	129371	129371	X06828	Hs.110802	von Willebrand factor
	129765	129765	M86933	Hs.1238	amelogenin (Y chromosome)
10	129884	129884	AF055581	Hs.13131	lysosomal
	130639	130639	AI557212	Hs.17132	ESTs, Moderately similar to I54374 gene
	130828	130828	AW631469	Hs.203213	ESTs
	131080	131080	NM_001955	Hs.2271	endothelin 1
	131182	131182	AI824144	Hs.23912	ESTs
15	131573	131573	AA040311	Hs.28959	ESTs
	131756	131756	AA443966	Hs.31595	ESTs
	131881	131881	AW361018	Hs.3383	upstream regulatory element binding prot
	132083	132083	BE386490	Hs.279663	Pirin
	132358	132358	NM_003542	Hs.46423	H4 histone family, member G
20	132456	132456	AB011084	Hs.48924	KIAA0512 gene product; ALEX2
	132676	132676	N92589	Hs.261038	ESTs, Weakly similar to I38022 hypotheti
	132718	132718	NM_004600	Hs.554	Sjogren syndrome antigen A2 (60kD, ribon
	132760	132760	AA125985	Hs.56145	thymosin, beta, identified in neuroblast
	132968	132968	AF234532	Hs.61638	myosin X
25	133061	133061	AI186431	Hs.296638	prostate differentiation factor
	133161	133161	AW021103	Hs.6631	hypothetical protein FLJ20373
	133260	133260	AA030345	Hs.6906	Homo sapiens cDNA: FLJ23197 fis, clone R
	133491	133491	BE19053	Hs.170001	eukaryotic translation initiation factor
	133550	133550	AI129903	Hs.74669	vesicle-associated membrane protein 5 (m
30	133614	133614	NM_003003	Hs.75232	SEC14 (S. cerevisiae)-like 1
	133691	133691	M85289	Hs.211573	heparan sulfate proteoglycan 2 (perlecan
	133913	133913	AU076964	Hs.7753	calumenin
	133985	133985	L34657	Hs.78146	platelet/endothelial cell adhesion molec
	134088	134088	AI379954	Hs.79025	KIAA0096 protein
35	134299	134299	AW580939	Hs.97199	complement component C1q receptor
	116470	116470	AI272141	Hs.83484	SRY (sex determining region Y)-box 4
	134989	134989	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi
	135073	135073	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f
	100114	100114	X02308	Hs.82962	thymidylate synthetase
40	100143	100143	AU076465	Hs.278441	KIAA0015 gene product
	100208	100208	NM_002933	Hs.78224	ribonuclease, RNase A family, 1 (pancrea
	100405	100405	AW291587	Hs.82733	nidogen 2
	100455	100455	AW888941	Hs.75789	N-myc downstream regulated
	100618	100618	AI752163	Hs.114599	collagen, type VIII, alpha 1
45	100658	100658	U56725	Hs.180414	heat shock 70kD protein 2
	100718	100718	BE295928	Hs.75424	inhibitor of DNA binding 1, dominant neg
	100828	100828	AL048753	Hs.303649	small inducible cytokine A2 (monocyte ch
	100991	100991	J03836	Hs.82085	serine (or cysteine) proteinase inhibito
	101110	101110	AI439011	Hs.86386	myeloid cell leukemia sequence 1 (BCL2-r
50	101156	101156	AA340987	Hs.75693	prolylcarboxypeptidase (angiotensinase C
	101184	101184	NM_001674	Hs.460	activating transcription factor 3
	101317	101317	L42176	Hs.8302	four and a half LIM domains 2
	101345	101345	NM_005795	Hs.152175	calcitonin receptor-like
	101475	101475	BE410405	Hs.76288	calpain 2, (m/II) large subunit
55	101496	101496	X12784	Hs.119129	collagen, type IV, alpha 1
	101543	101543	M31166	Hs.2050	pentaxin-related gene, rapidly induced b
	101560	101560	AW958272	Hs.347326	intercellular adhesion molecule 2
	101592	101592	AF064853	Hs.91299	guanine nucleotide binding protein (G pr
	101634	101634	AV650262	Hs.75765	GRO2 oncogene
60	101682	101682	AF043045	Hs.81008	filamin B, beta (actin-binding protein-2
	101720	101720	M69043	Hs.81328	nuclear factor of kappa light polypeptid
	101744	101744	AI879352	Hs.118625	hexokinase 1
	101837	101837	M92843	Hs.343586	zinc finger protein homologous to Zfp-36
	101840	101840	AA236291	Hs.183583	serine (or cysteine) proteinase inhibito
65	101864	101864	BE392588	Hs.75777	transgelin
	101966	101966	X96438	Hs.76095	immediate early response 3
	102013	102013	BE616287	Hs.178452	catenin (cadherin-associated protein), a
	102059	102059	AI752666	Hs.76669	nicotinamide N-methyltransferase
	102283	102283	AW161552	Hs.83381	guanine nucleotide binding protein 11
70	102378	102378	AU076887	Hs.28491	spermidine/spermine N1-acetyltransferase
	102460	102460	U48959	Hs.211582	myosin, light polypeptide kinase
	102499	102499	BE243877	Hs.76941	ATPase, Na+/K+ transporting, beta 3 poly
	102560	102560	R97457	Hs.63984	cadherin 13, H-cadherin (heart)
	102589	102589	AU076728	Hs.8867	cysteine-rich, angiogenic inducer, 61
75	102645	102645	AL119566	Hs.6721	lysosomal
	102693	102693	AA532780	Hs.183684	eukaryotic translation initiation factor
	102759	102759	NM_005100	Hs.788	A kinase (PRKA) anchor protein (gravin)

	102882	102882	AI767736	Hs.290070	gelsolin (amyloidosis, Finnish type)
	102915	102915	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin
	102960	102960	AI904738	Hs.76053	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep
5	103020	103020	X53416	Hs.195464	filamin A, alpha (actin-binding protein-
	103036	103036	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial
	103080	103080	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomatos
	103138	103138	X65965		gb:H.sapiens SOD-2 gene for manganese su
	103195	103195	AA351647	Hs.2642	eukaryotic translation elongation factor
10	103371	103371	X91247	Hs.13046	thioredoxin reductase 1
	103471	103471	Y00815	Hs.75216	protein tyrosine phosphatase, receptor t
	104447	104447	AW204145	Hs.156044	ESTs
	104783	104783	AA533513	Hs.93659	protein disulfide isomerase related prot
	104865	104865	T79340	Hs.22575	B-cell CLL/lymphoma 6, member B (zinc fi
15	104894	104894	AF065214	Hs.18858	phospholipase A2, group IVC (cytosolic,
	105113	105113	AB037816	Hs.8982	Homo sapiens, clone IMAGE:3506202, mRNA,
	105196	105196	W84893	Hs.9305	angiotensin receptor-like 1
	105263	105263	AW388633	Hs.6682	solute carrier family 7, (cationic amino
	105330	105330	AW338625	Hs.22120	ESTs
20	105492	105492	AI805717	Hs.289112	CGI-43 protein
	105594	105594	AB024334	Hs.25001	tyrosine 3-monooxygenase/tryptophan 5-mo
	105732	105732	AW504170	Hs.274344	hypothetical protein MGC12942
	105882	105882	W46802	Hs.81988	disabled (Drosophila) homolog 2 (mitogen
	106031	106031	X64116	Hs.171844	Homo sapiens cDNA: FLJ22296 fis, clone H
25	106222	106222	AA356392	Hs.21321	Homo sapiens clone FLB9213 PRO2474 mRNA,
	106263	106263	W21493	Hs.28329	hypothetical protein FLJ14005
	106366	106366	AA186715	Hs.336429	RIKEN cDNA 9130422N19 gene
	106634	106634	W25491	Hs.288909	hypothetical protein FLJ22471
	106793	106793	H94997	Hs.16450	ESTs
30	106842	106842	AF124251	Hs.26054	novel SH2-containing protein 3
	106890	106890	AA489245	Hs.88500	mitogen-activated protein kinase 8 inter
	106974	106974	AI817130	Hs.9195	Homo sapiens cDNA FLJ13698 fis, clone PL
	107061	107061	BE147611	Hs.6354	stromal cell derived factor receptor 1
	107216	107216	D51069	Hs.211579	melanoma cell adhesion molecule
35	107444	107444	W28391	Hs.343258	proliferation-associated 2G4, 38kD
	108507	108507	AI554545	Hs.68301	ESTs
	108931	108931	AA147186		gb:zo38d01.s1 Stratagene endothelial cel
	109195	109195	AF047033	Hs.132904	solute carrier family 4, sodium bicarbon
	109456	109456	AW966580	Hs.42699	ESTs
40	110411	110411	AW001579	Hs.9645	Homo sapiens mRNA for KIAA1741 protein,
	110906	110906	AA035211	Hs.17404	ESTs
	111091	111091	AA300067	Hs.33032	hypothetical protein DKFZp434N185
	111378	111378	AW160993	Hs.326292	hypothetical gene DKFZp434A1114
	111769	111769	AW629414	Hs.24230	ESTs
45	112951	112951	AA307634	Hs.6650	vacuolar protein sorting 45B (yeast homo
	113195	113195	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom
	113542	113542	H43374	Hs.7890	Homo sapiens mRNA for KIAA1671 protein,
	113847	113847	NM_005032	Hs.4114	plastin 3 (T isoform)
	113947	113947	W84768		gb:zh53d03.s1 Soares_fetal_liver_spleen_
50	115061	115061	AI751438	Hs.41271	Homo sapiens mRNA full length insert cDN
	115870	115870	NM_005985	Hs.48029	snail 1 (drosophila homolog), zinc finger
	116228	116228	AI767947	Hs.50841	ESTs
	116314	116314	AI799104	Hs.178705	Homo sapiens cDNA FLJ11333 fis, clone PL
	117023	117023	AW070211	Hs.102415	Homo sapiens mRNA; cDNA DKFZp586N0121 (f
55	117156	117156	W73853		ESTs
	117280	117280	M18217	Hs.172129	Homo sapiens cDNA: FLJ21409 fis, clone C
	119866	119866	AA496205	Hs.193700	Homo sapiens mRNA; cDNA DKFZp586I0324 (f
	121314	121314	W07343	Hs.182538	phospholipid scramblase 4
	121822	121822	AI743860		metallothionein 1E (functional)
60	122331	122331	AL133437	Hs.110771	Homo sapiens cDNA: FLJ21904 fis, clone H
	123160	123160	AA488687	Hs.284235	ESTs, Weakly similar to I38022 hypotheti
	124059	124059	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti
	124358	124358	AW070211	Hs.102415	Homo sapiens mRNA; cDNA DKFZp586N0121 (f
	124726	124726	NM_003654	Hs.104576	carbohydrate (keratan sulfate Gal-6) sul
65	125167	125167	AL137540	Hs.102541	netrin 4
	125307	125307	AW580945	Hs.330466	ESTs
	107985	107985	T40064	Hs.71968	Homo sapiens mRNA; cDNA DKFZp564F053 (fr
	125598	125598	T40064	Hs.71968	Homo sapiens mRNA; cDNA DKFZp564F053 (fr
	413731	413731	BE243845	Hs.75511	connective tissue growth factor
70	116024	116024	AA088767	Hs.83883	transmembrane, prostate androgen induced
	418000	418000	AA932794	Hs.83147	guanine nucleotide binding protein-like
	126399	126399	AA088767	Hs.83883	transmembrane, prostate androgen induced
	127566	127566	AI051390	Hs.116731	ESTs
	128453	128453	X02761	Hs.287820	fibronectin 1
75	128515	128515	BE395085	Hs.10086	type I transmembrane protein Fn14
	128623	128623	BE076608	Hs.105509	CTL2 gene
	128669	128669	W28493	Hs.180414	heat shock 70kD protein 8

	128914	128914	AW867491	Hs.107125	plasmalemma vesicle associated protein
	129188	129188	NM_001078	Hs.109225	vascular cell adhesion molecule 1
	129265	129265	AA530892	Hs.171695	dual specificity phosphatase 1
5	129468	129468	AW410538	Hs.111779	secreted protein, acidic, cysteine-rich
	101838	101838	BE243845	Hs.75511	connective tissue growth factor
	129619	129619	AA209534	Hs.284243	tetraspan NET-6 protein
	129762	129762	AA453694	Hs.12372	tripartite motif protein TRIM2
	130018	130018	AA353093		metallothionein 1L
10	130178	130178	U20982	Hs.1516	insulin-like growth factor-binding prote
	130431	130431	AW505214	Hs.155560	calnexin
	130553	130553	AF062649	Hs.252587	pituitary tumor-transforming 1
	130639	130639	AI557212	Hs.171132	ESTs, Moderately similar to I54374 gene
	130686	130686	BE548267	Hs.337986	Homo sapiens cDNA FLJ10934 fis, clone OV
15	130818	130818	AW190920	Hs.19928	hypothetical protein SP329
	130899	130899	AI077288	Hs.296323	serum/glucocorticoid regulated kinase
	131080	131080	NM_001955	Hs.2271	endothelin 1
	131091	131091	AJ271216	Hs.22880	dipeptidylpeptidase III
	131182	131182	AI824144	Hs.23912	ESTs
20	131319	131319	NM_003155	Hs.25590	stanniocalcin 1
	131328	131328	AW939251	Hs.25647	v-fos FBJ murine osteosarcoma viral onco
	131328	131328	AW939251	Hs.25647	v-fos FBJ murine osteosarcoma viral onco
	131555	131555	T47364	Hs.278613	interferon, alpha-inducible protein 27
	131573	131573	AA040311	Hs.28959	ESTs
25	131756	131756	AA443966	Hs.31595	ESTs
	131909	131909	NM_016558	Hs.274411	SCAN domain-containing 1
	132046	132046	AI359214	Hs.179260	chromosome 14 open reading frame 4
	132151	132151	BE379499	Hs.173705	Homo sapiens cDNA: FLJ22050 fis, clone H
	132187	132187	AA235709	Hs.4193	DKFZP586O1624 protein
30	132314	132314	AF112222	Hs.323806	pinin, desmosome associated protein
	132398	132398	AA876616	Hs.16979	ESTs, Weakly similar to A43932 mucin 2 p
	132490	132490	NM_001290	Hs.4980	LIM domain binding 2
	132546	132546	M24283	Hs.168383	intercellular adhesion molecule 1 (CD54)
35	132716	132716	BE379595	Hs.283738	casein kinase 1, alpha 1
	132883	132883	AA373314	Hs.5897	Homo sapiens mRNA; cDNA DKFZp586P1622 (f
	132989	132989	AA480074	Hs.331328	hypothetical protein FLJ13213
	133071	133071	BE384932	Hs.64313	ESTs, Weakly similar to AF257182 1 G-pro
	133099	133099	W16518	Hs.279518	amyloid beta (A4) precursor-like protein
40	133149	133149	AA370045	Hs.6607	AXIN1 up-regulated
	133200	133200	AB037715	Hs.183639	hypothetical protein FLJ10210
	133260	133260	AA403045	Hs.6906	Homo sapiens cDNA: FLJ23197 fis, clone R
	133349	133349	AW631255	Hs.8110	L-3-hydroxyacyl-Coenzyme A dehydrogenase
	133398	133398	NM_000499	Hs.72912	cytochrome P450, subfamily I (aromatic c
45	133454	133454	BE547647	Hs.177781	hypothetical protein MGC5618
	133491	133491	BE619053	Hs.170001	eukaryotic translation initiation factor
	133517	133517	NM_000165	Hs.74471	gap junction protein, alpha 1, 43kD (con
	133538	133538	NM_003257	Hs.74614	tight junction protein 1 (zona occludens
	133584	133584	D90209	Hs.181243	activating transcription factor 4 (tax-r
	133617	133617	BE244334	Hs.75249	ADP-ribosylation factor-like 6 interacti
50	133671	133671	AW503116	Hs.301819	zinc finger protein 146
	133681	133681	AI352558		tyrosine 3-monooxygenase/tryptophan 5-mo
	133730	133730	BE242779	Hs.179526	upregulated by 1,25-dihydroxyvitamin D-3
	133802	133802	AW239400	Hs.76297	G protein-coupled receptor kinase 6
	133838	133838	BE222494	Hs.180919	inhibitor of DNA binding 2, dominant neg
55	133889	133889	U48959	Hs.211582	myosin, light polypeptide kinase
	133975	133975	C18356	Hs.295944	tissue factor pathway inhibitor 2
	134039	134039	NM_002290	Hs.78672	laminin, alpha 4
	134081	134081	AL034349	Hs.79005	protein tyrosine phosphatase, receptor t
60	134203	134203	AA161219	Hs.799	diphtheria toxin receptor (heparin-bindi
	134299	134299	AW580939	Hs.97199	complement component C1q receptor
	134339	134339	R70429	Hs.81988	disabled (Drosophila) homolog 2 (mitogen
	134381	134381	AI557280	Hs.184270	capping protein (actin filament) muscle
	134416	134416	X68264	Hs.211579	melanoma cell adhesion molecule
	134558	134558	NM_001773	Hs.85289	CD34 antigen
65	134983	134983	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p
	135052	135052	AL136653	Hs.93675	decidual protein induced by progesterone
	135069	135069	AA876372	Hs.93961	Homo sapiens mRNA; cDNA DKFZp667D095 (fr
	135073	135073	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f
	135196	135196	C03577	Hs.9615	myosin regulatory light chain 2, smooth
70	134404	134404	AB000450	Hs.82771	vaccinia related kinase 2
	100082	100082	AA130080	Hs.4295	proteasome (prosome, macropain) 26S subu
	130150	130150	BE094848	Hs.15113	homogentisate 1,2-dioxygenase (homogenti
	130839	130839	AB011169	Hs.20141	similar to S. cerevisiae SSM4
	100113	100113	NM_001269	Hs.84746	chromosome condensation 1
75	100129	100129	AA469369	Hs.5831	tissue inhibitor of metalloproteinase 1
	100169	100169	AL037228	Hs.82043	D123 gene product
	100190	100190	M91401	Hs.178658	RAD23 (S. cerevisiae) homolog B

	100211	100211	D26528	Hs.123058	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep
	130283	130283	NM_012288	Hs.153954	TRAM-like protein
	100248	100248	NM_015156	Hs.78398	KIAA0071 protein
5	100262	100262	D38500	Hs.278468	postmeiotic segregation increased 2-like
	100281	100281	AF091035	Hs.184627	KIAA0118 protein
	100327	100327	D55640		gb:Human monocyte PABL (pseudautosomal
	134495	134495	D63477	Hs.84087	KIAA0143 protein
	135152	135152	M96954	Hs.182741	TIA1 cytotoxic granule-associated RNA-bi
10	100372	100372	NM_014791	Hs.184339	KIAA0175 gene product
	100394	100394	D84284	Hs.66052	CD38 antigen (p45)
	100418	100418	D86978	Hs.84790	KIAA0225 protein
	134347	134347	AF164142	Hs.82042	solute carrier family 23 (nucleobase tra
	100438	100438	AA013051	Hs.91417	topoisomerase (DNA) II binding protein
	100481	100481	X70377	Hs.121489	cystatin D
15	100591	100591	NM_004091	Hs.231444	Homo sapiens, Similar to hypothetical pr
	100662	100662	AI368680	Hs.816	SRY (sex determining region Y)-box 2
	100905	100905	L12260	Hs.172816	neuregulin 1
	100950	100950	AF128542	Hs.166846	polymerase (DNA directed), epsilon
20	135407	135407	J04029	Hs.99936	keratin 10 (epidermolytic hyperkeratosis
	131877	131877	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)
	134786	134786	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous
	134078	134078	L08895	Hs.78995	MADS box transcription enhancer factor 2
	134849	134849	BE409525	Hs.902	neurofibromin 2 (bilateral acoustic neur
25	101152	101152	AI984625	Hs.9884	spindle pole body protein
	131687	131687	BE297635	Hs.3069	heat shock 70kD protein 9B (mortalin-2)
	421155	421155	H87879	Hs.102267	lysyl oxidase
	133975	133975	C18356	Hs.295944	tissue factor pathway inhibitor 2
	130155	130155	AA101043	Hs.151254	kallikrein 7 (chymotryptic, stratum com
30	132813	132813	BE313625	Hs.57435	solute carrier family 11 (proton-coupled
	101300	101300	BE535511		transmembrane trafficking protein
	130344	130344	AW250122	Hs.154879	DiGeorge syndrome critical region gene D
	101381	101381	AW675039	Hs.1227	aminolevulinate, delta-, dehydratase
	133780	133780	AA557660	Hs.76152	decorin
	101447	101447	M21305		gb:Human alpha satellite and satellite 3
35	101470	101470	NM_000546	Hs.1846	tumor protein p53 (Li-Fraumeni syndrome)
	101478	101478	NM_002890	Hs.758	RAS p21 protein activator (GTPase activa
	133519	133519	AW583062	Hs.74502	chymotrypsinogen B1
	134116	134116	R84694	Hs.79194	cAMP responsive element binding protein
40	130174	130174	M29551	Hs.151531	protein phosphatase 3 (formerly 2B), cat
	132983	132983	M30269		nidogen (enactin)
	101543	101543	M31166	Hs.2050	pentaxin-related gene, rapidly induced b
	101620	101620	S55271	Hs.247930	Epsilon, IgE
	133595	133595	AA393273	Hs.75133	transcription factor 6-like 1 (mitochond
45	101700	101700	D90337	Hs.247916	natriuretic peptide precursor C
	134246	134246	D28459	Hs.80612	ubiquitin-conjugating enzyme E2A (RAD6 h
	133948	133948	X59960	Hs.77813	sphingomyelin phosphodiesterase 1, acid
	133948	133948	X59960	Hs.77813	sphingomyelin phosphodiesterase 1, acid
	133948	133948	X59960	Hs.77813	sphingomyelin phosphodiesterase 1, acid
50	101812	101812	BE439894	Hs.78991	DNA segment, numerous copies, expressed
	133396	133396	M96326	Hs.72885	azurocidin 1 (cationic antimicrobial pro
	129026	129026	AL120297	Hs.108043	Friend leukemia virus integration 1
	134831	134831	AA853479	Hs.89890	pyruvate carboxylase
	134395	134395	AA456539	Hs.8262	lysosomal
55	101977	101977	AF112213	Hs.184062	putative Rab5-interacting protein
	101998	101998	U01212	Hs.248153	olfactory marker protein
	102007	102007	U02556	Hs.75307	t-complex-associated-testis-expressed 1-
	416658	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara
	135389	135389	U05237	Hs.99872	fetal Alzheimer antigen
60	130145	130145	U34820	Hs.151051	mitogen-activated protein kinase 10
	420269	420269	U72937	Hs.96264	alpha thalassemia/mental retardation syn
	102123	102123	NM_001809	Hs.1594	centromere protein A (17kD)
	102133	102133	AU076845	Hs.155596	BCL2/adenovirus E1B 19kD-interacting pro
	102162	102162	AA450274	Hs.1592	CDC16 (cell division cycle 16, S. cerevi
65	427653	427653	AA159001	Hs.180069	nuclear respiratory factor 1
	102200	102200	AA232362	Hs.157205	branched chain aminotransferase 1, cytos
	102214	102214	U23752	Hs.32964	SRY (sex determining region Y)-box 11
	131319	131319	NM_003155	Hs.25590	stanniocalcin 1
	132316	132316	U28831	Hs.44566	KIAA1641 protein
70	134365	134365	AA568906	Hs.82240	syntaxin 3A
	102298	102298	AA382169	Hs.54483	N-myc (and STAT) interactor
	302344	302344	BE303044	Hs.192023	eukaryotic translation initiation factor
	102367	102367	U39656	Hs.118825	mitogen-activated protein kinase kinase
	102394	102394	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma
75	129521	129521	AF071076	Hs.112255	nucleoporin 98kD
	102251	102251	NM_004398	Hs.41706	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep
	133746	133746	AW410035	Hs.75862	MAD (mothers against decapentaplegic, Dr

	132828	132828	AB014615	Hs.57710	fibroblast growth factor 8 (androgen-ind
	132828	132828	AB014615	Hs.57710	fibroblast growth factor 8 (androgen-ind
	130441	130441	U63630	Hs.155637	protein kinase, DNA-activated, catalytic
	129350	129350	U50535	Hs.110630	Human BRCA2 region, mRNA sequence CG006
5	130457	130457	AB014595	Hs.155976	cullin 4B
	102560	102560	R97457	Hs.63984	cadherin 13, H-cadherin (heart)
	134305	134305	U61397	Hs.81424	ubiquitin-like 1 (sentrin)
	132736	132736	AW081883	Hs.211578	Homo sapiens cDNA: FLJ23037 fis, clone L
10	102663	102663	NM_002270	Hs.168075	karyopherin (importin) beta 2
	102735	102735	AF111106	Hs.3382	protein phosphatase 4, regulatory subuni
	101175	101175	U82671	Hs.36980	melanoma antigen, family A, 2
	132164	132164	AI752235	Hs.41270	procollagen-lysine, 2-oxoglutarate 5-dio
	102826	102826	NM_007274	Hs.8679	cytosolic acyl coenzyme A thioester hydr
15	102846	102846	BE264974	Hs.6566	thyroid hormone receptor interactor 13
	134161	134161	AA634543	Hs.79440	IGF-II mRNA-binding protein 3
	302363	302363	AW163799	Hs.198365	2,3-bisphosphoglycerate mutase
	125701	125701	T72104	Hs.93194	apolipoprotein A-I
	134656	134656	AI750878	Hs.87409	thrombospondin 1
20	102968	102968	AU076611	Hs.154672	methylene tetrahydrofolate dehydrogenase
	134037	134037	AI808780	Hs.227730	integrin, alpha 6
	103023	103023	AW500470	Hs.117950	multifunctional polypeptide similar to S
	130282	130282	BE245380	Hs.153952	5' nucleotidase (CD73)
	128568	128568	H12912	Hs.274691	adenylate kinase 3
25	103093	103093	S79876	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine
	129063	129063	X63094	Hs.283822	Rhesus blood group, D antigen
	133227	133227	AW977263	Hs.68257	general transcription factor IIIF, polype
	103184	103184	U43143	Hs.74049	fms-related tyrosine kinase 4
	103208	103208	AW411340	Hs.31314	retinoblastoma-binding protein 7
30	131486	131486	X6972	Hs.27372	BMX non-receptor tyrosine kinase
	103334	103334	NM_001260	Hs.25283	cyclin-dependent kinase 8
	135094	135094	NM_003304	Hs.250687	transient receptor potential channel 1
	103352	103352	H09366	Hs.78853	uracil-DNA glycosylase
	132173	132173	X89426	Hs.41716	endothelial cell-specific molecule 1
35	131584	131584	AA598509	Hs.29117	purine-rich element binding protein A
	103378	103378	AL119690	Hs.153618	HCGVIII-1 protein
	103410	103410	AA158294	Hs.295362	DR1-associated protein 1 (negative cofac
	103438	103438	AW175781	Hs.152720	M-phase phosphoprotein 6
	103452	103452	NM_006936	Hs.85119	SMT3 (suppressor of mif two 3, yeast) ho
40	135185	135185	AW404908	Hs.96038	Ric (Drosophila)-like, expressed in many
	134662	134662	NM_007048	Hs.284283	butyrophilin, subfamily 3, member A1
	103500	103500	AW408009	Hs.22580	alkylglycerone phosphate synthase
	132084	132084	NM_002267	Hs.3886	karyopherin alpha 3 (importin alpha 4)
	133152	133152	Z11695	Hs.324473	mitogen-activated protein kinase 1
45	103612	103612	BE336654	Hs.70937	H3 histone family, member A
	103692	103692	AW137912	Hs.227583	Homo sapiens chromosome X map Xp11.23 L-
	129796	129796	BE218319	Hs.5807	GTPase Rab14
	132683	132683	BE264633	Hs.143638	WD repeat domain 4
	103723	103723	BE274312	Hs.214783	Homo sapiens cDNA FLJ14041 fis, clone HE
50	133260	133260	AA403045	Hs.6906	Homo sapiens cDNA: FLJ23197 fis, clone R
	103766	103766	AI920783	Hs.191435	ESTs
	132051	132051	AA393968	Hs.180145	HSPC030 protein
	135289	135289	AW372569	Hs.9788	hypothetical protein MGC10924 similar to
	103794	103794	AF244135	Hs.30670	hepatocellular carcinoma-associated anti
55	134319	134319	BE304999	Hs.285754	fumarate hydratase
	119159	119159	AF142419	Hs.15020	homolog of mouse quaking QKI (KH domain
	103850	103850	AA187101	Hs.213194	hypothetical protein MGC10895
	322026	322026	AW024973	Hs.283675	NPD009 protein
	103861	103861	AA206236	Hs.4944	hypothetical protein FLJ12783
60	447735	447735	AA775268	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L
	131236	131236	AF043117	Hs.24594	ubiquitination factor E4B (homologous to
	129013	129013	AA371156	Hs.107942	DKFZP564M112 protein
	103988	103988	AA314389	Hs.342849	ADP-ribosylation factor-like 5
	425284	425284	AF155568	Hs.348043	NS1-associated protein 1
65	133281	133281	AK001601	Hs.69594	high-mobility group 20A
	108154	108154	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain
	135073	135073	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f
	129593	129593	AI338247	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f
	132064	132064	AA121098	Hs.3838	serum-inducible kinase
70	131427	131427	AF151879	Hs.26706	CGI-121 protein
	104282	104282	C14448	Hs.332338	EST
	130443	130443	D25216	Hs.155650	KIAA0014 gene product
	132837	132837	AA370362	Hs.57958	EGF-TM7-latrophilin-related protein
	104334	104334	D82614	Hs.78771	phosphoglycerate kinase 1
75	134731	134731	D89377	Hs.89404	msh (Drosophila) homeo box homolog 2
	131670	131670	H03514	Hs.15589	ESTs
	104402	104402	H56731	Hs.132956	ESTs

	129077	129077	N74724	Hs.108479	ESTs
	134927	134927	L36531	Hs.91296	integrin, alpha 8
	134498	134498	AW246273	Hs.84131	threonyl-tRNA synthetase
5	104488	104488	N56191	Hs.106511	protocadherin 17
	129214	129214	AL044335	Hs.109526	zinc finger protein 198
	104530	104530	AK001676	Hs.12457	hypothetical protein FLJ10814
	104544	104544	AI091173	Hs.222362	ESTs, Weakly similar to p40 [H.sapiens]
	104567	104567	AA040620	Hs.5672	hypothetical protein AF140225
10	129575	129575	F08282	Hs.278428	progesterone induced protein
	104599	104599	AW815036	Hs.151251	ESTs
	104667	104667	AI239923	Hs.63931	ESTs
	104764	104764	AI039243	Hs.278585	ESTs
	104787	104787	AA027317		gb:ze97d11.s1 Soares_fetal_heart_NbHH19W
15	104804	104804	AI858702	Hs.31803	ESTs, Weakly similar to N-WASP [H.sapien
	130828	130828	AW631469	Hs.203213	ESTs
	104943	104943	AF072873	Hs.114218	frizzled (Drosophila) homolog 6
	105024	105024	AA126311	Hs.9879	ESTs
	105038	105038	AW503733	Hs.9414	KIAA1488 protein
20	105096	105096	AL042506	Hs.21599	Kruppel-like factor 7 (ubiquitous)
	105169	105169	BE245294	Hs.180789	S164 protein
	130401	130401	BE396283	Hs.173987	eukaryotic translation initiation factor
	130114	130114	AA233393	Hs.14992	hypothetical protein FLJ11151
	105337	105337	AI468789	Hs.347187	myotubularin related protein 1
25	105376	105376	AW994032	Hs.8768	hypothetical protein FLJ10849
	131962	131962	AK000046	Hs.343877	hypothetical protein FLJ20039
	128658	128658	BE397354	Hs.324830	diphtheria toxin resistance protein requi
	105508	105508	AA173942	Hs.326416	Homo sapiens mRNA; cDNA DKFZp564H1916 (f
	135172	135172	AB028956	Hs.12144	KIAA1033 protein
30	132542	132542	AL137751	Hs.263671	Homo sapiens mRNA; cDNA DKFZp434I0812 (f
	105659	105659	AA283044	Hs.25625	hypothetical protein FLJ11323
	105674	105674	AI609530	Hs.279789	histone deacetylase 3
	105722	105722	AI922821	Hs.32433	ESTs
	115951	115951	BE546245	Hs.301048	sec13-like protein
35	105985	105985	AA406610		gb:zv15b10.s1 Soares_NhHMPu_S1 Homo sapi
	131216	131216	AI815486	Hs.243901	Homo sapiens cDNA FLJ20738 fis, clone HE
	113689	113689	AB037850	Hs.16621	DKFZP434I116 protein
	130839	130839	AB011169	Hs.20141	similar to S. cerevisiae SSM4
	130777	130777	AW135049	Hs.26285	Homo sapiens cDNA FLJ10643 fis, clone NT
40	106196	106196	AA525993	Hs.173699	ESTs, Weakly similar to ALU1_HUMAN ALU S
	133200	133200	AB037715	Hs.183639	hypothetical protein FLJ10210
	106328	106328	AL079559	Hs.28020	KIAA0766 gene product
	106423	106423	AB020722	Hs.16714	Rho guanine exchange factor (GEF) 15
	439608	439608	AW864696	Hs.301732	hypothetical protein MGC5306
45	106503	106503	AB033042	Hs.29679	cofactor required for Sp1 transcriptiona
	106543	106543	AA676939	Hs.69285	neuropilin 1
	106589	106589	AK000933	Hs.28661	Homo sapiens cDNA FLJ10071 fis, clone HE
	106596	106596	AA452379		ESTs, Moderately similar to ALU7_HUMAN A
	106636	106636	AW958037	Hs.286	ribosomal protein L4
50	131353	131353	AW754182		gb:RC2-CT0321-131199-011-c01 CT0321 Homo
	131710	131710	NM_015368	Hs.30985	pannexin 1
	131775	131775	AB014548	Hs.31921	KIAA0648 protein
	106773	106773	AA478109	Hs.188833	ESTs
	106817	106817	D61216	Hs.18672	ESTs
55	106848	106848	AA449014	Hs.121025	chromosome 11 open reading frame 5
	418699	418699	BE539639	Hs.173030	ESTs, Weakly similar to ALU8_HUMAN ALU S
	130638	130638	AW021276	Hs.17121	ESTs
	107059	107059	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E. coli Re
	107115	107115	BE379623	Hs.27693	peptidylprolyl isomerase (cyclophilin)-I
60	107156	107156	AA137043	Hs.9663	programmed cell death 6-interacting prot
	130621	130621	AW513087	Hs.16803	LUC7 (S. cerevisiae)-like
	132626	132626	AW504732	Hs.21275	hypothetical protein FLJ11011
	131610	131610	AA357879	Hs.29423	scavenger receptor with C-type lectin
	107295	107295	AA186629	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp
65	107315	107315	AA316241	Hs.90691	nucleophosmin/nucleoplasmin 3
	107328	107328	AW959891	Hs.76591	KIAA0887 protein
	134715	134715	U48263	Hs.89040	prepronociceptin
	129938	129938	AW003668	Hs.135587	Human clone 23629 mRNA sequence
	130074	130074	AL038596	Hs.250745	polymerase (RNA) III (DNA directed) (62k
70	132036	132036	AL157433	Hs.37706	hypothetical protein DKFZp434E2220
	113857	113857	AW243158	Hs.5297	DKFZP564A2416 protein
	130419	130419	AF037448	Hs.155489	NS1-associated protein 1
	132616	132616	BE262677	Hs.283558	hypothetical protein PRO1855
	132358	132358	NM_003542	Hs.46423	H4 histone family, member G
75	125827	125827	NM_003403	Hs.97496	YY1 transcription factor
	107609	107609	R75654	Hs.164797	hypothetical protein FLJ13693
	107714	107714	AA015761	Hs.60642	ESTs

	107832	107832	AA021473		gb:ze66c11.s1 Soares retina N2b4HR Homo
	124337	124337	N23541	Hs.281561	Homo sapiens cDNA: FLJ23582 fis, clone L
	129577	129577	N75346	Hs.306121	CDC20 (cell division cycle 20, S. cerevi
	132000	132000	AW247017	Hs.36978	melanoma antigen, family A, 3
5	107935	107935	AA029428	Hs.61555	ESTs
	131461	131461	AA992841	Hs.27263	KIAA1458 protein
	108029	108029	AA040740	Hs.62007	ESTs
	108084	108084	AA058944	Hs.116602	Homo sapiens, clone IMAGE:4154008, mRNA,
10	108168	108168	AI453137	Hs.63176	ESTs
	108189	108189	AW376061	Hs.63335	ESTs, Moderately similar to A46010 X-lin
	108203	108203	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone C
	108217	108217	AA058686	Hs.62588	ESTs
	108277	108277	AA064859		gb:zm50f03.s1 Stratagene fibroblast (937
15	108309	108309	AA069818		gb:zm67e03.r1 Stratagene neuroepithelium
	108340	108340	AA069820	Hs.180909	peroxiredoxin 1
	108427	108427	AA076382		gb:zm91g08.s1 Stratagene ovarian cancer
	108439	108439	AA078986		gb:zm92h01.s1 Stratagene ovarian cancer
	108469	108469	AA079487		gb:zm97f08.s1 Stratagene colon HT29 (937
20	108501	108501	AA083256		gb:zm08g12.s1 Stratagene hNT neuron (937
	108562	108562	AA100796		gb:zm26c06.s1 Stratagene pancreas (93720
	130890	130890	AI907537	Hs.76698	stress-associated endoplasmic reticulum
	130385	130385	AW067800	Hs.155223	stanniocalcin 2
	108807	108807	AI652236	Hs.49376	hypothetical protein FLJ20644
25	108833	108833	AF188527	Hs.61661	ESTs, Weakly similar to AF174605 1 F-box
	108846	108846	AL117452	Hs.44155	DKFZP586G1517 protein
	131474	131474	L46353	Hs.2726	high-mobility group (nonhistone chromoso
	108941	108941	AA148650		gb:zo09e06.s1 Stratagene neuroepithelium
	108996	108996	AW995610	Hs.332436	EST
30	131183	131183	AI611807	Hs.285107	hypothetical protein FLJ13397
	109022	109022	AA157291	Hs.21479	ubiquitin 1
	109068	109068	AA164293	Hs.72545	ESTs
	129021	129021	AL044675	Hs.173081	KIAA0530 protein
	109146	109146	AA176589	Hs.142078	EST
35	131080	131080	NM_001955	Hs.2271	endothelin 1
	109222	109222	AA192833	Hs.333512	similar to rat myomegalin
	109481	109481	AA878923	Hs.289069	hypothetical protein FLJ21016
	109516	109516	AI471639	Hs.71913	ESTs
	109556	109556	AI925294	Hs.87385	ESTs
40	109578	109578	F02208	Hs.27214	ESTs
	109625	109625	H29490	Hs.22697	ESTs
	109648	109648	H17800	Hs.7154	ESTs
	109699	109699	H18013	Hs.167483	ESTs
	109933	109933	R52417	Hs.20945	Homo sapiens clone 24993 mRNA sequence
	110039	110039	H11938	Hs.21907	histone acetyltransferase

TABLE 2A

Table 2A shows the accession numbers for those pkeys lacking unigenelD's for Table 2. The pkeys in Table 7 lacking unigenelD's are represented within Tables 1-6A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

10	Pkey: CAT number: Accession:	Unique Eos probeset identifier number Gene cluster number Genbank accession numbers	
15	Pkey	CAT Number	Accession
	108469	116761_1	AA079487 AA128547 AA128291 AA079587 AA079600
	108501	13684_-12	AA083256
	108562	36375_1	AA100796 AF020589 AA074629 AA075946 AA100849 AA085347 AA126309 AA079311 AA079323 AA085274
20	101300	4669_1	BE535511 M62098 AA306787 WB891766 AA348998 AA338869 AA344013 AW956561 AW389343 AW403607 L40391 AW408435 AA121738 AI568978 H13317 R20373 AW948724 AW948744 AA335023 AA436722 AA448690 C21404 AW884390 AA345454 AA303292 AA174174 BE092290 T90614 AA035104 R76028 AA126924 AA741086 AW022056 AW118940 AA121666 AI832409 AA683475 AI140901 AI623576 AW519064 AW474125 AI953923 AI735349 AW150109 AI436154 AW118130 AW270782 AI804073 N27434 AA876543 AA937815 AI051166 AA505378 AI041975 AI335355 AI089540 AA662243 AI127912 AI925604 AI250880 AI366874 AI564386 AI815196 AI683526 AI435885 AI160934 H79030 AI801493 AA448691 AI673767 AI076042 AI804327 AA813438 AA680002 AI274492 T16177 AI287337 AI935050 AA907805 AA911493 AI589411 AI371358 AW576236 AI078866 AW516168 AA346372 AI560185 AA471009 R75857 AA296025 AA523155 AA853168 AI696593 AI658482 AI566601 AW072797 AA128047 AA035502 AW243274 AA992517 R43760
25			W73853 AA928112 W77887 AW889237 AA148524 AI749182 AI754442 AI338392 AI253102 AI079403 AI370541 AI697341 H97538 AW188021 AI927669 W72716 AI051402 AI188071 AI335900 N21488 AW770478 W92522 AI691028 AI913512 AI144448 W73819 AA604358 N28900 W95221 AI868132 H98465 AA148793 R20840 R20839
30	117156	145392_1	M30269 NM_002508 X82245 AI078760 AW957003 D78945 M27445 AA650439 AL048816 AV660256 AV660347 AA333052 BE295257 T60999 AA383049 AW369677 Z26985 AW175704 AA343326 AW747957 AI818389 W17308 W17302 H15591 AA371284 AA370412 W94966 BE384365 T28498 R80714 R16959 H21723 AW835154 D56097 D56381 W21232 AA190565 AW379755 AW067895
35			AI352558 Z82248 X78138 NM_003405 AU077248 AA223125 S80794 D78577 AI124697 AW403970 BE614089 BE296713 BE621334 L20422 X80536 D54224 D54950 X57345 N29226 AA127798 AA340253 F08031 AA192540 H67636 AA321827 AW950283 AA084159 BE538808 AW401377 AA256774 C03366 W46595 W47608 AA305009 H69431 H69456 AL120082 H11706 AA303717 AA361357 H22042 H78020 AW999584 AA134368 AA322911 AA322961 H60980 N85248 N31547 H79624 T11718 W85826 AW894663 AW894624 BE167441 BE170015 AA304626 AW602163 AW998929 AA156681 AA151067 BE002724 AA608688 H82692 BE155392 AW383636 BE155394 AA487004 AW383504 AI342365 R82553 W16498 BE155344 AI143938 R69901 AA322873 AW340648 R25364 AA367935 AI559406 AA033522 AA374252 AW835019 AI922133 AI697089 N99662 AW189078 AI199076 AW151598 W59944 AA662875 W94022 AA299055 AI039008 AI829449 AA583503 AI635674 AW131665 AI473820 AW273118 AW900930 AA908944 AI688035 AW170272 AI082545 AW468176 AI608761 AI082748 AI911682 AI248943 AI831016 AA192465 AI218477 AA938406 AA385288 AI809817 AA905196 AI191245 AI470204 AI188296 AI421367 AI125315 AI087141 AA629032 AA740589 AI554181 AA150830 AI248541 AI077943 AA775958 AA864930 AI261476 AI123121 AI310394 AA862331 AA872478 BE537084 AI205606 AA720684 AI872093 AW150042 AL120538 AA219627 AA988608 C21397 AI359337 H25337 AI089749 AA605146 AI359620 AA150478 AI359738 AW383642 AW995424 AI766457 R56892 AI089839 W61343 N69107 W46459 AA565955 N20527 AI279782 W46596 AA776573 H23204 AI866231 AI083995 N21530 AA126874 D82630 W65437 AI086917 AW382095 AI086877 H69844 AW340217 W85827 L08439 AA262704 AA505380 W47413 W94135 AA223241 AW089153 AA084101 BE538000 AA096126 T28031 AA491574 R84813 AA774536 AW383522 AA155615 AW383529 AA491520 AW028427 AA171496 AI469689 AW664539 AI811102 AI811116 BE464590 BE350791 H78021 T15405 H21979 AA219489 H13301 AA505883 AI864305 AI423963 AW084401 F04963 R69858 H67097 AI917740 AI655561 H69864 AA033631 AW383484 AI886261 H25293 AA513281 AW271187 H11617 N79982 AI174338 AI904207 AI904208 BE614558 W94127 W65436 AI272249 AA700018 AI579932 AI085941 AW152629
40			AA404418 AI217248 AA353093 AW957317 AW872498 AI560785 AI289110 AW135512 X97261 T68873 AI743860 N49543 AW027759 BE349467 AI656284 BE463975 R35022 AA370031 AW955302 AL042109 N53092 AI611424 AL079362 AI969290 AI928016 BE394912 BE504220 BE467505 AI611611 AI611407 AI611452 W56437 AI284566 AI583349 AW183058 AI308085 AI074952 AA437315 AA628161 AW301728 AI150224 AA400137 AA437279 AI223355 AA639462 AI261373 AI432414 AI984994 AI539335 AA401550 AA358757 AI609976 AA442357 AA359393 AA437046 AA370301 AA429328 AW272055 AI580502 AI832944 AI038530 AA425107 AI014986 AI148349 AW237721 AW779756 AW137877 AI125293 AA400404 R28554
45			AA069818 AA069971 AA069923 AA069908
50	121335	279548_1	AA021473
	130018	18986_1	AA608588
	121822	244391_1	
55			
60			
65	108309	111495_1	
	107832	genbank_AA021473	AA021473
	123523	genbank_AA608588	AA608588
70	123964	genbank_C13961	C13961
	118475	genbank_N66845	N66845
	104787	genbank_AA027317	AA027317
	106596	304084_1	AI583948 AA578212 AW303715 AA653450 AA456981 AI400385 W88533 AI224133 AW272145 AA088686 R94698
	113947	genbank_W84768	W84768
75	108277	genbank_AA064859	AA064859

	108427	genbank_AA076382	AA076382
	108439	genbank_AA078986	AA078986
	131353	231290_1	AW411259 H23555 AW015049 AI684275 AW015886 AW068953 AW014085 AI027260 R52686 AA918278 AI129462 AA969360 N34869 AI948416 AA534205 AA702483 AA705292
5	101447	entrez_M21305	M21305
	108931	genbank_AA147186	AA147186
	108941	genbank_AA148650	AA148650
	103138	entrez_X65965	X65965
10	119174	genbank_R71234	R71234
	119416	genbank_T97186	T97186
	105985	genbank_AA406610	AA406610
	100327	entrez_D55640	D55640

TABLE 3:

5	Pkey:	Unique Eos probeset identifier number			
	Accession:	Accession number used for previous patent filings			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
10	Pkey	Accession	ExAccn	UniGene	UnigeneTitle
	100405	D86425	AW291587	Hs.82733	nidogen 2
	100420	D86983	D86983	Hs.118893	Melanoma associated gene
15	100481	HG1098-HT1098	X70377	Hs.121489	cystatin D
	100484	HG1103-HT1103	NM_005402	Hs.288757	v-rat simian leukemia viral oncogene hom
	100718	HG3342-HT3519	BE295928	Hs.75424	inhibitor of DNA binding 1, dominant neg
	100991	J03764	J03836	Hs.82085	serine (or cysteine) proteinase inhibito
20	101097	L06797	BE245301	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus
	101168	L15388	NM_005308	Hs.211569	G protein-coupled receptor kinase 5
	101194	L20971	L20971	Hs.188	phosphodiesterase 4B, cAMP-specific (dun
	101261	L35545	D30857	Hs.82353	protein C receptor, endothelial (EPCR)
	101345	L76380	NM_005795	Hs.152175	calcitonin receptor-like
	101447	M21305	M21305		gb:Human alpha satellite and satellite 3
25	101485	M24736	AA296520	Hs.89546	selectin E (endothelial adhesion molecucl
	101543	M31166	M31166	Hs.2050	pentaxin-related gene, rapidly induced b
	101550	M31551	Y00630	Hs.75716	serine (or cysteine) proteinase inhibito
	101560	M32334	AW958272	Hs.347326	intercellular adhesion molecule 2
	101674	M61916	NM_002291	Hs.82124	laminin, beta 1
30	101714	M68874	M68874	Hs.211587	phospholipase A2, group IVA (cytosolic,
	101741	M74719	NM_003199	Hs.326198	transcription factor 4
	101838	M92934	BE243845	Hs.75511	connective tissue growth factor
	101857	M94856	BE550723	Hs.153179	fatty acid binding protein 5 (psoriasis-s
	102012	U03057	BE259035	Hs.118400	singed (Drosophila)-like (sea urchin fas
35	102024	U03877	AA301867	Hs.76224	EGF-containing fibulin-like extracellula
	102164	U18300	NM_000107	Hs.77602	damage-specific DNA binding protein 2 (4
	102241	U27109	NM_007351	Hs.268107	multimerin
	102283	U31384	AW161552	Hs.83381	guanine nucleotide binding protein 11
	102303	U33053	U33053	Hs.2499	protein kinase C-like 1
40	102564	U59423	U59423	Hs.79067	MAD (mothers against decapentaplegic, Dr
	102663	U70322	NM_002270	Hs.168075	karyopherin (importin) beta 2
	102759	U81607	NM_005100	Hs.788	A kinase (PRKA) anchor protein (gravin)
	102778	U83463	AF000652	Hs.8180	syndecan binding protein (syntenin)
	102804	U89942	NM_002318	Hs.83354	lysyl oxidase-like 2
45	102887	X04729	J03836	Hs.82085	serine (or cysteine) proteinase inhibito
	102898	X06256	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,
	102915	X07820	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin
	103036	X54925	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial
50	103037	X54936	BE018302	Hs.2894	placental growth factor, vascular endoth
	103095	X60957	NM_005424	Hs.78824	tyrosine kinase with immunoglobulin and
	103158	X67235	BE242587	Hs.118651	hematopoietically expressed homeobox
	103166	X67951	AA159248	Hs.180909	peroxiredoxin 1
	103185	X69910	NM_006825	Hs.74368	transmembrane protein (63kD), endoplasmic
	103280	X79981	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula
55	103554	Z18951	AI878826	Hs.74034	caveolin 1, caveolae protein, 22kD
	103850	AA187101	AA187101	Hs.213194	hypothetical protein MGC10895
	104465	N24990	Z44203	Hs.26418	ESTs
	104592	R81003	AW630488	Hs.25338	protease, serine, 23
	104764	AA025351	AI039243	Hs.278585	ESTs
60	104786	AA027168	AA027167	Hs.10031	KIAA0955 protein
	104850	AA040465	AL133035	Hs.8728	hypothetical protein DKFZp434G171
	104865	AA045136	T79340	Hs.22575	B-cell CLL/lymphoma 6, member B (zinc fi
	104894	AA054087	AF065214	Hs.18858	phospholipase A2, group IVC (cytosolic,
	104952	AA071089	AW076098	Hs.345588	desmoplakin (DPI, DPLI)
65	104974	AA085918	Y12059	Hs.278675	bromodomain-containing 4
	105178	AA187490	AA313825	Hs.21941	AD036 protein
	105263	AA227926	AW388633	Hs.6682	solute carrier family 7, (cationic amino
	105330	AA234743	AW388625	Hs.22120	ESTs
	105376	AA236559	AW994032	Hs.8768	hypothetical protein FLJ10849
70	105729	AA292694	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds
	105826	AA398243	AA478756	Hs.194477	E3 ubiquitin ligase SMURF2
	105977	AA406363	AK001972	Hs.30822	hypothetical protein FLJ11110
	106008	AA411465	AB033888	Hs.8619	SRV (sex determining region Y)-box 18
	106031	AA412284	X64116	Hs.171844	Homo sapiens cDNA: FLJ22296 fis, clone H
75	106124	AA423987	H93366	Hs.7567	Homo sapiens cDNA: FLJ21962 fis, clone H

	106155	AA425309	AA425414	Hs.33287	nuclear factor I/B
	106302	AA435896	AA398859	Hs.18397	hypothetical protein FLJ23221
	106423	AA448238	AB020722	Hs.16714	Rho guanine exchange factor (GEF) 15
5	106793	AA478778	H94997	Hs.16450	ESTs
	107174	AA621714	BE122762	Hs.25338	ESTs
	107216	D51069	D51069	Hs.211579	melanoma cell adhesion molecule
	107295	T34527	AA186629	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp
	107385	U97519	NM_005397	Hs.16426	podocalyxin-like
10	108756	AA127221	AA127221	Hs.117037	ESTs
	108846	AA132983	AL117452	Hs.44155	DKFZP586G1517 protein
	108888	AA135606	AA135606	Hs.189384	gb:zl10a05.s1 Soares_pregnant_uterus_NbH
	109001	AA156125	AI056548	Hs.72116	hypothetical protein FLJ20992 similar to
	109166	AA179845	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines
15	109456	AA232645	AW956580	Hs.42699	ESTs
	109768	F10399	F06838	Hs.14763	ESTs
	110107	H16772	AW151660	Hs.31444	ESTs
	110906	N39584	AA035211	Hs.17404	ESTs
	110984	N52006	AW613287	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp
20	111006	N53375	BE387014	Hs.166146	Homer, neuronal immediate early gene, 3
	111018	N54067	AI287912	Hs.3628	mitogen-activated protein kinase kinase
	111133	N64436	AW580939	Hs.97199	complement component C1q receptor
	111760	R26892	BE551929	Hs.268754	Homo sapiens cDNA FLJ11949 fis, clone HE
	113073	T33637	N39342	Hs.103042	microtubule-associated protein 1B
25	113195	T57112	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom
	113923	W80763	AW953484	Hs.3849	hypothetical protein FLJ22041 similar to
	114521	AA046808	AW139036	Hs.108957	40S ribosomal protein S27 isoform
	115061	AA253217	AI751438	Hs.41271	Homo sapiens mRNA full length insert cDN
	115096	AA255991	AI683069	Hs.175319	ESTs
30	115145	AA258138	AA740907	Hs.88297	ESTs
	115819	AA426573	AA486620	Hs.41135	endomucin-2
	115947	AA443793	R47479	Hs.94761	KIAA1691 protein
	116314	AA490588	AI799104	Hs.178705	Homo sapiens cDNA FLJ11333 fis, clone PL
	116339	AA496257	AK000290	Hs.44033	dipeptidyl peptidase 8
35	116430	AA609717	AK001531	Hs.66048	hypothetical protein FLJ10669
	116589	D59570	AI557212	Hs.17132	ESTs, Moderately similar to I54374 gene
	116733	F13787	AL157424	Hs.61289	synaptojanin 2
	117023	H88157	AW070211	Hs.102415	Homo sapiens mRNA; cDNA DKFZp586N0121 (f
	117186	H98988	H98988	Hs.42612	ESTs, Weakly similar to ALU1_HUMAN ALU S
40	117563	N34287	AF055634	Hs.44553	unc5 (C.elegans homolog) c
	117997	N52090	N52090	Hs.47420	EST
	118475	N66845	N66845		gb:za46c11.s1 Soares fetal liver spleen
	118581	N68905	N68905		gb:za69b09.s1 Soares_fetal_lung_NbHL19W
	119073	R32894	BE245360	Hs.279477	ESTs
45	119155	R61715	R61715	Hs.310598	ESTs, Moderately similar to ALU1_HUMAN A
	119174	R71234	R71234		gb:yi54c08.s1 Soares placenta Nb2HP Homo
	119221	R98105	C14322	Hs.250700	trypsin beta 1
	119416	T97186	T97186		gb:ye50h09.s1 Soares fetal liver spleen
	119866	W80814	AA496205	Hs.193700	Homo sapiens mRNA; cDNA DKFZp586I0324 (f
50	121335	AA404418	AA404418		gb:zw37e02.s1 Soares_total_fetus_Nb2HF8_
	121381	AA405747	AW088642	Hs.97984	hypothetical protein FLJ22252 similar to
	123160	AA488687	AA488687	Hs.284235	ESTs, Weakly similar to I38022 hypothi
	123473	AA599143	AA599143		gb:ae52d04.s1 Stratagene lung carcinoma
	123523	AA608588	AA608588		gb:ae54e06.s1 Stratagene lung carcinoma
55	123533	AA608751	AA608751		gb:ae56h07.s1 Stratagene lung carcinoma
	123964	C13961	C13961		gb:C13961 Clontech human aorta polyA+ mR
	124006	D60302	AI147155	Hs.270016	ESTs
	124315	H94892	NM_005402	Hs.288757	v-ral simian leukemia viral oncogene hom
	124659	N93521	AI680737	Hs.289068	Homo sapiens cDNA FLJ11918 fis, clone HE
60	124669	N95477	AI571594	Hs.102943	hypothetical protein MGC12916
	124847	R60044	W07701	Hs.304177	Homo sapiens clone FLB8503 PRO2286 mRNA,
	124875	R70506	AI887664	Hs.285814	sprouty (Drosophila) homolog 4
	125091	T91518	T91518		gb:ye20f05.s1 Stratagene lung (937210) H
	125103	T95333	AA570056	Hs.122730	ESTs, Moderately similar to KIAA1215 pro
65	125355	R45630	R60547	Hs.170098	KIAA0372 gene product
	125565	R20839	R20840		gb:yg05c08.r1 Soares infant brain 1NIB H
	125590	R23858	R23858	Hs.143375	Homo sapiens, clone IMAGE:3840937, mRNA,
	126511	AI024874	T92143	Hs.57958	EGF-TM7-latrophilin-related protein
	126563	W26247	AA516391	Hs.181368	U5 snRNP-specific protein (220 kD), orth
70	126649	AA856990	AA001860	Hs.279531	ESTs
	126872	AA136653	AW450979		gb:UI-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su
	127402	AA358869	AA358869	Hs.227949	SEC13 (S. cerevisiae)-like 1
	127651	AI123976	AA382523	Hs.105689	MSTP031 protein
	127759	AI369384	AI369384	Hs.292441	ESTs
75	128062	AA379500	AA379621	Hs.105547	neural proliferation, differentiation an
	128992	R49693	H04150	Hs.107708	ESTs
	129046	AA195678	AB029290	Hs.108258	actin binding protein; macrophin (microf

	129188	M30257	NM_001078	Hs.109225	vascular cell adhesion molecule 1
	129314	AA028131	BE622768	Hs.290356	mesoderm development candidate 1
	129371	M10321	X06828	Hs.110802	von Willebrand factor
5	129468	J03040	AW410538	Hs.111779	secreted protein, acidic, cysteine-rich
	129765	M86933	M86933	Hs.1238	amelogenin (Y chromosome)
	129805	AA012933	AA012848	Hs.12570	tubulin-specific chaperone d
	129884	AA286710	AF055581	Hs.13131	lysosomal
10	130495	AA243278	AW250380	Hs.109059	mitochondrial ribosomal protein L12
	130639	D59711	AI557212	Hs.17132	ESTs, Moderately similar to I54374 gene
	130657	T94452	AW337575	Hs.201591	ESTs
	130828	AA053400	AW631469	Hs.203213	ESTs
	130972	AA370302	D81866	Hs.21739	Homo sapiens mRNA; cDNA DKFZp58611518 (f
	131080	J05008	NM_001955	Hs.2271	endothelin 1
	131137	U85193	W27392	Hs.33287	nuclear factor I/B
15	131182	AA256153	AI824144	Hs.23912	ESTs
	131486	X83107	F06972	Hs.27372	BMX non-receptor tyrosine kinase
	131573	AA046593	AA040311	Hs.28959	ESTs
	131647	AA410480	AA359615	Hs.30089	ESTs
	131756	D45304	AA443966	Hs.31595	ESTs
20	131859	M90657	AW960564		transmembrane 4 superfamily member 1
	131881	AA010163	AW361018	Hs.3383	upstream regulatory element binding prot
	132050	AA136353	AI267615	Hs.38022	ESTs
	132083	Y07867	BE386490	Hs.279663	Pirin
25	132164	U84573	AI752235	Hs.41270	procollagen-lysine, 2-oxoglutarate 5-dio
	132358	X60486	NM_003542	Hs.46423	H4 histone family, member G
	132413	AA132969	AW361383	Hs.260116	metalloprotease 1 (pitrilysin family)
	132456	AA114250	AB011084	Hs.48924	KIAA0512 gene product; ALEX2
	132490	F13782	NM_001290	Hs.4980	LIM domain binding 2
30	132676	AA283035	N92589	Hs.261038	ESTs, Weakly similar to I38022 hypotheti
	132687	AB002301	AB002301	Hs.54985	KIAA0303 protein
	132718	AA056731	NM_004600	Hs.554	Sjogren syndrome antigen A2 (60kD, ribon
	132736	U68019	AW081883	Hs.211578	Homo sapiens cDNA: FLJ23037 fis, clone L
	132760	H99198	AA125985	Hs.56145	thymosin, beta, identified in neuroblast
	132933	AA598702	BE263252	Hs.6101	hypothetical protein MGC3178
35	132968	N77151	AF234532	Hs.61638	myosin X
	132994	AA505133	AA112748	Hs.279905	clone HQ0310 PRO0310p1
	133081	AB000584	AI186431	Hs.296638	prostate differentiation factor
	133147	D12763	AA026533	Hs.66	interleukin 1 receptor-like 1
40	133161	AA253193	AW021103	Hs.6631	hypothetical protein FLJ20373
	133200	AA432248	AB037715	Hs.183639	hypothetical protein FLJ10210
	133260	AA083572	AA403045	Hs.6906	Homo sapiens cDNA: FLJ23197 fis, clone R
	133363	AA479713	AI866286	Hs.71962	ESTs, Weakly similar to B36298 proline-r
	133491	L40395	BE619053	Hs.170001	eukaryotic translation initiation factor
45	133517	X52947	NM_000165	Hs.74471	gap junction protein, alpha 1, 43kD (con
	133550	W80846	AI129903	Hs.74669	vesicle-associated membrane protein 5 (m
	133607	M34539	BE273749		FK506-binding protein 1A (12kD)
	133614	D67029	NM_003003	Hs.75232	SEC14 (S. cerevisiae)-like 1
	133627	U09587	NM_002047	Hs.75280	glycyl-tRNA synthetase
50	133691	M85289	M85289	Hs.211573	heparan sulfate proteoglycan 2 (perlecan
	133696	D10522	AI878921	Hs.75607	myristoylated alanine-rich protein kinas
	133913	W84712	AU076964	Hs.7753	calumenin
	133975	D29992	C18356	Hs.295944	tissue factor pathway inhibitor 2
	133985	L34657	L34657	Hs.78146	platelet/endothelial cell adhesion molec
55	134039	S78569	NM_002290	Hs.78672	laminin, alpha 4
	134088	D43636	AI379954	Hs.79025	KIAA0096 protein
	134161	U97188	AA634543	Hs.79440	IGF-II mRNA-binding protein 3
	134299	AA487558	AW580939	Hs.97199	complement component C1q receptor
	134416	M28882	X68264	Hs.211579	melanoma cell adhesion molecule
60	134453	X70683	AI272141	Hs.83484	SRY (sex determining region Y)-box 4
	134656	X14787	AI750878	Hs.87409	thrombospondin 1
	134989	AA236324	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi
	135051	C15324	AI272141	Hs.83484	SRY (sex determining region Y)-box 4
	135073	AA452000	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f
65	135349	D83174	AA114212	Hs.9930	serine (or cysteine) proteinase inhibito
	100114	D00596	X02308	Hs.82962	thymidylate synthetase
	100130	D11428	NM_000304	Hs.103724	peripheral myelin protein 22
	100143	D13640	AU076465	Hs.278441	KIAA0015 gene product
	100168	D14874	H73444	Hs.394	adrenomedullin
70	100208	D26129	NM_002933	Hs.78224	ribonuclease, RNase A family, 1 (pancrea
	100224	D28476	AL121516	Hs.138617	thyroid hormone receptor interactor 12
	100405	D86425	AW291587	Hs.82733	nidogen 2
	100420	D86983	D86983	Hs.118893	Melanoma associated gene
	100455	D87953	AW888941	Hs.75789	N-myc downstream regulated
75	100529	HG1862-HT1897	BE313693	Hs.334330	calmodulin 2 (phosphorylase kinase, delt
	100618	HG2614-HT2710	AI752163	Hs.114599	collagen, type VIII, alpha 1
	100619	HG2639-HT2735	N24433	Hs.241567	RNA binding motif, single stranded inter

	100658	HG2855-HT2995	U56725	Hs.180414	heat shock 70kD protein 2
	100676	HG3044-HT3742	X02761	Hs.287820	fibronectin 1
	100718	HG3342-HT3519	BE295928	Hs.75424	inhibitor of DNA binding 1, dominant neg
5	100752	HG3543-HT3739	T81309		insulin-like growth factor 2 (somatomedi
	100828	HG4069-HT4339	AL048753	Hs.303649	small inducible cytokine A2 (monocyte ch
	100850	HG417-HT417	AA836472	Hs.297939	cathepsin B
	100991	J03764	J03836	Hs.82085	serine (or cysteine) proteinase inhibito
	101097	L06797	BE245301	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus
10	101110	L08246	AI439011	Hs.86386	myeloid cell leukemia sequence 1 (BCL2-r
	101142	L12711	L12711	Hs.89643	transketolase (Wernicke-Korsakoff syndro
	101156	L13977	AA340987	Hs.75693	prolylcarboxypeptidase (angiotensinase C
	101168	L15388	NM_005308	Hs.211569	G protein-coupled receptor kinase 5
	101184	L19871	NM_001674	Hs.460	activating transcription factor 3
	101192	L20859	BE247295	Hs.78452	solute carrier family 20 (phosphate tran
15	101317	L42176	L42176	Hs.8302	four and a half LIM domains 2
	101336	L49169	NM_006732	Hs.75678	FBJ murine osteosarcoma viral oncogene h
	101345	L76380	NM_005795	Hs.152175	calcitonin receptor-like
	101400	M15990	M15990	Hs.194148	v-yes-1 Yamaguchi sarcoma viral oncogene
20	101475	M23254	BE410405	Hs.76288	calpain 2, (mII) large subunit
	101485	M24736	AA296520	Hs.89546	selectin E (endothelial adhesion molecu
	101496	M26576	X12784	Hs.119129	collagen, type IV, alpha 1
	101505	M27396	AA307680	Hs.75692	asparagine synthetase
	101543	M31166	M31166	Hs.2050	pentaxin-related gene, rapidly induced b
25	101557	M31994	BE293116	Hs.76392	aldehyde dehydrogenase 1 family, member
	101560	M32334	AW958272	Hs.347326	intercellular adhesion molecule 2
	101587	M35878	AI752416	Hs.77326	insulin-like growth factor binding prote
	101592	M36429	AF064853	Hs.91299	guanine nucleotide binding protein (G pr
	101633	M57730	NM_004428	Hs.1624	ephrin-A1
30	101634	M57731	AV650262	Hs.75765	GRO2 oncogene
	101667	M60858	NM_005381		nucleolin
	101682	M62994	AF043045	Hs.81008	filamin B, beta (actin-binding protein-2
	101714	M68874	M68874	Hs.211587	phospholipase A2, group IVA (cytosolic,
	101720	M69043	M69043	Hs.81328	nuclear factor of kappa light polypeptid
	101741	M74719	NM_003199	Hs.326198	transcription factor 4
35	101744	M75126	AI879352	Hs.118625	hexokinase 1
	101793	M84349	W01076	Hs.278573	CD59 antigen p18-20 (antigen identified
	101837	M92843	M92843	Hs.343586	zinc finger protein homologous to Zfp-36
	101838	M92934	BE243845	Hs.75511	connective tissue growth factor
40	101840	M93056	AA236291	Hs.183583	serine (or cysteine) proteinase inhibito
	101857	M94856	BE550723	Hs.153179	fatty acid binding protein 5 (psoriasis-
	101864	M95787	BE392588	Hs.75777	transgelin
	101931	S76965	NM_006823	Hs.75209	protein kinase (cAMP-dependent, catalyti
	101966	S81914	X96438	Hs.76095	immediate early response 3
45	102012	U03057	BE259035	Hs.118400	singed (Drosophila)-like (sea urchin fas
	102013	U03100	BE616287	Hs.178452	catenin (cadherin-associated protein), a
	102024	U03877	AA301867	Hs.76224	EGF-containing fibulin-like extracellular
	102059	U08021	AI752666	Hs.76669	nicotinamide N-methyltransferase
	102121	U14391	NM_004998	Hs.82251	myosin IE
50	102283	U31384	AW161552	Hs.83381	guanine nucleotide binding protein 11
	102300	U32944	AI929721	Hs.5120	dynein, cytoplasmic, light polypeptide
	102378	U40369	AU076887	Hs.28491	spermidine/spermine N1-acetyltransferase
	102395	U41767	AU077005	Hs.92208	a disintegrin and metalloproteinase doma
	102460	U48959	U48959	Hs.211582	myosin, light polypeptide kinase
55	102491	U51010	U51010		gb:Human nicotinamide N-methyltransferas
	102499	U51478	BE243877	Hs.76941	ATPase, Na+/K+ transporting, beta 3 poly
	102523	U53445	U53445	Hs.15432	downregulated in ovarian cancer 1
	102560	U59289	R97457	Hs.63984	cadherin 13, H-cadherin (heart)
	102564	U59423	U59423	Hs.79067	MAD (mothers against decapentaplegic, Dr
60	102589	U62015	AU076728	Hs.8867	cysteine-rich, angiogenic inducer, 61
	102600	U63825	AI984144	Hs.66713	hepatitis delta antigen-interacting prot
	102645	U67963	AL119566	Hs.6721	lysosomal
	102687	U73379	NM_007019	Hs.93002	ubiquitin carrier protein E2-C
	102693	U73824	AA532780	Hs.183684	eukaryotic translation initiation factor
65	102709	U77604	AA122237	Hs.81874	microsomal glutathione S-transferase 2
	102759	U81607	NM_005100	Hs.788	A kinase (PRKA) anchor protein (gravin)
	102804	U89942	NM_002318	Hs.83354	lysyl oxidase-like 2
	102882	X04412	AI767736	Hs.290070	gelsolin (amyloidosis, Finnish type)
	102907	X06985	BE409861	Hs.202833	heme oxygenase (decycling) 1
	102915	X07820	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin
70	102927	X12876	BE512730	Hs.65114	keratin 18
	102960	X15729	AI904738	Hs.76053	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep
	103011	X52541	AJ243425	Hs.326035	early growth response 1
	103020	X53416	X53416	Hs.195464	filamin A, alpha (actin-binding protein-
75	103029	X54489	AW800726	Hs.789	GRO1 oncogene (melanoma growth stimulat
	103036	X54925	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial
	103056	X57206	Y18024	Hs.78877	inositol 1,4,5-trisphosphate 3-kinase B

5	103080	X59798	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomatos
	103095	X60957	NM_005424	Hs.78824	tyrosine kinase with immunoglobulin and
	103138	X65965	X65965		gb:H.sapiens SOD-2 gene for manganese su
	103176	X69111	AL021154	Hs.76884	inhibitor of DNA binding 3, dominant neg
	103195	X70940	AA351647	Hs.2642	eukaryotic translation-elongation factor
10	103347	X87838	AU077309	Hs.171271	catenin (cadherin-associated protein), b
	103371	X91247	X91247	Hs.13046	thioredoxin reductase 1
	103432	X97748	X97748		gb:H.sapiens PTX3 gene promotor region.
	103471	Y00815	Y00815	Hs.75216	protein tyrosine phosphatase, receptor t
	103967	AA303711	AL120051	Hs.144700	ephrin-B1
15	104447	L44538	AW204145	Hs.156044	ESTs
	104764	AA025351	AI039243	Hs.278585	ESTs
	104783	AA027050	AA533513	Hs.93659	protein disulfide isomerase related prot
	104798	AA029462	AW952619	Hs.17235	Homo sapiens clone TCCCA00176 mRNA sequ
	104865	AA045136	T79340	Hs.22575	B-cell CLL/lymphoma 6, member B (zinc fi
20	104877	AA047437	AI138635	Hs.22968	Homo sapiens clone IMAGE:451939, mRNA se
	104894	AA054087	AF065214	Hs.18858	phospholipase A2, group IVC (cytosolic,
	104952	AA071089	AW076098	Hs.345588	desmoplakin (DPI, DPLI)
	105113	AA156450	AB037816	Hs.8982	Homo sapiens, clone IMAGE:3506202, mRNA,
	105178	AA187490	AA313825	Hs.21941	AD036 protein
25	105196	AA195031	W84893	Hs.9305	angiotensin receptor-like 1
	105215	AA205724	AA205759	Hs.10119	hypothetical protein FLJ14957
	105263	AA227926	AW388633	Hs.6682	solute carrier family 7, (cationic amino
	105271	AA227986	AA807881	Hs.25329	ESTs
	105330	AA234743	AW338625	Hs.22120	ESTs
30	105461	AA253216	BE539071	Hs.69388	hypothetical protein FLJ20505
	105492	AA256210	AI805717	Hs.289112	CGI-43 protein
	105493	AA256268	AL047586	Hs.10283	RNA binding motif protein 8B
	105594	AA279397	AB024334	Hs.25001	tyrosine 3-monooxygenase/tryptophan 5-mo
	105727	AA292379	AL135159	Hs.20340	KIAA1002 protein
35	105732	AA292717	AW504170	Hs.274344	hypothetical protein MGC12942
	105767	AA346551	AW370946	Hs.23457	ESTs
	105882	AA400292	W46802	Hs.81988	disabled (Drosophila) homolog 2 (mitogen
	105936	AA404338	AI678765	Hs.21812	ESTs
	106031	AA412284	X64116	Hs.171844	Homo sapiens cDNA: FLJ22296 fis, clone H
40	106124	AA423987	H93366	Hs.7567	Homo sapiens cDNA: FLJ21962 fis, clone H
	106222	AA428594	AA356392	Hs.21321	Homo sapiens clone FLB9213 PRO2474 mRNA,
	106241	AA430108	BE019681	Hs.6019	Homo sapiens cDNA: FLJ21288 fis, clone C
	106263	AA431462	W21493	Hs.28329	hypothetical protein FLJ14005
	106264	AA431470	AL046859	Hs.3407	protein kinase (cAMP-dependent, catalyti
45	106366	AA443756	AA186715	Hs.336429	RIKEN cDNA 9130422N19 gene
	106454	AA449479	NM_014038	Hs.5216	HSPC028 protein
	106634	AA459916	W25491	Hs.288909	hypothetical protein FLJ22471
	106724	AA465226	N48670	Hs.28631	Homo sapiens cDNA: FLJ22141 fis, clone H
	106793	AA478778	H94997	Hs.16450	ESTs
50	106799	AA479037	BE313412	Hs.7951	Homo sapiens clone 25012 mRNA sequence
	106842	AA482597	AF124251	Hs.26054	novel SH2-containing protein 3
	106868	AA487561	BE185536	Hs.301183	molecule possessing ankyrin repeats indu
	106890	AA489245	AA489245	Hs.88500	mitogen-activated protein kinase 8 inter
	106961	AA504110	AW243614	Hs.18063	Homo sapiens cDNA FLJ10768 fis, clone NT
55	106974	AA520989	AI817130	Hs.9195	Homo sapiens cDNA FLJ13698 fis, clone PL
	107030	AA599434	AL117424	Hs.25035	chloride intracellular channel 4
	107061	AA608649	BE147611	Hs.6354	stromal cell derived factor receptor 1
	107086	AA609519	NM_012331	Hs.26458	methionine sulfoxide reductase A
	107216	D51069	D51069	Hs.211579	melanoma cell adhesion molecule
60	107385	U97519	NM_005397	Hs.16426	podocalyxin-like
	107444	W28391	W28391	Hs.343258	proliferation-associated 2G4, 38kD
	107985	AA035638	T40064	Hs.71968	Homo sapiens mRNA; cDNA DKFZp564F053 (fr
	108507	AA083514	AI554545	Hs.68301	ESTs
	108695	AA121315	AB029000	Hs.70823	KIAA1077 protein
65	108931	AA147186	AA147186		gb:z038d01.s1 Stratagene endothelial cel
	109001	AA156125	AI056548	Hs.72116	hypothetical protein FLJ20992 similar to
	109195	AA188932	AF047033	Hs.132904	solute carrier family 4, sodium bicarbon
	109390	AA219653	AW007485	Hs.87125	EH-domain containing 3
	109456	AA232645	AW956580	Hs.42699	ESTs
70	109737	F10078	AA055415	Hs.13233	ESTs, Moderately similar to A47582 B-cel
	110411	H48032	AW001579	Hs.9645	Homo sapiens mRNA for KIAA1741 protein,
	110660	H82117	AA782114	Hs.28043	ESTs
	110906	N39584	AA035211	Hs.17404	ESTs
	111018	N54067	AI287912	Hs.3628	mitogen-activated protein kinase kinase
75	111091	N59858	AA300067	Hs.33032	hypothetical protein DKFZp434N185
	111356	N90933	BE301871	Hs.4867	mannosyl (alpha-1,3)-glycoprotein beta-
	111378	N93764	AW160993	Hs.326292	hypothetical gene DKFZp434A1114
	111741	R26124	AB020653	Hs.24024	KIAA0846 protein
	111769	R27957	AW629414	Hs.24230	ESTs
	112318	R55470	AW083384	Hs.11067	ESTs, Highly similar to T46395 hypotheti

	112951	T16550	AA307634	Hs.6650	vacuolar protein sorting 45B (yeast homo
	113057	T26674	AW194301	Hs.339283	Human DNA sequence from clone RP1-187J11
	113195	T57112	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom
5	113490	T88700	BE178110	Hs.173374	Homo sapiens cDNA FLJ10500 fis, clone NT
	113542	T90527	H43374	Hs.7890	Homo sapiens mRNA for KIAA1671 protein,
	113803	W42789	AW880709	Hs.283683	chromosome 8 open reading frame 4
	113847	W60002	NM_005032	Hs.4114	plastin 3 (T isoform)
	113910	W78175	AA113262	Hs.17901	Homo sapiens, clone IMAGE:3937015, mRNA,
10	113947	W84768	W84768		gb:zh53d03.s1 Soares_fetal_liver_spleen_
	114047	W94427	AL035858	Hs.3807	FXD domain-containing ion transport reg
	115061	AA253217	AI751438	Hs.41271	Homo sapiens mRNA full length insert cDN
	115819	AA426573	AA486620	Hs.41135	endomucin-2
	115870	AA432374	NM_005985	Hs.48029	snail 1 (drosophila homolog), zinc finger
15	115964	AA446622	AA987568	Hs.74313	KIAA1265 protein
	116228	AA478771	AI767947	Hs.50841	ESTs
	116264	AA482594	D51174	Hs.272239	lysosomal
	116314	AA490588	AI799104	Hs.178705	Homo sapiens cDNA FLJ11333 fis, clone PL
	116589	D59570	AI557212	Hs.17132	ESTs, Moderately similar to I54374 gene
20	117023	H88157	AW070211	Hs.102415	Homo sapiens mRNA; cDNA DKFZp586N0121 (f
	117112	H94648	AW969999	Hs.293658	ESTs
	117156	H97538	W73853		ESTs
	117176	H98670	H45100	Hs.49753	uveal autoantigen with coiled coil domai
	117280	N22107	M18217	Hs.172129	Homo sapiens cDNA: FLJ21409 fis, clone C
25	119559	W38197	W38197		Empirically selected from AFFX single pr
	119866	W80814	AA486205	Hs.193700	Homo sapiens mRNA; cDNA DKFZp586I0324 (f
	120655	AA287347	AA305599	Hs.238205	hypothetical protein PRO2013
	121314	AA402799	W07343	Hs.182538	phospholipid scramblase 4
	121335	AA404418	AA404418		gb:zw37e02.s1 Soares_total_fetus_Nb2HF8_
30	121822	AA425107	AI743860		metallothionein 1E (functional)
	121835	AA425435	AB033030	Hs.300670	KIAA1204 protein
	122331	AA442872	AL133437	Hs.110771	Homo sapiens cDNA: FLJ21904 fis, clone H
	122577	AA452860	AA829725	Hs.334437	hypothetical protein MGC4248
	123160	AA488687	AA488687	Hs.284235	ESTs, Weakly similar to I38022 hypotheti
35	123486	AA599674	BE019072	Hs.334802	Homo sapiens cDNA FLJ14680 fis, clone NT
	124059	F13673	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti
	124339	H99093	H99093	Hs.343411	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep
	124358	N22495	AW070211	Hs.102415	Homo sapiens mRNA; cDNA DKFZp586N0121 (f
	124364	N23031	AF265555	Hs.250646	baculoviral IAP repeat-containing 6
40	124726	R15740	NM_003654	Hs.104576	carbohydrate (keratan sulfate Gal-6) sul
	124763	R39610	BE410405	Hs.76288	calpain 2, (m/l) large subunit
	125167	W45560	AL137540	Hs.102541	netrin 4
	125304	Z39833	AL359573	Hs.124940	GTP-binding protein
	125307	Z40583	AW580945	Hs.330466	ESTs
45	125329	AA825437	AA825437	Hs.58875	ESTs
	125598	R66613	T40064	Hs.71968	Homo sapiens mRNA; cDNA DKFZp564F053 (fr
	125609	AA868063	AA868063	Hs.104576	carbohydrate (keratan sulfate Gal-6) sul
	418245	AA128075	AA088767	Hs.83883	transmembrane, prostate androgen induced
	127435	N66570	X69086	Hs.286161	Homo sapiens cDNA FLJ13613 fis, clone PL
50	127566	AI051390	AI051390	Hs.116731	ESTs
	127619	AA627122	AA627122	Hs.163787	ESTs
	128453	X02761	X02761	Hs.287820	fibronectin 1
	128495	AF010193	NM_005904	Hs.100602	MAD (mothers against decapentaplegic, Dr
	128515	AA149044	BE395085	Hs.10086	type I transmembrane protein Fn14
55	128580	U82108	U82108	Hs.101813	solute carrier family 9 (sodium/hydrogen
	128623	D78676	BE076608	Hs.105509	CTL2 gene
	128642	L35240	Z28913	Hs.102948	enigma (LIM domain protein)
	128669	AA598737	W28493	Hs.180414	heat shock 70kD protein 8
	128903	R69417	AW150717	Hs.345728	STAT induced STAT inhibitor 3
60	128914	AA232837	AW867491	Hs.107125	plasmalemma vesicle associated protein
	129087	N72695	AI348027	Hs.108557	hypothetical protein PP1057
	129188	M30257	NM_001078	Hs.109225	vascular cell adhesion molecule 1
	129226	M96843	BE222494	Hs.180919	inhibitor of DNA binding 2, dominant neg
	129265	X68277	AA530892	Hs.171695	dual specificity phosphatase 1
65	129345	AA292440	R22497	Hs.110571	growth arrest and DNA-damage-inducible,
	129468	J03040	AW410538	Hs.111779	secreted protein, acidic, cysteine-rich
	129488	AA228107	AW966728	Hs.54642	methionine adenosyltransferase II, beta
	129498	AA449789	AA449789	Hs.75511	connective tissue growth factor
	129557	W01367	AL045404	Hs.46366	KIAA0948 protein
70	129619	AA610116	AA209534	Hs.284243	tetraspan NET-6 protein
	129627	AA258308	T40064	Hs.71968	Homo sapiens mRNA; cDNA DKFZp564F053 (fr
	129762	AA460273	AA453694	Hs.12372	tripartite motif protein TRIM2
	129884	AA286710	AF055581	Hs.13131	lysosomal
	130018	T68873	AA353093		metallothionein 1L
75	130147	D63476	D63476	Hs.172813	PAK-interacting exchange factor beta
	130178	M62403	U20982	Hs.1516	insulin-like growth factor-binding prote
	130282	X55740	BE245380	Hs.153952	5' nucleotidase (CD73)

	130431	L10284	AW505214	Hs.155560	calnexin
	130495	AA243278	AW250380	Hs.109059	mitochondrial ribosomal protein L12
	130553	AA430032	AF062649	Hs.252587	pituitary tumor-transforming 1
5	130638	H16402	AW021276	Hs.17121	ESTs
	130639	D59711	AI557212	Hs.17132	ESTs, Moderately similar to I54374 gene
	130657	T94452	AW337575	Hs.201591	ESTs
	130686	AA431571	BE548267	Hs.337986	Homo sapiens cDNA FLJ10934 fis, clone OV
	130776	R79356	AF167706	Hs.19280	cysteine-rich motor neuron 1
10	130818	AA280375	AW190920	Hs.19928	hypothetical protein SP329
	130840	Z49269	BE048821	Hs.20144	small inducible cytokine subfamily A (Cy
	130899	Z41740	AI077288	Hs.296323	serum/glucocorticoid regulated kinase
	131002	AA121543	AL050295	Hs.22039	KIAA0758 protein
	131080	J05008	NM_001955	Hs.2271	endothelin 1
	131084	AA101878	NM_017413	Hs.303084	apelin; peptide ligand for APJ receptor
15	131091	T35341	AJ271216	Hs.22880	dipeptidylpeptidase III
	131107	N87590	BE620886	Hs.75354	GCN1 (general control of amino-acid synt
	131182	AA256153	AI824144	Hs.23912	ESTs
	131207	W74533	AF104266	Hs.24212	latrophilin
20	131319	U25997	NM_003155	Hs.25590	stanniocalcin 1
	131328	V01512	AW939251	Hs.25647	v-fos FBJ murine osteosarcoma viral onco
	131328	V01512	AW939251	Hs.25647	v-fos FBJ murine osteosarcoma viral onco
	131328	V01512	AW939251	Hs.25647	v-fos FBJ murine osteosarcoma viral onco
	131328	V01512	AW939251	Hs.25647	v-fos FBJ murine osteosarcoma viral onco
25	131509	X56681	X56681	Hs.2780	jun D proto-oncogene
	131555	AA161292	T47364	Hs.278613	interferon, alpha-inducible protein 27
	131564	AA491465	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL
	131573	AA046593	AA040311	Hs.28959	ESTs
	131692	D50914	BE559681	Hs.30736	KIAA0124 protein
	131756	D45304	AA443966	Hs.31595	ESTs
30	131859	M90657	AW960564		transmembrane 4 superfamily member 1
	131909	W69127	NM_016558	Hs.274411	SCAN domain-containing 1
	131915	AA316186	AI161383	Hs.34549	ESTs, Highly similar to S94541 1 clone 4
	132046	AA384503	AI359214	Hs.179260	chromosome 14 open reading frame 4
	132050	AA136353	AI267615	Hs.38022	ESTs
35	132151	AA044755	BE379499	Hs.173705	Homo sapiens cDNA: FLJ22050 fis, clone H
	132164	U84573	AI752235	Hs.41270	procollagen-lysine, 2-oxoglutarate 5-dio
	132187	AA058911	AA235709	Hs.4193	DKFZP586O1624 protein
	132303	AA620962	BE177330	Hs.325093	Homo sapiens cDNA: FLJ21210 fis, clone C
40	132314	AA285290	AF112222	Hs.323806	pinin, desmosome associated protein
	132358	X60486	NM_003542	Hs.46423	H4 histone family, member G
	132398	R31641	AA876616	Hs.16979	ESTs, Weakly similar to A43932 mucin 2 p
	132421	AA489190	AW163483	Hs.48320	double ring-finger protein, Dorfin
	132490	F13782	NM_001290	Hs.4980	LIM domain binding 2
45	132520	AA257993	AA257992	Hs.50651	Janus kinase 1 (a protein tyrosine kinas
	132546	M24283	M24283	Hs.168383	intercellular adhesion molecule 1 (CD54)
	132610	AA443114	AA160511	Hs.5326	amino acid system N transporter 2; porcu
	132716	T35289	BE379595	Hs.283738	casein kinase 1, alpha 1
	132840	N23817	BE218319	Hs.5807	GTPase Rab14
50	132883	AA047151	AA373314	Hs.5897	Homo sapiens mRNA; cDNA DKFZp586P1622 (f
	132968	N77151	AF234532	Hs.61638	myosin X
	132989	AA480074	AA480074	Hs.331328	hypothetical protein FLJ13213
	132999	Y00787	Y00787	Hs.624	interleukin 8
	133071	T99789	BE384932	Hs.64313	ESTs, Weakly similar to AF257182 1 G-pro
55	133076	W84341	AW946276	Hs.6441	Homo sapiens mRNA; cDNA DKFZp586J021 (fr
	133099	L09209	W16518	Hs.279518	amyloid beta (A4) precursor-like protein
	133147	D12763	AA026533	Hs.66	Interleukin 1 receptor-like 1
	133149	T16484	AA370045	Hs.6607	AXIN1 up-regulated
	133161	AA253193	AW021103	Hs.6631	hypothetical protein FLJ20373
60	133200	AA432248	AB037715	Hs.183639	hypothetical protein FLJ10210
	133220	X82200	NM_006074	Hs.318501	Homo sapiens mRNA full length insert cDN
	133260	AA083572	AA403045	Hs.6906	Homo sapiens cDNA: FLJ23197 fis, clone R
	133295	L00352	AI147861	Hs.213289	low density lipoprotein receptor (famili
	133349	N75791	AW631255	Hs.8110	L-3-hydroxyacyl-Coenzyme A dehydrogenase
65	133391	X57579	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a
	133398	X02612	NM_000499	Hs.72912	cytochrome P450, subfamily I (aromatic c
	133436	H44631	BE294068	Hs.737	immediate early protein
	133454	AA090257	BE547647	Hs.177781	hypothetical protein MGC5618
	133478	X83703	X83703	Hs.31432	cardiac ankyrin repeat protein
70	133491	L40395	BE619053	Hs.170001	eukaryotic translation initiation factor
	133510	AA227913	AW880841	Hs.96908	p53-induced protein
	133517	X52947	NM_000165	Hs.74471	gap junction protein, alpha 1, 43kD (con
	133526	M11313	AU077051	Hs.74561	alpha-2-macroglobulin
	133538	L14837	NM_003257	Hs.74614	tight junction protein 1 (zona occludens
75	133562	M60721	M60721	Hs.74870	H2.0 (Drosophila)-like homeo box 1
	133584	D90209	D90209	Hs.181243	activating transcription factor 4 (tax-r
	133590	T67986	T70956	Hs.75106	clusterin (complement lysis inhibitor, S

133617	AA148318	BE244334	Hs.75249	ADP-ribosylation factor-like 6 interacti
133651	U97105	AI301740	Hs.173381	dihydropyrimidinase-like 2
133671	T25747	AW503116	Hs.301819	zinc finger protein 146
133678	K02574	AW247252		nucleoside phosphorylase
133681	D78577	AI352558		tyrosine 3-monooxygenase/tryptophan 5-mo
133722	X53331	AW969976	Hs.279009	matrix Gla protein
133730	S73591	BE242779	Hs.179526	upregulated by 1,25-dihydroxyvitamin D-3
133750	X95735	BE410769	Hs.75873	zyxin
133802	L16862	AW239400	Hs.76297	G protein-coupled receptor kinase 6
133825	U44975	BE616902	Hs.285313	core promoter element binding protein
133838	M97796	BE222494	Hs.180919	inhibitor of DNA binding 2, dominant neg
133859	U86782	U86782	Hs.178761	26S proteasome-associated pad1 homolog
133889	AA099391	U48959	Hs.211582	myosin, light polypeptide kinase
133960	M19267	M19267	Hs.77899	tropomyosin 1 (alpha)
133975	D29992	C18356	Hs.295944	tissue factor pathway inhibitor 2
133977	L19314	AI125639	Hs.250666	hairy (Drosophila)-homolog
134039	S78569	NM_002290	Hs.78672	laminin, alpha 4
134075	U28811	NM_012201	Hs.78979	Golgi apparatus protein 1
134081	L77886	AL034349	Hs.79005	protein tyrosine phosphatase, receptor t
134164	C14407	AW245540	Hs.79516	brain abundant, membrane attached signal
134203	M60278	AA161219	Hs.799	diphtheria toxin receptor (heparin-bindi
134238	R81509	AA102179	Hs.160726	Homo sapiens cDNA FLJ11680 fis, clone HE
134299	AA487558	AW580939	Hs.97199	complement component C1q receptor
134332	D86962	D86962	Hs.81875	growth factor receptor-bound protein 10
134339	AA478971	R70429	Hs.81988	disabled (Drosophila) homolog 2 (mitogen
134343	D50683	D50683	Hs.82028	transforming growth factor, beta recepto
134381	U56637	AI557280	Hs.184270	capping protein (actin filament) muscle
134403	M61199	AA334551		sperm specific antigen 2
134416	M28882	X68264	Hs.211579	melanoma cell adhesion molecule
134493	X15183	M30627	Hs.289088	heat shock 90kD protein 1, alpha
134558	S53911	NM_001773	Hs.85289	CD34 antigen
134817	U20734	AU076592	Hs.198951	jun B proto-oncogene
134983	D28235	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p
134989	AA236324	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi
135052	AA148923	AL136653	Hs.93675	decidual protein induced by progesterone
135062	AA174183	AK000967	Hs.93872	KIAA1682 protein
135069	AA456311	AA876372	Hs.93961	Homo sapiens mRNA; cDNA DKFZp667D095 (fr
135071	L08069	W27190	Hs.94	DnaJ (Hsp40) homolog, subfamily A, membe
135073	AA452000	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f
135170	AA282140	T53169	Hs.9587	Homo sapiens cDNA: FLJ22290 fis, clone H
135196	J02854	C03577	Hs.9615	myosin regulatory light chain 2, smooth
135348	AA442054	U80983	Hs.268177	phospholipase C, gamma 1 (formerly subty
134404	AB000450	AB000450	Hs.82771	vaccinia related kinase 2
439561	AB002380	AF180681	Hs.6582	Rho guanine exchange factor (GEF) 12
100082	AB003103	AA130080	Hs.4295	proteasome (prosome, macropain) 26S subu
132817	AB004884	N27852	Hs.57553	tousled-like kinase 2
130150	AF000573	BE094848	Hs.15113	homogentisate 1,2-dioxygenase (homogenti
100104	AF008937	AF008937		syntaxin 16
447973	AF009301	AB011169	Hs.20141	similar to S. cerevisiae SSM4
332613	AF009368	AF029674	Hs.173422	KIAA1605 protein
100113	D00591	NM_001269	Hs.84746	chromosome condensation 1
133980	D00760	AA294921	Hs.348024	v-ral simian leukemia viral oncogene hom
100129	D11139	AA469369	Hs.5831	tissue inhibitor of metalloproteinase 1
100154	D14657	H60720	Hs.81892	KIAA0101 gene product
100169	D14878	AL037228	Hs.82043	D123 gene product
129718	D17716	NM_002410	Hs.121502	mannosyl (alpha-1,6-)-glycoprotein beta-
100190	D21090	M91401	Hs.178658	RAD23 (S. cerevisiae) homolog B
134742	D26135	NM_001346	Hs.89462	diacylglycerol kinase, gamma (90kD)
100211	D26528	D26528	Hs.123058	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep
100238	D30742	L24959	Hs.348	calcium/calmodulin-dependent protein kin
130283	D31762	NM_012288	Hs.153954	TRAM-like protein
134237	D31765	D31765	Hs.170114	KIAA0061 protein
100248	D31888	NM_015156	Hs.78398	KIAA0071 protein
100256	D38128	D25418	Hs.393	prostaglandin I2 (prostaglandin) receptor
100262	D38500	D38500	Hs.278468	postmeiotic segregation increased 2-like
134329	D38551	N92036	Hs.81848	RAD21 (S. pombe) homolog
100281	D42087	AF091035	Hs.184627	KIAA0118 protein
100294	D49396	AA331881	Hs.75454	peroxiredoxin 3
100327	D55640	D55640		gb:Human monocyte PABL (pseudautosomal
100335	D63391	AW247529	Hs.6793	platelet-activating factor acetylhydrola
134495	D63477	D63477	Hs.84087	KIAA0143 protein
100338	D63483	D86864	Hs.57735	acetyl LDL receptor; SREC
135152	D64015	M96954	Hs.182741	TIA1 cytotoxic granule-associated RNA-bi
134269	D79990	NM_014737	Hs.80905	Ras association (RalGDS/AF-6) domain fam
100372	D79997	NM_014791	Hs.184339	KIAA0175 gene product
134304	D80010	BE613486	Hs.81412	lipin 1

	100394	D84276	D84284	Hs.66052	CD38 antigen (p45)
	100405	D86425	AW291587	Hs.82733	nidogen 2
	100418	D86978	D86978	Hs.84790	KIAA0225 protein
5	133154	D87012	D87012	Hs.194685	topoisomerase (DNA) III beta
	134347	D87075	AF164142	Hs.82042	solute carrier family 23 (nucleobase tra
	444099	D87432	D87432	Hs.10315	solute carrier family 7 (cationic amino
	100438	D87448	AA013051	Hs.91417	topoisomerase (DNA) II binding protein
	134593	D87845	NM_000437	Hs.234392	platelet-activating factor acetylhydrola
10	100481	HG1098-HT1098	X70377	Hs.121489	cystatin D
	100552	HG2167-HT2237	AA019521	Hs.301946	lysosomal
	100591	HG2415-HT2511	NM_004091	Hs.231444	Homo sapiens, Similar to hypothetical pr
	100652	HG2825-HT2949	BE613608	Hs.142653	ret finger protein
	100662	HG2887-HT3031	AI368680	Hs.816	SRY (sex determining region Y)-box 2
15	100899	HG4660-HT5073	AL039123	Hs.103042	microtubule-associated protein 1B
	100905	HG4704-HT5146	L12260	Hs.172816	neuregulin 1
	100945	HG884-HT884	AF002225	Hs.180686	ubiquitin protein ligase E3A (human papi
	100950	HG919-HT919	AF128542	Hs.166846	polymerase (DNA directed), epsilon
	100964	J00212	J00212		Empirically selected from AFFX single pr
20	135407	J04029	J04029	Hs.99936	keratin 10 (epidermolytic hyperkeratosis
	130149	J04031	AW067805	Hs.172665	methylene tetrahydrofolate dehydrogenase
	131877	J04088	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)
	101016	J04543	J04543	Hs.78637	annexin A7
	134786	L06139	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous
25	134100	L07540	AA460085	Hs.171075	replication factor C (activator 1) 5 (36
	134078	L08895	L08895	Hs.78995	MADS box transcription enhancer factor 2
	101132	L11239	L11239	Hs.36993	gastrulation brain homeo box 1
	134849	L11353	BE409525	Hs.902	neurofibromin 2 (bilateral acoustic neur
	332736	L13773	Z83689	Hs.114765	myeloid/lymphoid or mixed-lineage leukem
30	101152	L13800	AI984625	Hs.9884	spindle pole body protein
	135397	L14922	L14922	Hs.166563	replication factor C (activator 1) 1 (14
	432642	L15189	BE297635	Hs.3069	heat shock 70kD protein 9B (mortalin-2)
	101168	L15388	NM_005308	Hs.211569	G protein-coupled receptor kinase 5
	421155	L16895	H87879	Hs.102267	lysyl oxidase
35	101226	L27476	AF083892	Hs.75608	tight junction protein 2 (zona occludens
	415138	L27624	C18356	Hs.295944	tissue factor pathway inhibitor 2
	134739	L32976	NM_002419	Hs.89449	mitogen-activated protein kinase kinase
	130155	L33404	AA101043	Hs.151254	kalikrein 7 (chymotryptic, stratum com
	440538	L35263	W76332	Hs.79107	mitogen-activated protein kinase 14
40	409916	L37347	BE313625	Hs.57435	solute carrier family 11 (proton-coupled
	101294	L40371	AF168418	Hs.116784	thyroid hormone receptor interactor 4
	101300	L40391	BE535511		transmembrane trafficking protein
	101310	L41607	L41607	Hs.934	glucosaminyl (N-acetyl) transferase 2, I
	130344	L77566	AW250122	Hs.154879	DiGeorge syndrome critical region gene D
45	101381	M13928	AW675039	Hs.1227	aminolevulinic acid, delta-, dehydratase
	101381	M13928	AW675039	Hs.1227	aminolevulinic acid, delta-, dehydratase
	415678	M14016	AW005903	Hs.78601	uroporphyrinogen decarboxylase
	133780	M14219	AA557660	Hs.76152	decorin
	101396	M15796	BE267931	Hs.78996	proliferating cell nuclear antigen
50	101447	M21305	M21305		gb:Human alpha satellite and satellite 3
	101458	M22092	M22092		gb:Human neural cell adhesion molecule (
	101470	M22898	NM_000546	Hs.1846	tumor protein p53 (Li-Fraumeni syndrome)
	134604	M22995	NM_002884	Hs.865	RAP1A, member of RAS oncogene family
	101478	M23379	NM_002890	Hs.758	RAS p21 protein activator (GTPase activa
55	133519	M24400	AW583062	Hs.74502	chymotrypsinogen B1
	131185	M25753	BE280074	Hs.23960	cyclin B1
	134116	M27691	R84694	Hs.79194	cAMP responsive element binding protein
	133999	M28213	AA535244	Hs.78305	RAB2, member RAS oncogene family
	130174	M29550	M29551	Hs.151531	protein phosphatase 3 (formerly 2B), cat
60	129963	M29971	M29971	Hs.1384	O-6-methylguanine-DNA methyltransferase
	132983	M30269	M30269		nidogen (enactin)
	133900	M31158	M31158	Hs.77439	protein kinase, cAMP-dependent, regulato
	101543	M31166	M31166	Hs.2050	pentaxin-related gene, rapidly induced 'b
	101545	M31210	BE246154	Hs.154210	endothelial differentiation, sphingolipi
65	101620	M55420	S55271	Hs.247930	Epsilon, IgE
	134691	M59979	AW382987	Hs.88474	prostaglandin-endoperoxide synthase 1 (p
	133595	M62810	AA393273	Hs.75133	transcription factor 6-like 1 (mitochond
	101700	M64710	D90337	Hs.247916	natriuretic peptide precursor C
	101714	M68874	M68874	Hs.211587	phospholipase A2, group IVA (cytosolic,
70	134246	M74524	D28459	Hs.80612	ubiquitin-conjugating enzyme E2A (RAD6 h
	101760	M80254	M80254	Hs.173125	peptidylprolyl isomerase F (cyclophilin
	415022	M81780	X59960	Hs.77813	sphingomyelin phosphodiesterase 1, acid
	415022	M81780	X59960	Hs.77813	sphingomyelin phosphodiesterase 1, acid
	415022	M81780	X59960	Hs.77813	sphingomyelin phosphodiesterase 1, acid
75	415022	M81780	X59960	Hs.77813	sphingomyelin phosphodiesterase 1, acid
	415022	M81780	X59960	Hs.77813	sphingomyelin phosphodiesterase 1, acid
	101791	M83822	M83822	Hs.62354	cell division cycle 4-like

	101812	M86934	BE439894	Hs.78991	DNA segment, numerous copies, expressed
	101813	M87338	NM_002914	Hs.139226	replication factor C (activator 1) 2 (40
	133396	M96326	M96326	Hs.72885	azurocidin 1 (cationic antimicrobial pro
5	428161	M96954	M96954	Hs.182741	TIA1 cytotoxic granule-associated RNA-bi
	129026	M98833	AL120297	Hs.108043	Friend leukemia virus integration 1
	101901	S66793	H38026	Hs.308	arrestin 3, retinal (X-arrestin)
	134831	S72370	AA853479	Hs.89890	pyruvate carboxylase
	134039	S78569	NM_002290	Hs.78672	laminin, alpha 4
10	442355	S79873	AA456539	Hs.8262	lysosomal-associated membrane protein 2
	101975	S83325	AA079717	Hs.283664	aspartate beta-hydroxylase
	101977	S83364	AF112213	Hs.184062	putative Rab5-interacting protein
	101978	S83365	BE561610	Hs.5809	putative transmembrane protein; homolog
	101998	U01212	U01212	Hs.248153	olfactory marker protein
	102003	U01922	U01922	Hs.125565	translocase of inner mitochondrial membr
15	102007	U02556	U02556	Hs.75307	t-complex-associated-testis-expressed 1-
	102009	U02680	BE245149	Hs.82643	protein tyrosine kinase 9
	416658	U03272	U03272	Hs.79432	fibrillin 2 (congenital contractural ara
	132951	U04209	AW821182	Hs.61418	microfibrillar-associated protein 1
20	135389	U05237	U05237	Hs.99872	fetal Alzheimer antigen
	102048	U07225	U07225	Hs.339	purinergic receptor P2Y, G-protein coupl
	130145	U07620	U34820	Hs.151051	mitogen-activated protein kinase 10
	303153	U09759	U09759	Hs.246857	mitogen-activated protein kinase 9
	420269	U09820	U72937	Hs.96264	alpha thalassemia/mental retardation syn
	102095	U11313	U11313	Hs.75760	sterol carrier protein 2
25	102123	U14518	NM_001809	Hs.1594	centromere protein A (17kD)
	102126	U14575	AW950870	Hs.78961	protein phosphatase 1, regulatory (inhib
	102133	U15173	AU076845	Hs.155596	BCL2/adenovirus E1B 19kD-interacting pro
	102139	U15932	NM_004419	Hs.2128	dual specificity phosphatase 5
	102162	U18291	AA450274	Hs.1592	CDC16 (cell division cycle 16, S. cerevi
30	102164	U18300	NM_000107	Hs.77602	damage-specific DNA binding protein 2 (4
	427653	U18383	AA159001	Hs.180069	nuclear respiratory factor 1
	131817	U20536	U20536	Hs.3280	caspase 6, apoptosis-related cysteine pr
	102200	U21551	AA232362	Hs.157205	branched chain aminotransferase 1, cytos
35	102210	U23028	BE619413	Hs.2437	eukaryotic translation initiation factor
	102214	U23752	U23752	Hs.32964	SRY (sex determining region Y)-box 11
	132811	U25435	U25435	Hs.57419	CCCTC-binding factor (zinc finger protei
	131319	U25997	NM_003155	Hs.25590	stanniocalcin 1
	102256	U28251	U28251	Hs.53237	ESTs, Highly similar to Z169_HUMAN ZINC
40	132316	U28831	U28831	Hs.44566	KIAA1641 protein
	102269	U30245	U30245		gb:Human myelomonocytic specific protein
	417526	U32315	AA568906	Hs.82240	syntaxin 3A
	102293	U32439	AF090116	Hs.79348	regulator of G-protein signalling 7
	102298	U32849	AA382169	Hs.54483	N-myc (and STAT) interactor
45	102325	U35139	AI815867	Hs.50130	neodin (mouse) homolog
	428734	U36764	BE303044	Hs.192023	eukaryotic translation initiation factor
	102361	U39400	AA223616	Hs.75859	chromosome 11 open reading frame 4
	102367	U39657	U39656	Hs.118825	mitogen-activated protein kinase kinase
	102388	U41344	AA362907	Hs.76494	proline arginine-rich end leucine-rich r
50	102394	U41766	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma
	129829	U41813	AF010258	Hs.127428	homeo box A9
	102409	U43286	BE300330	Hs.118725	selenophosphate synthetase 2
	133746	U44378	AW410035	Hs.75862	MAD (mothers against decapentaplegic, Dr
	102423	U44754	Z47542	Hs.179312	small nuclear RNA activating complex, po
55	132828	U47011	AB014615	Hs.57710	fibroblast growth factor 8 (androgen-ind
	132828	U47011	AB014615	Hs.57710	fibroblast growth factor 8 (androgen-ind
	132828	U47011	AB014615	Hs.57710	fibroblast growth factor 8 (androgen-ind
	132828	U47011	AB014615	Hs.57710	fibroblast growth factor 8 (androgen-ind
	425322	U47077	U63630	Hs.155637	protein kinase, DNA-activated, catalytic
60	102450	U48251	U48251	Hs.75871	protein kinase C binding protein 1
	129350	U50535	U50535	Hs.110630	Human BRCA2 region, mRNA sequence CG006
	102534	U56833	U96759	Hs.198307	von Hippel-Lindau binding protein 1
	130457	U58091	AB014595	Hs.155976	cullin 4B
	135065	U58837	AA019401	Hs.93909	cyclic nucleotide gated channel beta 1
65	102560	U59289	R97457	Hs.63984	cadherin 13, H-cadherin (heart)
	102567	U59863	U63830	Hs.146847	TRAF family member-associated NFKB activ
	417173	U67122	U61397	Hs.81424	ubiquitin-like 1 (sentrin)
	102638	U67319	U67319	Hs.9216	caspase 7, apoptosis-related cysteine pr
	132736	U68019	AW081883	Hs.211578	Homo sapiens cDNA: FLJ23037 fis, clone L
70	133070	U69611	U92649	Hs.64311	a disintegrin and metalloproteinase doma
	102663	U70322	NM_002270	Hs.168075	karyopherin (importin) beta 2
	134660	U73524	U73524	Hs.87465	ATP/GTP-binding protein
	102735	U79267	AF111106	Hs.3382	protein phosphatase 4, regulatory subuni
	102741	U79291	AW959829	Hs.83572	hypothetical protein MGC14433
	130564	U82671	U82671	Hs.36980	melanoma antigen, family A, 2
75	130564	U82671	U82671	Hs.36980	melanoma antigen, family A, 2
	132164	U84573	AI752235	Hs.41270	procollagen-lysine, 2-oxoglutarate 5-dio

	102823	U90914	D85390	Hs.5057	carboxypeptidase D
	102826	U91316	NM_007274	Hs.8679	cytosolic acyl coenzyme A thioester hydr
	102831	U91932	AA262170	Hs.80917	adaptor-related protein complex 3, sigma
5	102846	U96131	BE264974	Hs.6566	thyroid hormone receptor interactor 13
	129777	U97018	U97018	Hs.12451	echinoderm microtubule-associated protei
	134161	U97188	AA634543	Hs.79440	IGF-II mRNA-binding protein 3
	134854	V00503	J03464	Hs.179573	collagen, type I, alpha 2
	429257	X04327	AW163799	Hs.198365	2,3-bisphosphoglycerate mutase
10	413985	X06389	AI018666	Hs.75667	synaptophysin
	419768	X07496	T72104	Hs.93194	apolipoprotein A-I
	102915	X07820	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin
	134656	X14787	AI750878	Hs.87409	thrombospondin 1
	413858	X15525	NM_001610	Hs.75589	acid phosphatase 2, lysosomal
15	102968	X16396	AU076611	Hs.154672	methylene tetrahydrofolate dehydrogenase
	102971	X16609	X16609	Hs.183805	ankyrin 1, erythrocytic
	134037	X53586	AI808780	Hs.227730	integrin, alpha 6
	134037	X53586	AI808780	Hs.227730	integrin, alpha 6
	103023	X53793	AW500470	Hs.117950	multifunctional polypeptide similar to S
	103037	X54936	BE018302	Hs.2894	placental growth factor, vascular endoth
20	130282	X55740	BE245380	Hs.153952	5' nucleotidase (CD73)
	134542	X57025	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi
	128568	X60673	H12912	Hs.274691	adenylate kinase 3
	128568	X60673	H12912	Hs.274691	adenylate kinase 3
25	103093	X60708	S79876	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine
	413076	X62048	U10564	Hs.75188	wee1 (S. pombe) homolog
	129063	X63097	X63094	Hs.283822	Rhesus blood group, D antigen
	424460	X63563	BE275979	Hs.296014	polymerase (RNA) II (DNA directed) polyp
	411077	X64037	AW977263	Hs.68257	general transcription factor IIF, polype
30	103181	X69636	X69636	Hs.334731	Homo sapiens, clone IMAGE:3448306, mRNA,
	103184	X69878	U43143	Hs.74049	fms-related tyrosine kinase 4
	103194	X70649	NM_004939	Hs.78580	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep
	103208	X72841	AW411340	Hs.31314	retinoblastoma-binding protein 7
	129698	X74987	BE242144	Hs.12013	ATP-binding cassette, sub-family E (OABP
35	131486	X83107	F06972	Hs.27372	BMX non-receptor tyrosine kinase
	130729	X84194	AI963747	Hs.18573	acylphosphatase 1, erythrocyte (common)
	103334	X85753	NM_001260	Hs.25283	cyclin-dependent kinase 8
	132645	X87870	AI654712	Hs.54424	hepatocyte nuclear factor 4, alpha
	135094	X89066	NM_003304	Hs.250687	transient receptor potential channel 1
40	103352	X89398	H09366	Hs.78853	uracil-DNA glycosylase
	103352	X89398	H09366	Hs.78853	uracil-DNA glycosylase
	103353	X89399	X89399	Hs.119274	RAS p21 protein activator (GTPase activa
	132173	X89426	X89426	Hs.41716	endothelial cell-specific molecule 1
	103371	X91247	X91247	Hs.13046	thioredoxin reductase 1
45	131584	X91648	AA598509	Hs.29117	purine-rich element binding protein A
	103376	X92098	AL036166	Hs.323378	coated vesicle membrane protein
	103378	X92110	AL119690	Hs.153618	HCGVIII-1 protein
	128510	X94703	X94703		RAB28, member RAS oncogene family
	103410	X96506	AA158294	Hs.295362	DR1-associated protein 1 (negative cofac
50	133490	X97230	AF022044	Hs.274601	killer cell immunoglobulin-like receptor
	332689	X97230	AF022044	Hs.274601	killer cell immunoglobulin-like receptor
	103438	X98263	AW175781	Hs.152720	M-phase phosphoprotein 6
	103440	X98296	X98296	Hs.77578	ubiquitin specific protease 9, X chromos
	103452	X99584	NM_006936	Hs.85119	SMT3 (suppressor of mif two 3, yeast) ho
55	133536	Y00264	W25797.comp		Hs.177486 amyloid beta (A4) precursor protein (pro
	420234	Y07566	AW404908	Hs.96038	Ric (Drosophila)-like, expressed in many
	426502	Y07759	Y07759	Hs.170157	myosin VA (heavy polypeptide 12, myoxin)
	134662	Y07827	NM_007048	Hs.284283	butyrophilin, subfamily 3, member A1
	132083	Y07867	BE386490	Hs.279663	Pirin
60	103500	Y09443	AW408009	Hs.22580	alkylglycerone phosphate synthase
	134389	Y09858	Y09858	Hs.82577	spindlin-like
	132084	Y12394	NM_002267	Hs.3886	karyopherin alpha 3 (importin alpha 4)
	103540	Z11559	NM_002197	Hs.154721	aconitase 1, soluble
	133152	Z11695	Z11695	Hs.324473	mitogen-activated protein kinase 1
65	103548	Z15005	Z15005	Hs.75573	centromere protein E (312kD)
	103612	Z46261	BE336654	Hs.70937	H3 histone family, member A
	129092	AA011243	D56365	Hs.63525	poly(rC)-binding protein 2
	103692	AA018418	AW137912	Hs.227583	Homo sapiens chromosome X map Xp11.23 L-
	103695	AA018758	AW207152	Hs.186600	ESTs
70	129796	AA018804	BE218319	Hs.5807	GTPase Rab14
	434993	AA031993	AA306325	Hs.4311	SUMO-1 activating enzyme subunit 2
	132683	AA044217	BE264633	Hs.143638	WD repeat domain 4
	131887	AA046548	W17064	Hs.332848	SWI/SNF related, matrix associated, acti
	103723	AA057447	BE274312	Hs.214783	Homo sapiens cDNA FLJ14041 fis, clone HE
	453368	AA058376	W20296	Hs.288178	Homo sapiens cDNA FLJ11968 fis, clone HE
75	133260	AA083572	AA403045	Hs.6906	Homo sapiens cDNA: FLJ23197 fis, clone R
	103765	AA085696	AA085696	Hs.169600	KIAA0826 protein

	103766	AA088744	AI920783	Hs.191435	ESTs
	103767	AA089688	BE244667		CGI-100 protein
	132051	AA091284	AA393968	Hs.180145	HSPC030 protein
5	103773	AA092700	AI219323	Hs.101077	ESTs, Weakly similar to T22363 hypothe
	135289	AA092968	AW372569	Hs.9788	hypothetical protein MGC10924 similar to
	409659	AA094800	AW970843	Hs.55682	eukaryotic translation initiation factor
	103794	AA100219	AF244135	Hs.30670	hepatocellular carcinoma-associated anti
	131471	AA114885	AA164842	Hs.192619	KIAA1600 protein
10	134319	AA129547	BE304999	Hs.285754	fumarate hydratase
	103807	AA133016	AW958264	Hs.103832	similar to yeast Upf3, variant B
	446392	AA149507	AF142419	Hs.15020	homolog of mouse quaking QKI (KH domain
	129863	AA151005	BE379765	Hs.129872	sperm associated antigen 9
	103850	AA187101	AA187101	Hs.213194	hypothetical protein MGC10895
	103855	AA195179	W02363		hypothetical protein FLJ10330
15	103861	AA206236	AA206236	Hs.4944	hypothetical protein FLJ12783
	130634	AA227621	AI769067	Hs.127824	ESTs, Weakly similar to T28770 hypothe
	447735	AA248283	AA775268	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L
	103909	AA249611	AA249611	Hs.47438	SH3 domain binding glutamic acid-rich pr
20	458928	AA282640	AF043117	Hs.24594	ubiquitination factor E4B (homologous to
	415824	AA287199	D42039	Hs.78871	mesoderm development candidate 2
	129013	AA313990	AA371156	Hs.107942	DKFZP564M112 protein
	129435	AA314256	AF151852	Hs.111449	CGI-94 protein
	103988	AA314389	AA314389	Hs.342849	ADP-ribosylation factor-like 5
25	104000	AA324364	AI146527	Hs.80475	polymerase (RNA) II (DNA directed) polyp
	425284	AA329211	AF155568	Hs.348043	NS1-associated protein 1
	128629	AA399187	AL096748	Hs.102708	DKFZP434A043 protein
	133281	AA421079	AK001601	Hs.69594	high-mobility group 20A
	104104	AA422029	AA422029	Hs.143640	ESTs, Weakly similar to hyperpolarizatio
30	332455	AA425230	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain
	132091	AA447052	AW954243		KIAA0251 protein
	135073	AA452000	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f
	131367	AA456687	AI750575	Hs.173933	nuclear factor I/A
	129593	AA487015	AI338247	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f
35	133505	C01527	AI630124	Hs.324504	Homo sapiens mRNA; cDNA DKFZp586J0720 (f
	132064	C01714	AA121098	Hs.3838	serum-inducible kinase
	442351	C01811	W52642	Hs.8261	hypothetical protein FLJ22393
	131427	C02352	AF151879	Hs.26706	CGI-121 protein
	433892	C02375	AI929357	Hs.323966	Homo sapiens clone H63 unknown mRNA
40	104282	C14448	C14448	Hs.332338	EST
	134827	D16611	BE314037	Hs.89866	coproporphyrinogen oxidase (coproporphyr
	425330	D25216	D25216	Hs.155650	KIAA0014 gene product
	131742	D31352	AA961420	Hs.31433	ESTs
	456935	D58024	AA370362	Hs.57958	EGF-TM7-latrophilin-related protein
45	425218	D80897	NM_014909	Hs.155182	KIAA1036 protein
	104334	D82614	D82614	Hs.78771	phosphoglycerate kinase 1
	134593	D87845	NM_000437	Hs.234392	platelet-activating factor acetylhydrola
	134731	D89377	D89377	Hs.89404	msh (Drosophila) homeo box homolog 2
	445776	H06583	NM_001310	Hs.13313	cAMP responsive element binding protein-
50	131670	H40732	H03514	Hs.15589	ESTs
	104394	H46617	AA129551	Hs.172129	Homo sapiens cDNA: FLJ21409 fis, clone C
	104402	H56731	H56731	Hs.132956	ESTs
	439130	H75570	AA306090	Hs.124707	ESTs
	129077	H78886	N74724	Hs.108479	ESTs
55	104417	H81241	AI819448	Hs.320861	Kruppel-like factor 8
	134927	L36531	L36531	Hs.91296	integrin, alpha 8
	129280	M63154	M63154	Hs.110014	gastric intrinsic factor (vitamin B synt
	134498	M63180	AW246273	Hs.84131	threonyl-tRNA synthetase
	104460	M91504	AW955705	Hs.62604	Homo sapiens, clone IMAGE:4299322, mRNA,
60	104488	N56191	N56191	Hs.106511	protocadherin 17
	131248	N78483	AI038989	Hs.332633	Bardet-Biedl syndrome 2
	130017	R14652	AK000096	Hs.143198	inhibitor of growth family, member 3
	104530	R20459	AK001676	Hs.12457	hypothetical protein FLJ10814
	104534	R22303	R22303		gb:yh26b09.r1 Soares placenta Nb2HP Homo
65	104544	R33779	AI091173	Hs.222362	ESTs, Weakly similar to p40 [H.sapiens]
	133328	R36553	AW452738	Hs.265327	hypothetical protein DKFZp7611141
	104567	R64534	AA040620	Hs.5672	hypothetical protein AF140225
	129575	R70621	F08282	Hs.278428	progesterin induced protein
	130776	R79356	AF167706	Hs.19280	cysteine-rich motor neuron 1
70	104599	R84933	AW815036	Hs.151251	ESTs
	104660	AA007160	BE298665	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (fr
	104667	AA007234	AI239923	Hs.63931	ESTs
	104718	AA018409	AI143020	Hs.36250	ESTs, Weakly similar to I38022 hypothe
	104764	AA025351	AI039243	Hs.278585	ESTs
75	104786	AA027168	AA027167	Hs.10031	KIAA0955 protein
	104787	AA027317	AA027317		gb:ze97d11.s1 Soares_fetal_heart_NbHH19W
	134079	AA029423	AK001751	Hs.171835	hypothetical protein FLJ10889

	104804	AA031357	AI858702	Hs.31803	ESTs, Weakly similar to N-WASP [H.sapien
	104865	AA045136	T79340	Hs.22575	B-cell CLL/lymphoma 6, member B (zinc fi
	130828	AA053400	AW631469	Hs.203213	ESTs
5	104907	AA055829	AA055829	Hs.196701	ESTs, Weakly similar to ALU1_HUMAN ALU S
	104943	AA065217	AF072873	Hs.114218	frizzled (Drosophila) homolog 6
	105013	AA116054	H63789	Hs.296288	ESTs, Weakly similar to KIAA0638 protein
	105024	AA126311	AA126311	Hs.9879	ESTs
	132592	AA129390	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H
10	105038	AA130273	AW503733	Hs.9414	KIAA1488 protein
	105077	AA142919	W55946	Hs.234863	Homo sapiens cDNA FLJ12082 fis, clone HE
	105096	AA150205	AL042506	Hs.21599	Kruppel-like factor 7 (ubiquitous)
	129215	AA176867	AB040930	Hs.126085	KIAA1497 protein
	105169	AA180321	BE245294	Hs.180789	S164 protein
15	132796	AA180487	NM_006283	Hs.173159	transforming, acidic coiled-coil contain
	427210	AA187634	BE396283	Hs.173987	eukaryotic translation initiation factor
	105200	AA195399	AA328102	Hs.24641	cytoskeleton associated protein 2
	130114	AA234717	AA233393	Hs.14992	hypothetical protein FLJ11151
	105330	AA234743	AW338625	Hs.22120	ESTs
20	105337	AA234957	AI468789	Hs.347187	myotubularin related protein 1
	422040	AA235604	AA172106	Hs.110950	Rag C protein
	105376	AA236559	AW994032	Hs.8768	hypothetical protein FLJ10849
	105397	AA242868	AA814807	Hs.7395	hypothetical protein FLJ23182
	431679	AA251776	AK000046	Hs.343877	hypothetical protein FLJ20039
25	131991	AA251909	AF053306	Hs.36708	budding uninhibited by benzimidazoles 1
	421305	AA252672	BE397354	Hs.324830	diphtheria toxin resistance protein requi
	105489	AA256157	AA256157	Hs.24115	Homo sapiens cDNA FLJ14178 fis, clone NT
	105508	AA256680	AA173942	Hs.326416	Homo sapiens mRNA; cDNA DKFZp564H1916 (f
	105539	AA258873	AB040884	Hs.109694	KIAA1451 protein
30	135172	AA262727	AB028956	Hs.12144	KIAA1033 protein
	131569	AA281451	AL389951	Hs.271623	nucleoporin 50kD
	431129	AA281545	AL137751	Hs.263671	Homo sapiens mRNA; cDNA DKFZp434I0812 (f
	105643	AA282069	BE621719	Hs.173802	KIAA0603 gene product
	105659	AA283044	AA283044	Hs.25625	hypothetical protein FLJ11323
35	105666	AA283930	AA426234	Hs.34906	ESTs, Weakly similar to T17210 hypotheti
	105674	AA284755	AI609530	Hs.279789	histone deacetylase 3
	105709	AA291268	AI928962	Hs.26761	DKFZP586L0724 protein
	105722	AA291927	AI922821	Hs.32433	ESTs
	105765	AA343514	AA299688	Hs.24183	ESTs
40	115951	AA398109	BE546245	Hs.301048	sec13-like protein
	130884	AA398109	BE546245	Hs.301048	sec13-like protein
	105962	AA405737	AW880358	Hs.339808	hypothetical protein FLJ10120
	105985	AA406610	AA406610		gb:zv15b10.s1 Soares_NhHMPu_S1 Homo sapi
	106008	AA411465	AB033888	Hs.8619	SRY (sex determining region Y)-box 18
45	457322	AA416886	AI815486	Hs.243901	Homo sapiens cDNA FLJ20738 fis, clone HE
	134222	AA424013	AW855861	Hs.8025	Homo sapiens clone 23767 and 23782 mRNA
	446954	AA424148	AB037850	Hs.16621	DKFZP434I116 protein
	106141	AA424558	AF031463	Hs.9302	phosducin-like
	447973	AA424961	AB011169	Hs.20141	similar to S. cerevisiae SSM4
50	106157	AA425367	W37943	Hs.34892	KIAA1323 protein
	428314	AA425921	AW135049	Hs.26285	Homo sapiens cDNA FLJ10643 fis, clone NT
	446727	AA426220	AB011095	Hs.16032	KIAA0523 protein
	106196	AA427735	AA525993	Hs.173699	ESTs, Weakly similar to ALU1_HUMAN ALU S
	457714	AA430673	AA083764		hypothetical protein MGC3178
55	133200	AA432248	AB037715	Hs.183639	hypothetical protein FLJ10210
	106302	AA435896	AA398859	Hs.18397	hypothetical protein FLJ23221
	106328	AA436705	AL079559	Hs.28020	KIAA0766 gene product
	450534	AA446561	AI570189	Hs.25132	KIAA0470 gene product
	106423	AA448238	AB020722	Hs.16714	Rho guanine exchange factor (GEF) 15
60	439608	AA449756	AW864696	Hs.301732	hypothetical protein MGC5306
	106477	AA450303	R23324	Hs.41693	DnaJ (Hsp40) homolog, subfamily B, membe
	106503	AA452411	AB033042	Hs.29679	cofactor required for Sp1 transcriptiona
	446999	AA454566	AA151520		hypothetical protein MGC4485
	106543	AA454667	AA676939	Hs.69285	neuropilin 1
65	442007	AA456437	AA301116	Hs.142838	nucleolar phosphoprotein Nopp34
	106589	AA456646	AK000933	Hs.28661	Homo sapiens cDNA FLJ10071 fis, clone HE
	106593	AA456826	AW296451	Hs.24605	ESTs
	106596	AA456981	AA452379		ESTs, Moderately similar to ALU7_HUMAN A
	423064	AA458959	AF265208	Hs.8740	SWI/SNF related, matrix associated, acti
70	106636	AA459950	AW958037	Hs.286	ribosomal protein L4
	106654	AA460449	AW075485	Hs.286049	phosphoserine aminotransferase
	131353	AA463910	AW754182		gb:RC2-CT0321-131199-011-c01 CT0321 Homo
	106707	AA464603	AK000566	Hs.98135	hypothetical protein FLJ20559
	452909	AA464606	NM_015368	Hs.30985	pannexin 1
75	106717	AA465093	AA600357	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi
	453141	AA465692	AB014548	Hs.31921	KIAA0648 protein
	106747	AA476473	NM_007118	Hs.171957	triple functional domain (PTPRF) interact

	106773	AA478109	AA478109	Hs.188833	ESTs
	106781	AA478474	AA330310	Hs.24181	ESTs
	106817	AA480889	D61216	Hs.18672	ESTs
5	106846	AA485223	AB037744	Hs.34892	KIAA1323 protein
	106848	AA485254	AA449014	Hs.121025	chromosome 11 open reading frame 5
	106856	AA486183	W58353	Hs.285123	Homo sapiens mRNA full length insert cDN
	418699	AA496936	BE539639	Hs.173030	ESTs, Weakly similar to ALU8_HUMAN ALU S
	107001	AA598589	AI926520	Hs.31016	putative DNA binding protein
10	442853	AA598831	AW021276	Hs.17121	ESTs
	107054	AA600150	AI076459	Hs.15978	KIAA1272 protein
	107059	AA608545	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re
	107080	AA609210	AL122043	Hs.19221	hypothetical protein DKFZp566G1424
	107115	AA610108	BE379623	Hs.27693	peptidylprolyl isomerase (cyclophilin)-I
15	107130	AA620582	AB033106	Hs.12913	KIAA1280 protein
	107156	AA621239	AA137043	Hs.9663	programmed cell death 6-interacting prot
	107174	AA621714	BE122762	Hs.25338	ESTs
	130621	AA621718	AW513087	Hs.16803	LUC7 (S. cerevisiae)-like
	107190	D19673	AA836401	Hs.87860	ESTs
20	132626	D25755	AW504732	Hs.21275	hypothetical protein FLJ11011
	107217	D51095	AL080235	Hs.35861	DKFZP586E1621 protein
	332584	D60272	AA357879	Hs.29423	ESTs; Weakly similar to macrophage lecti
	444655	T08879	AF088886	Hs.11590	cathepsin F
	107295	T34527	AA186629	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp
25	107299	T40327	BE277457	Hs.30661	hypothetical protein MGC4606
	107315	T62771	AA316241	Hs.90691	nucleophosmin/nucleoplasmin 3
	107316	T63174	T63174	Hs.193700	Homo sapiens mRNA; cDNA DKFZp586I0324 (f
	107328	T83444	AW959891	Hs.76591	KIAA0887 protein
	107334	T93641	T93597	Hs.187429	ESTs
30	456340	U48263	U48263	Hs.89040	prepronociceptin
	128636	U49065	U49065	Hs.102865	interleukin 1 receptor-like 2
	129938	U79300	AW003668	Hs.135587	Human clone 23629 mRNA sequence
	107375	U88573	BE011845	Hs.251064	high-mobility group (nonhistone chromoso
	130074	U93867	AL038596	Hs.250745	polymerase (RNA) III (DNA directed) (62k
35	107387	W01094	D86983	Hs.118893	Melanoma associated gene
	132036	W01568	AL157433	Hs.37706	hypothetical protein DKFZp434E2220
	107426	W26853	W26853	Hs.291003	hypothetical protein MGC4707
	135388	W27965	W27965	Hs.99865	epimorphin
	130419	W36280	AF037448	Hs.155489	NS1-associated protein 1
40	107469	W47063	W47063	Hs.94668	ESTs
	434203	W79060	BE262677	Hs.283558	hypothetical protein PRO1855
	107506	W88550	AB028981	Hs.8021	KIAA1058 protein
	132358	X60486	NM_003542	Hs.46423	H4 histone family, member G
	107522	X78931	X78931	Hs.99971	zinc finger protein 272
45	456495	Z14077	NM_003403	Hs.97496	YY1 transcription factor
	107582	AA002147	AA002147	Hs.59952	EST
	107609	AA004711	R75654	Hs.164797	hypothetical protein FLJ13693
	107661	AA010383	AA010383	Hs.60389	ESTs
	107714	AA015761	AA015761	Hs.60642	ESTs
50	107775	AA018772	AW008846	Hs.60857	ESTs
	107832	AA021473	AA021473		gb:ze66c11.s1 Soares retina N2b4HR Homo
	107859	AA024835	AW732573	Hs.47584	potassium voltage-gated channel, delayed
	107914	AA027229	AA027229	Hs.61329	ESTs, Weakly similar to T16370 hypotheti
	107935	AA029428	AA029428	Hs.61555	ESTs
55	410196	AA035143	AI936442	Hs.59838	hypothetical protein FLJ10808
	131461	AA035237	AA992841	Hs.27263	KIAA1458 protein
	108007	AA039347	AA039347	Hs.61916	EST
	108029	AA040740	AA040740	Hs.62007	ESTs
	108040	AA041551	AL121031	Hs.159971	SWI/SNF related, matrix associated, acti
60	108084	AA045513	AA058944	Hs.116602	Homo sapiens, clone IMAGE:4154008, mRNA,
	108088	AA045745	AA045745	Hs.62886	ESTs
	108168	AA055348	AI453137	Hs.63176	ESTs
	130719	AA056582	AA679262	Hs.14235	hypothetical protein FLJ20008; KIAA1839
	108189	AA056697	AW376061	Hs.63335	ESTs, Moderately similar to A46010 X-fin
	108190	AA056746	AA056746	Hs.63338	EST
65	108203	AA057678	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone C
	108216	AA058681	AA524743	Hs.44883	ESTs
	108217	AA058686	AA058686	Hs.62588	ESTs
	108245	AA062840	BE410285	Hs.89545	proteasome (prosome, macropain) subunit,
70	108277	AA064859	AA064859		gb:zm50f03.s1 Stratagene fibroblast (937
	108280	AA065069	AA065069		gb:zm12e11.s1 Stratagene pancreas (93720
	108309	AA069923	AA069818		gb:zm67e03.r1 Stratagene neuroepithelium
	108340	AA070815	AA069820	Hs.180909	peroxiredoxin 1
	108403	AA075374	AA075374		gb:zm87a01.s1 Stratagene ovarian cancer
	108427	AA076382	AA076382		gb:zm91g08.s1 Stratagene ovarian cancer
75	108435	AA078787	T82427	Hs.194101	Homo sapiens cDNA: FLJ20869 fis, clone A
	108439	AA078986	AA078986		gb:zm92h01.s1 Stratagene ovarian cancer

	108465	AA079393	AA079393	Hs.3462	cytochrome c oxidase subunit VIc
	108469	AA079487	AA079487		gb:zm97f08.s1 Stratagene colon HT29 (937
	108500	AA083207	AA083207	Hs.68270	EST
5	108501	AA083256	AA083256		gb:zn08g12.s1 Stratagene hNT neuron (937
	108533	AA084415	AA084415		gb:zn06g09.s1 Stratagene hNT neuron (937
	108562	AA085274	AA100796		gb:zm26c06.s1 Stratagene pancreas (93720
	108589	AA088678	AI732404	Hs.68846	ESTs
	130890	AA100925	AI907537	Hs.76698	stress-associated endoplasmic reticulum
10	432645	AA101255	D14041	Hs.347340	H-2K binding factor-2
	130385	AA126474	AW067800	Hs.155223	stanniocalcin 2
	108749	AA127017	AA127017	Hs.71052	ESTs
	108807	AA129968	AI652236	Hs.49376	hypothetical protein FLJ20644
	108808	AA130240	AA045088	Hs.62738	ESTs
15	108833	AA131866	AF188527	Hs.61661	ESTs, Weakly similar to AF174605 1 F-box
	108846	AA132983	AL117452	Hs.44155	DKFZP586G1517 protein
	108857	AA133250	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act
	131474	AA133583	L46353	Hs.2726	high-mobility group (nonhistone chromoso
	108894	AA135941	AK001431	Hs.5105	hypothetical protein FLJ10569
20	108941	AA148650	AA148650		gb:zo09e06.s1 Stratagene neuroepithelium
	108968	AA151110	AI304870	Hs.188680	ESTs
	108996	AA155754	AW995610	Hs.332436	EST
	109001	AA156125	AI056548	Hs.72116	hypothetical protein FLJ20992 similar to
	131183	AA156289	AI611807	Hs.285107	hypothetical protein FLJ13397
25	109019	AA156997	AA156755	Hs.72150	ESTs
	109022	AA157291	AA157291	Hs.21479	ubiquitin 1
	109023	AA157293	AA157293	Hs.72168	ESTs
	109068	AA164293	AA164293	Hs.72545	ESTs
	109072	AA164676	AI732585	Hs.22394	hypothetical protein FLJ10893
30	426981	AA167375	AL044675	Hs.173081	KIAA0530 protein
	130346	AA167550	H05769	Hs.188757	Homo sapiens, clone MGC:5564, mRNA, comp
	109146	AA176589	AA176589	Hs.142078	EST
	109172	AA180448	AA180448	Hs.144300	EST
	428438	AA187144	NM_001955	Hs.2271	endothelin 1
35	129208	AA189170	AI587376	Hs.109441	MSTP033 protein
	109222	AA192757	AA192833	Hs.333512	similar to rat myomegalin
	109300	AA205650	AA418276	Hs.170142	ESTs
	109481	AA233342	AA878923	Hs.289069	hypothetical protein FLJ21016
	109485	AA233472	BE619092	Hs.28465	Homo sapiens cDNA: FLJ21869 fis, clone H
40	109516	AA234110	AI471639	Hs.71913	ESTs
	109537	D80981	AI858695	Hs.34898	ESTs
	109556	F01660	AI925294	Hs.87385	ESTs
	109577	F02206	F02206	Hs.296639	Homo sapiens potassium channel subunit (
45	109578	F02208	F02208	Hs.27214	ESTs
	109595	F02544	AA078629	Hs.27301	ESTs
	109625	F03918	H29490	Hs.22697	ESTs
	428376	F04258	AF119665	Hs.184011	pyrophosphatase (inorganic)
	109648	F04600	H17800	Hs.7154	ESTs
	109671	F08998	R59210	Hs.26634	ESTs
50	109699	F09605	H18013	Hs.167483	ESTs
	109820	F11115	AW016809	Hs.119021	ESTs
	109933	H06371	R52417	Hs.20945	Homo sapiens clone 24993 mRNA sequence
	110014	H10995	AL109666	Hs.7242	Homo sapiens mRNA full length insert cDN
	110039	H11938	H11938	Hs.21907	histone acetyltransferase
55	110099	H16568	R44557	Hs.23748	ESTs
	110107	H16772	AW151660	Hs.31444	ESTs
	110155	H18951	AI559626	Hs.93522	Homo sapiens mRNA for KIAA1647 protein,
	110197	H20859	AW090386	Hs.112278	arrestin, beta 1
	110223	H23747	H19836	Hs.31697	ESTs
60	110306	H38087	H38087	Hs.105509	CTL2 gene
	110335	H40331	H65490	Hs.18845	ESTs
	110342	H40567	H40961	Hs.33008	ESTs
	110395	H46966	AA025116	Hs.33333	ESTs
	110511	H56640	H56640	Hs.221460	ESTs
65	110523	H57154	AI040384	Hs.19102	ESTs, Weakly similar to organic anion tr
	110715	H96712	H96712	Hs.269029	ESTs
	110754	N20814	AW302200	Hs.6336	KIAA0672 gene product
	428454	N25249	U55936	Hs.184376	synaptosomal-associated protein, 23kD
70	431663	N27100	NM_016569	Hs.267182	TBX3-iso protein
	134263	N39616	AW973443	Hs.8086	RNA (guanine-7-) methyltransferase
	110938	N48982	N48982	Hs.38034	Homo sapiens cDNA FLJ12924 fis, clone NT
	110983	N51957	NM_015367	Hs.10267	MIL1 protein
	111081	N59435	AI146349	Hs.271614	CGI-112 protein
	111128	N64139	AW505364	Hs.19074	LATS (large tumor suppressor, Drosophila
75	431548	N66981	AI834273	Hs.9711	novel protein
	111216	N68640	AW139408	Hs.152940	ESTs
	437562	N69352	AB001636	Hs.5683	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep

	111399	R00138	AW270776	Hs.18857	ESTs
	111514	R07998	R07998		gb:yf16g11.s1 Soares fetal liver spleen
	428744	R08929	BE267033	Hs.192853	ubiquitin-conjugating enzyme E2G 2 (homo
5	111574	R10307	AI024145	Hs.188526	ESTs
	111804	R33354	AA482478	Hs.181785	ESTs
	111831	R36083	R36095	Hs.268695	ESTs
	426773	R37938	NM_015556	Hs.172180	KIAA0440 protein
	111904	R39330	Z41572		gb:HSCZYB122 normalized infant brain cDN
10	428371	R40816	AB012193	Hs.183874	cullin 4A
	112033	R43162	R49031	Hs.22627	ESTs
	130987	R45698	BE613269	Hs.21893	hypothetical protein DKFZp761N0624
	112300	R54554	H24334	Hs.26125	ESTs
	112513	R68425	R68425	Hs.13809	hypothetical protein FLJ10648
15	112514	R68568	R68568	Hs.183373	src homology 3 domain-containing protein
	112522	R68763	R68857	Hs.265499	ESTs
	112540	R70467	R69751		gb:yi40a10.s1 Soares placenta Nb2HP Homo
	428655	R73565	H05769	Hs.188757	Homo sapiens, clone MGC:5564, mRNA, comp
	129534	R73640	AK002126	Hs.11260	hypothetical protein FLJ11264
20	112597	R78376	R78376	Hs.29733	EST
	112732	R92453	R92453	Hs.34590	ESTs
	451798	T03865	BE297567	Hs.27047	hypothetical protein FLJ20392
	112888	T03872	AW195317	Hs.107716	hypothetical protein FLJ22344
	131863	T10072	AI656378	Hs.33461	ESTs
25	112911	T10080	AW732747	Hs.13493	like mouse brain protein E46
	132215	T10132	AL035703	Hs.4236	KIAA0478 gene product
	112931	T15343	T02966	Hs.167428	ESTs
	112984	T23457	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p
	112998	T23555	H11257	Hs.22968	Homo sapiens clone IMAGE:451939, mRNA se
30	133376	T23670	BE618768	Hs.7232	acetyl-Coenzyme A carboxylase alpha
	113026	T23948	AA376654		eukaryotic translation initiation factor
	113070	T33464	AB032977	Hs.6298	KIAA1151 protein
	410781	T34413	AI375672	Hs.165028	ESTs
	113074	T34611	AK001335	Hs.31137	protein tyrosine phosphatase, receptor t
35	113095	T40920	AA828380	Hs.126733	ESTs
	113179	T55182	BE622021	Hs.152571	ESTs, Highly similar to IGF-II mRNA-bind
	113337	T77453	T77453	Hs.302234	ESTs
	113421	T84039	AI769400	Hs.189729	ESTs
	113454	T86458	AI022166	Hs.16188	ESTs
40	113481	T87693	T87693	Hs.204327	EST
	453345	T89350	AA302862	Hs.90063	neurocalcin delta
	113557	T90945	H66470	Hs.16004	ESTs
	113559	T90987	T79763	Hs.14514	ESTs
	113589	T91863	AI078554	Hs.15682	ESTs
45	113591	T91881	T91881	Hs.200597	KIAA0563 gene product
	113619	T93783	R08665	Hs.17244	hypothetical protein FLJ13605
	113683	T96687	AB035335	Hs.144519	T-cell leukemia/lymphoma 6
	113692	T96944	AL360143	Hs.17936	DKFZP434H132 protein
	113702	T97307	T97307		gb:ye53h05.s1 Soares fetal liver spleen
50	113717	T97764	T99513	Hs.187447	ESTs
	113824	W48817	AI631964	Hs.34447	ESTs
	113840	W58343	R72137	Hs.7949	DKFZP586B2420 protein
	113844	W59949	AI369275	Hs.243010	Homo sapiens cDNA FLJ14445 fis, clone HE
	113902	W74644	AA340111	Hs.100009	acyl-Coenzyme A oxidase 1, palmitoyl
55	113904	W74761	AF125044	Hs.19196	ubiquitin-conjugating enzyme HBUCE1
	113905	W74802	R81733	Hs.33106	ESTs
	113931	W81205	BE255499	Hs.3496	hypothetical protein MGC15749
	113932	W81237	AA256444	Hs.126485	hypothetical protein FLJ12604; KIAA1692
	131965	W90146	W79283	Hs.35962	ESTs
60	114035	W92798	W92798	Hs.269181	ESTs
	114106	Z38412	AW602528		gb:RC5-BT0562-260100-011-A02 BT0562 Homo
	457308	Z38709	AI416988	Hs.238272	inositol 1,4,5-triphosphate receptor, ty
	114161	Z38904	BE548222	Hs.299883	hypothetical protein FLJ23399
	424949	Z39103	AF052212	Hs.153934	core-binding factor, runt domain, alpha
65	457548	Z39930	AW069534	Hs.279583	CGI-81 protein
	128937	Z39939	AA251380	Hs.10726	ESTs, Weakly similar to ALU1_HUMAN ALU S
	432554	Z40012	AI479813	Hs.278411	NCK-associated protein 1
	114277	Z40377	AI052229	Hs.25373	ESTs, Weakly similar to T20410 hypotheti
	114304	Z40820	AI934204	Hs.16129	ESTs
70	114364	Z41680	AL117427	Hs.172778	Homo sapiens mRNA; cDNA DKFZp566P013 (fr
	432620	AA005112	AA777749	Hs.5978	LIM domain only 7
	129034	AA005432	AA481157	Hs.108110	DKFZP547E2110 protein
	131881	AA010163	AW361018	Hs.3383	upstream regulatory element binding prot
	332421	AA026356	AI909968	Hs.108106	transcription factor
	114465	AA026901	BE621056	Hs.131731	hypothetical protein FLJ11099
75	451271	AA036867	AK001644	Hs.26156	hypothetical protein FLJ10782
	332498	AA044644	AA303661		lymphocyte-specific protein 1

	431555	AA046426	AI815470	Hs.260024	Cdc42 effector protein 3
	132944	AA054515	T96641	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L
	114618	AA084162	AW979261	Hs.291993	ESTs
5	332509	AA085749	AA128376	Hs.153884	ATP binding protein associated with cell
	114648	AA101056	AA101056		gb:zn25b03.s1 Stratagene neuroepithelium
	114658	AA102746	AA102383	Hs.249190	tumor necrosis factor receptor superfamI
	132456	AA114250	AB011084	Hs.48924	KIAA0512 gene product; ALEX2
	450847	AA126561	NM_003155	Hs.25590	stanniocalcin 1
10	132225	AA128980	AA128980		gb:zo09a11.s1 Stratagene neuroepithelium
	437197	AA129757	W38586		guanine nucleotide binding protein (G pr
	114709	AA129921	AA397651	Hs.301959	proline synthetase co-transcribed (bacte
	456926	AA133331	AB018284	Hs.158688	KIAA0741 gene product
	114750	AA135958	AA887211	Hs.129467	ESTs
15	426806	AA136524	T19228	Hs.172572	hypothetical protein FLJ20093
	114763	AA147044	AA810755	Hs.102500	hypothetical protein dJ511E16.2
	114767	AA148885	AI859865	Hs.154443	minichromosome maintenance deficient (S.
	114774	AA150043	AV656017	Hs.184325	CGI-76 protein
	129388	AA151621	AA662477	Hs.110964	hypothetical protein FLJ23471
20	457742	AA155743	BE561824	Hs.273369	uncharacterized hematopoietic stem/proge
	456200	AA156335	AA768242	Hs.80618	hypothetical protein
	130207	AA156336	AF044209	Hs.144904	nuclear receptor co-repressor 1
	114798	AA159181	AA159181	Hs.54900	serologically defined colon cancer antig
	114800	AA159825	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypotheli
25	114828	AA234185	AA252937	Hs.283522	Homo sapiens mRNA; cDNA DKFZp434J1912 (f
	114846	AA234929	BE018682	Hs.166196	ATPase, Class I, type 8B, member 1
	114848	AA234935	BE614347	Hs.169615	hypothetical protein FLJ20989
	114902	AA236359	AW275480	Hs.39504	hypothetical protein MGC4308
	132271	AA236466	AB030034	Hs.115175	sterile-alpha motif and leucine zipper c
30	114907	AA236535	N29390	Hs.13804	hypothetical protein dJ462O23.2
	420170	AA236935	U43374	Hs.95631	Human normal keratinocyte mRNA
	132204	AA236942	AA235827	Hs.42265	ESTs
	114928	AA237018	AA237018	Hs.94869	ESTs
	132481	AA237025	W93378	Hs.49614	ESTs
35	114932	AA242751	AA871436	Hs.16218	KIAA0903 protein
	314162	AA242760	BE041820	Hs.38516	Homo sapiens, clone MGC:15887, mRNA, com
	131006	AA242763	AF064104	Hs.22116	CDC14 (cell division cycle 14, S. cerevi
	114935	AA242809	H23329	Hs.290880	ESTs, Weakly similar to ALU1_HUMAN ALU S
	408908	AA243133	BE296227	Hs.250822	serine/threonine kinase 15
40	437754	AA243495	R60366	Hs.5822	Homo sapiens cDNA: FLJ22120 fis, clone H
	114957	AA243706	AW170425	Hs.87680	ESTs
	114974	AA250848	AW966931	Hs.302649	nucleosome assembly protein 1-like 1
	114977	AA250868	AW296978	Hs.87787	ESTs
	114995	AA251152	AA769266	Hs.193657	ESTs
45	115005	AA251544	AI760825	Hs.153042	ESTs
	417177	AA251792	NM_004458	Hs.81452	fatty-acid-Coenzyme A ligase, long-chain
	115026	AA252144	AA251972	Hs.188718	ESTs
	115045	AA252524	AW014549	Hs.58373	ESTs
	115068	AA253461	AW512260	Hs.87767	ESTs
50	133138	AA255522	AV657594	Hs.181161	Homo sapiens cDNA FLJ14643 fis, clone NT
	332668	AA255522	AV657594	Hs.181161	ESTs
	115114	AA256468	AA527548	Hs.7527	small fragment nuclease
	129584	AA256528	AV656017	Hs.184325	CGI-76 protein
	115137	AA257976	AW968304	Hs.56156	ESTs
55	417187	AA258296	AB011151	Hs.334659	hypothetical protein MGC14139
	115166	AA258409	AF095727	Hs.287832	myelin protein zero-like 1
	115167	AA258421	AA749209	Hs.43728	hypothetical protein
	436719	AA262077	Y11192	Hs.5299	aldehyde dehydrogenase 5 family, member
	115239	AA278650	BE251328	Hs.73291	hypothetical protein FLJ10881
60	115243	AA278766	AA806600	Hs.116665	KIAA1842 protein
	428419	AA280791	U49436		KIAA1856 protein
	115322	AA280819	L08895	Hs.78995	MADS box transcription enhancer factor 2
	413303	AA280828	AW836130	Hs.75277	hypothetical protein FLJ13910
	115372	AA282195	AW014385	Hs.88678	ESTs, Weakly similar to Unknown [H.sapie
65	409962	AA283127	U82671	Hs.57698	Target CAT
	130269	AA284694	F05422	Hs.168352	nucleoporin-like protein 1
	456570	AA291137	AA286914	Hs.183299	ESTs
	332675	AA291708	BE439944		ESTs
	407864	AA293495	AF069291	Hs.40539	chromosome 8 open reading frame 1
70	115536	AA347193	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), act
	408799	AA398474	AA059412	Hs.47986	hypothetical protein MGC10940
	115575	AA398512	AA393254	Hs.43619	ESTs
	115601	AA400277	AA148984	Hs.48849	ESTs, Weakly similar to ALU4_HUMAN ALU S
	434428	AA400896	D14540	Hs.199160	myeloid/lymphoid or mixed-lineage leukem
75	115683	AA410345	AF255910	Hs.54650	junctional adhesion molecule 2
	115715	AA416733	BE395161	Hs.1390	proteasome (prosome, macropain) subunit,
	132952	AA425154	AI658580	Hs.61426	Homo sapiens mesenchymal stem cell prote

	115819	AA426573	AA486620	Hs.41135	endomucin-2
	409124	AA431418	AW292809	Hs.50727	N-acetylglucosaminidase, alpha- (Sanfill
	115895	AA436182	AB033035	Hs.51965	KIAA1209 protein
5	458073	AA437099	AA192669	Hs.45032	ESTs
	115962	AA446585	AI636361	Hs.179520	hypothetical protein MGC10702
	115967	AA446887	AI745379	Hs.42911	ESTs
	115974	AA447224	BE513442	Hs.238944	hypothetical protein FLJ10631
	115985	AA447709	AA447709	Hs.268115	ESTs, Weakly similar to T08599 probable
10	129254	AA453624	AA252468	Hs.1098	DKFZp434J1813 protein
	446730	AA455044	BE384932	Hs.64313	ESTs, Weakly similar to AF257182 1 G-pro
	116095	AA456045	AA043429	Hs.62618	ESTs
	426856	AA460454	R19768	Hs.172788	ALEX3 protein
	116210	AA476494	BE622792	Hs.172788	ALEX3 protein
15	116213	AA476738	AA292105	Hs.326740	hypothetical protein MGC10947
	432645	AA481422	D14041	Hs.347340	H-2K binding factor-2
	116265	AA482595	BE297412	Hs.55189	hypothetical protein
	129334	AA485084	AW157022	Hs.343551	hypothetical protein FLJ22584
	116274	AA485431	AI129767	Hs.182874	guanine nucleotide binding protein (G pr
20	426002	AA489638	BE514376	Hs.165998	PAI-1 mRNA-binding protein
	116331	AA491000	N41300	Hs.71616	Homo sapiens mRNA; cDNA DKFZp586N1720 (f
	116333	AA491250	AF155827	Hs.203963	hypothetical protein FLJ10339
	132994	AA505133	AA112748	Hs.279905	clone HQ0310 PRO0310p1
	418538	AA598447	BE244323	Hs.85951	exportin, tRNA (nuclear export receptor
25	116391	AA599243	T86558	Hs.75113	general transcription factor IIIA
	116394	AA599574	NM_006033	Hs.65370	lipase, endothelial
	134531	AA600153	AI742845	Hs.110713	DEK oncogene (DNA binding)
	116417	AA609309	AW499664		Human clone 23826 mRNA sequence
	116429	AA609710	AF191018	Hs.279923	putative nucleotide binding protein, est
30	116439	AA610068	AA251594	Hs.43913	PIBF1 gene product
	116459	AA621399	R80137	Hs.302738	Homo sapiens cDNA: FLJ21425 fis, clone C
	427505	AA621752	AA361562	Hs.178761	26S proteasome-associated pad1 homolog
	409633	C21523	AW449822	Hs.55200	ESTs
	116541	D12160	D12160	Hs.249212	polymerase (RNA) III (DNA directed) (155
35	132557	D19708	AA114926	Hs.169531	ESTs
	414964	D25801	AA337548	Hs.333402	hypothetical protein MGC12760
	116571	D45652	D45652	Hs.211604	gb:HUMGS02848 Human adult lung 3' direct
	451522	D60208	BE565817	Hs.26498	hypothetical protein FLJ21657
	421919	D80504	AJ224901	Hs.109526	zinc finger protein 198
40	116643	F03010	AI367044	Hs.153638	myeloid/lymphoid or mixed-lineage leukem
	116661	F04247	R61504		gb:yh16a03.s1 Soares infant brain 1NIB H
	116715	F10966	AL117440	Hs.170263	tumor protein p53-binding protein, 1
	116729	F13700	BE549407	Hs.115823	ribonuclease P, 40kD subunit
	318709	H05063	R52576	Hs.285280	Homo sapiens cDNA: FLJ22096 fis, clone H
45	418999	H16758	NM_000121	Hs.89548	erythropoietin receptor
	116773	H17315	AI823410	Hs.343581	karyopherin alpha 1 (importin alpha 5)
	116780	H22566	H22566	Hs.63931	ESTs
	453884	H48459	AA355925	Hs.36232	KIAA0186 gene product
	116819	H53073	H53073	Hs.93698	EST
50	427278	H56559	AL031428	Hs.174174	KIAA0601 protein
	407833	H57957	AW955632	Hs.66666	ESTs, Weakly similar to S19560 proline-r
	116844	H64938	H64938	Hs.337434	ESTs, Weakly similar to A46010 X-linked
	116845	H64973	AA649530	Hs.348148	gb:ns44f05.s1 NCL_CGAP_Alvl1 Homo sapiens
	116892	H69535	AI573283	Hs.38458	ESTs
55	116925	H73110	H73110	Hs.260603	ESTs, Moderately similar to A47582 B-cel
	116981	H81783	N29218	Hs.40290	ESTs
	453133	H86259	AC005757	Hs.31809	hypothetical protein
	117031	H88353	H88353	Hs.347265	gb:yw21a02.s1 Morton Fetal Cochlea Homo
	117034	H88639	U72209		YY1-associated factor 2
60	431129	H88675	AL137751	Hs.263671	Homo sapiens mRNA; cDNA DKFZp434I0812 (f
	417861	H93708	AA334551		sperm specific antigen 2
	117280	N22107	M18217	Hs.172129	Homo sapiens cDNA: FLJ21409 fis, clone C
	117344	N24046	R19085	Hs.210706	Homo sapiens cDNA FLJ13182 fis, clone NT
	117422	N27028	AI355562	Hs.43880	ESTs, Weakly similar to A46010 X-linked
65	117475	N30205	N30205	Hs.93740	ESTs, Weakly similar to I38022 hypothe
	117487	N30621	N30621	Hs.44203	ESTs
	117937	N33258	AF044209	Hs.144904	nuclear receptor co-repressor 1
	130207	N33258	AF044209	Hs.144904	nuclear receptor co-repressor 1
	117549	N33390	N33390	Hs.44483	EST
70	117683	N40180	N40180		gb:yy44d02.s1 Soares_multiple_sclerosis_
	117710	N45198	N45198	Hs.47248	ESTs, Highly similar to similar to Cdc14
	117791	N48325	N48325	Hs.93956	EST
	117822	N48913	AA706282	Hs.93963	ESTs
	422544	N49394	AB018259	Hs.118140	KIAA0716 gene product
	117895	N50656	AW450348	Hs.93996	ESTs, Highly similar to SORL_HUMAN SORTI
75	452259	N50721	AA317439	Hs.28707	signal sequence receptor, gamma (translo
	133057	N53143	AA465131	Hs.64001	Homo sapiens clone 25218 mRNA sequence

	118103	N55326	AA401733	Hs.184134	ESTs
	118111	N55493	N55493		gb:yv50c02.s1 Soares fetal liver spleen
	118129	N57493	N57493		gb:yy54c08.s1 Soares_multiple_sclerosis_
5	118278	N62955	N62955	Hs.316433	Homo sapiens cDNA FLJ11375 fis, clone HE
	118329	N63520	N63520		gb:yy62f01.s1 Soares_multiple_sclerosis_
	118336	N63604	BE327311	Hs.47166	HT021
	417098	N64166	AB017365	Hs.173859	frizzled (Drosophila) homolog 7
	118363	N64168	AI183838	Hs.48938	hypothetical protein FLJ21802
10	118364	N64191	N46114	Hs.29169	hypothetical protein FLJ22623
	118475	N66845	N66845		gb:za46c11.s1 Soares fetal liver spleen
	118491	N67135	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H
	118500	N67295	W32889	Hs.154329	ESTs
	118584	N68963	AW136928		gb:UI-H-B11-adp-d-08-0-UI.s1 NCI_CGAP_Su
15	456647	N69331	AI252640	Hs.110364	peptidylprolyl isomerase C (cyclophilin
	118661	N70777	AL137554	Hs.49927	protein kinase NYD-SP15
	118684	N71364	N71313	Hs.163986	Homo sapiens cDNA: FLJ22765 fis, clone K
	118689	N71545	AW390601	Hs.184544	Homo sapiens, clone IMAGE:3355383, mRNA,
	118690	N71571	N71571	Hs.269142	ESTs
20	118766	N74456	N74456	Hs.50499	EST
	118793	N75594	N75594	Hs.285921	ESTs, Moderately similar to T47135 hypot
	118817	N79035	AI668658	Hs.50797	ESTs
	118844	N80279	AL035364	Hs.50891	hypothetical protein
	118919	N91797	AW452696	Hs.130760	myosin phosphatase, target subunit 2
25	129558	N92454	AW580922	Hs.180446	karyopherin (importin) beta 1
	407604	N94581	AW191962	Hs.288061	collagen, type VIII, alpha 2
	118996	N94746	N94746	Hs.274248	hypothetical protein FLJ20758
	119021	N98238	N98238	Hs.55185	ESTs
	119039	R02384	AI160570	Hs.252097	pregnancy specific beta-1-glycoprotein 6
30	119063	R16833	R16833	Hs.53106	ESTs, Moderately similar to ALU1_HUMAN A
	332622	R41828	R10674		CSR1 protein
	119111	R43203	T02865	Hs.328321	EST
	415115	R46395	AA214228	Hs.127751	hypothetical protein
	119146	R58863	R58863	Hs.91815	ESTs
35	449224	R78248	AW995911	Hs.299883	hypothetical protein FLJ23399
	119239	T11483	T11483		gb:CHR90049 Chromosome 9 exon Homo sapie
	119281	T16896	AI692322	Hs.65373	ESTs, Weakly similar to T02345 hypotheti
	119298	T23820	NM_001241	Hs.155478	cyclin T2
	126502	T30222	T10077	Hs.13453	hypothetical protein FLJ14753
40	419983	W15275	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f
	119558	W38194	W38194		Empirically selected from AFFX single pr
	429641	W42414	AW081883	Hs.211578	Homo sapiens cDNA: FLJ23037 fis, clone L
	419445	W49632	AA884471	Hs.90449	Human clone 23908 mRNA sequence
	119650	W57613	R82342	Hs.79856	ESTs, Weakly similar to S65657 alpha-1C-
45	119654	W57759	W57759		gb:zd20g11.s1 Soares_fetal_heart_NbHH19W
	119683	W61118	W65379	Hs.57835	ESTs
	119694	W65344	AA041350	Hs.57847	ESTs, Moderately similar to ICE4_HUMAN C
	119718	W69216	W69216	Hs.92848	ESTs
	410365	W69379	AI287518		Homo sapiens mRNA; cDNA DKFZp586D0923 (f
50	119938	W86728	AW014862	Hs.58885	ESTs
	120128	Z38499	BE379320	Hs.91448	MKP-1 like protein tyrosine phosphatase
	120130	Z38630	AA045767	Hs.5300	bladder cancer associated protein
	120148	Z39494	F02806	Hs.65765	ESTs
	120155	Z39623	Z39623	Hs.65783	ESTs
55	451979	Z40071	F06972	Hs.27372	BMX non-receptor tyrosine kinase
	120183	Z40174	AW082866	Hs.65882	ESTs
	120184	Z40182	Z40182	Hs.65885	EST
	120211	Z40904	Z40904	Hs.66012	EST
	120245	AA166965	AW959615	Hs.111045	ESTs
60	120247	AA167500	AA167500	Hs.103939	EST
	120254	AA169599	W90403	Hs.111054	ESTs
	120259	AA171724	AW014786	Hs.192742	hypothetical protein FLJ12785
	120260	AA171739	AK000061	Hs.101590	hypothetical protein
	120275	AA177105	AA177105	Hs.78457	solute carrier family 25 (mitochondrial
65	120284	AA182626	AA179656		gb:zp54e11.s1 Stratagene NT2 neuronal pr
	417735	AA186324	AA188175	Hs.82506	KIAA1254 protein
	422137	AA192099	AJ236885		zinc finger protein 148 (pHZ-52)
	120302	AA192173	AA837098	Hs.269933	ESTs
	120303	AA192415	AI216292	Hs.96184	ESTs
70	120305	AA192553	AW295096	Hs.101337	uncoupling protein 3 (mitochondrial, pro
	120319	AA194851	T57776	Hs.191094	ESTs
	408729	AA195520	AA195764	Hs.72639	ESTs
	120326	AA196300	AA196300	Hs.21145	hypothetical protein RG083M05.2
	133145	AA196549	H94227	Hs.6592	Homo sapiens, clone IMAGE:2961368, mRNA,
75	120327	AA196721	AK000292	Hs.130732	hypothetical protein FLJ20285
	120328	AA196979	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi
	120340	AA206828	AA206828		gb:zq80b08.s1 Stratagene hNT neuron (937

	417122	AA207123	AI906291	Hs.81234	immunoglobulin superfamily, member 3
	131522	AA214539	AI380040	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi
	421787	AA226914	AA227068	Hs.108301	nuclear receptor subfamily 2, group C, m
5	120375	AA227260	AF028706	Hs.111227	Zic family member 3 (odd-paired Drosophi
	120376	AA227469	AA227469		gb:zr18a07.s1 Stratagene NT2 neuronal pr
	120390	AA233122	AA837093	Hs.111460	calcium/calmodulin-dependent protein kin
	410804	AA233334	U64820	Hs.66521	Machado-Joseph disease (spinocerebellar
	434223	AA233347	AI825842	Hs.3776	zinc finger protein 216
10	312771	AA233714	AA018515	Hs.264482	Homo sapiens mRNA; cDNA DKFZp761A0411 (f
	120396	AA233796	AA134006	Hs.79306	eukaryotic translation initiation factor
	120409	AA235050	AA235050		gb:zs38e04.s1 Soares_NhHMPu_S1 Homo sapi
	120414	AA235704	AW137156	Hs.181202	hypothetical protein FLJ10038
	120420	AA236031	AI128114	Hs.112885	spinal cord-derived growth factor-B
	120422	AA236352	AL133097	Hs.301717	hypothetical protein DKFZp434N1928
15	419326	AA236390	W94915	Hs.42419	ESTs
	120423	AA236453	AA236453	Hs.18978	Homo sapiens cDNA: FLJ22822 fis, clone K
	120435	AA243370	AA243370	Hs.96450	EST
	120453	AA250947	AA250947	Hs.170263	tumor protein p53-binding protein, 1
20	120455	AA251083	AA251720	Hs.104347	ESTs, Weakly similar to ALUC_HUMAN !!!!
	120456	AA251113	AA488750	Hs.88414	BTB and CNC homology 1, basic leucine zi
	120473	AA251973	AA251973	Hs.269988	ESTs
	128922	AA252023	AI244901	Hs.9589	ubiquitin 1
	120477	AA252414	AA252414	Hs.43141	DKFZP727C091 protein
25	120479	AA252650	AF006689	Hs.110299	mitogen-activated protein kinase kinase
	120488	AA255523	AW952916	Hs.63510	KIAA0141 gene product
	120510	AA258128	AI796395	Hs.111377	ESTs
	120527	AA262105	AA262105	Hs.4094	Homo sapiens cDNA FLJ14208 fis, clone NT
	120528	AA262107	AI923511	Hs.104413	ESTs
	120529	AA262235	AI434823	Hs.104415	ESTs
30	120541	AA278298	W07318	Hs.240	M-phase phosphoprotein 1
	120544	AA278721	BE548277	Hs.103104	ESTs
	120562	AA280036	BE244580	Hs.342307	hypothetical protein FLJ10330
	120569	AA280648	AA807544	Hs.24970	ESTs, Weakly similar to B34323 GTP-bind
35	120571	AA280738	AB037744	Hs.34892	KIAA1323 protein
	120572	AA280794	H39599	Hs.294008	ESTs
	129434	AA280837	AW967495	Hs.186644	ESTs
	130529	AA280886	AA178953	Hs.309648	gb:zp39e03.s1 Stratagene muscle 937209 H
	120575	AA280934	AW978022	Hs.238911	hypothetical protein DKFZp762E1511; KIAA
40	409339	AA281535	AB020686	Hs.54037	ectonucleotide pyrophosphatase/phosphodi
	120591	AA281797	AF078847	Hs.191356	general transcription factor IIH, polype
	120593	AA282047	AA748355	Hs.193522	ESTs
	430275	AA283002	Z11773	Hs.237786	zinc finger protein 187
	440303	AA283709	AA306166	Hs.7145	calpain 7
45	120609	AA283902	AW978721	Hs.266076	ESTs, Weakly similar to A46010 X-linked
	409702	AA284108	AI752244		eukaryotic translation elongation factor
	456870	AA284109	AI241084	Hs.154353	nonselective sodium potassium/proton exc
	132614	AA284371	AA284371	Hs.118064	similar to rat nuclear ubiquitous casein
	458750	AA284744	AA115496	Hs.336898	Homo sapiens, Similar to RIKEN cDNA 1810
50	135376	AA284784	BE617856	Hs.99756	mitochondrial ribosome recycling factor
	120621	AA284840	AW961294	Hs.143818	hypothetical protein FLJ23459
	452279	AA286844	AA286844	Hs.61260	hypothetical protein FLJ13164
	332484	AA287032	AW172431	Hs.13012	ESTs
	120644	AA287038	AI869129	Hs.96616	ESTs
55	120660	AA287546	AA286785	Hs.99677	ESTs
	135370	AA287553	BE622187	Hs.99670	ESTs, Weakly similar to I38022 hypotheti
	120661	AA287556	AA287556	Hs.263412	ESTs, Weakly similar to ALUB_HUMAN !!!!
	429828	AA287564	AB019494	Hs.225767	IDN3 protein
	452291	AA291015	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi
60	120699	AA291716	AI683243	Hs.97258	ESTs, Moderately similar to S29539 ribos
	100690	AA291749	AA383256	Hs.1657	estrogen receptor 1
	120726	AA293656	AA293655	Hs.21198	ESTs
	120737	AA302430	AL049176	Hs.82223	chordin-like
	120745	AA302809	AA302809		gb:EST10426 Adipose tissue, white I Homo
65	443574	AA302820	U83993	Hs.321709	purinergic receptor P2X, ligand-gated io
	120750	AA310499	AI191410	Hs.96693	ESTs, Moderately similar to 2109260A B c
	120761	AA321890	AA321890		branched chain keto acid dehydrogenase E
	120768	AA340589	AA340589	Hs.104560	EST
	120769	AA340622	AI769467	Hs.9475	ESTs
70	135232	AA342457	AL038812	Hs.96800	ESTs, Moderately similar to ALU7_HUMAN A
	120793	AA342864	AA342864	Hs.96812	ESTs
	120796	AA342973	AI247356	Hs.96820	ESTs
	120809	AA346495	AA346495		gb:EST52657 Fetal heart II Homo sapiens
	332633	AA347573	AL120071	Hs.48998	fibronectin leucine rich transmembrane p
	120825	AA347614	AI280215	Hs.96885	ESTs
75	120827	AA347717	AA382525	Hs.132967	Human EST clone 122887 mariner transpos
	120839	AA348913	AA348913		gb:EST55442 Infant adrenal gland II Homo

	120850	AA349647	AA349647	Hs.96927	Homo sapiens cDNA FLJ12573 fis, clone NT
	120852	AA349773	AA349773	Hs.191564	ESTs
	128852	AA350541	R40622	Hs.106601	ESTs
5	135240	AA357159	AA357159	Hs.96986	EST
	120870	AA357172	AA357172	Hs.292581	ESTs, Moderately similar to ALU1_HUMAN A
	120894	AA370132	AA370132	Hs.97063	ESTs
	435737	AA370472	AF229839	Hs.173202	I-kappa-B-interacting Ras-like protein 1
	120897	AA370867	AA370867	Hs.97079	ESTs, Moderately similar to AF174605 1 F
10	120915	AA377296	AL135556	Hs.97104	ESTs
	120935	AA383902	AL048409	Hs.97177	ESTs, Weakly similar to ALU1_HUMAN ALU S
	120936	AA385934	AA385934	Hs.97184	EST, Highly similar to (define not avai
	120937	AA386255	AA386255	Hs.97186	EST
	120938	AA386260	AA386260	Hs.104632	EST
15	417632	AA386266	R20855	Hs.5422	glycoprotein M6B
	120960	AA398014	AA398014	Hs.104684	EST
	120985	AA398222	AI219896	Hs.97592	ESTs
	120988	AA398235	AA398235	Hs.97631	ESTs
	121008	AA398348	AA398348	Hs.130546	Human DNA sequence from clone RP11-251J8
20	121029	AA398482	AA398482	Hs.97641	EST
	121032	AA398504	AA393037	Hs.161798	ESTs
	121033	AA398505	AA398505	Hs.97360	ESTs
	121034	AA398507	AL389951	Hs.271623	nucleoporin 50kD
	121035	AA398523	AA398523	Hs.210579	ESTs
25	121058	AA398625	AA398625	Hs.97391	ESTs
	121060	AA398632	AA398632	Hs.97395	ESTs
	121061	AA398633	AA393288	Hs.97396	ESTs
	121091	AA398894	AA398894	Hs.97657	ESTs, Moderately similar to ALU8_HUMAN A
	121092	AA398895	AA398895	Hs.97658	EST
30	121094	AA398900	AA402505		gb:zt62h10.r1 Soares_testis_NHT Homo sap
	121096	AA398904	AA398904	Hs.332690	ESTs
	121115	AA399122	AA398187	Hs.104682	ESTs, Weakly similar to mitochondrial ci
	121121	AA399371	AA399371	Hs.189095	similar to SALL1 (sal (Drosophila)-like
	121122	AA399373	AI126713	Hs.192233	ESTs, Highly similar to T00337 hypotheti
35	121125	AA399441	AL042981	Hs.251278	KIAA1201 protein
	121151	AA399636	AA399636	Hs.143629	ESTs
	121153	AA399640	AA399640	Hs.97694	ESTs
	121163	AA399680	AI676062	Hs.111902	ESTs
	121176	AA400080	AL121523	Hs.97774	ESTs
40	121192	AA400262	AA400262	Hs.190093	ESTs
	121223	AA400725	AI002110	Hs.97169	ESTs, Weakly similar to dJ667H12.2.1 [H.
	121227	AA400748	AA400748	Hs.97823	Homo sapiens mRNA; cDNA DKFZp434D024 (fr
	121231	AA400780	AA814948	Hs.96343	ESTs, Weakly similar to ALUC_HUMAN !!!!
	121278	AA401631	AA037121	Hs.98518	Homo sapiens cDNA FLJ11490 fis, clone HE
45	121279	AA401688	AA292873	Hs.177996	ESTs
	121282	AA401695	AA401695	Hs.97334	ESTs
	121299	AA402227	AA402227	Hs.22826	tropomodulin 3 (ubiquitous)
	121301	AA402329	NM_006202	Hs.89901	phosphodiesterase 4A, cAMP-specific (dun
	121302	AA402398	AA402587	Hs.325520	LAT1-3TM protein
50	121304	AA402449	AA293863	Hs.97316	EST
	121305	AA402468	AA402468	Hs.291557	ESTs
	134721	AA403268	AK000112	Hs.89306	hypothetical protein FLJ20105
	121323	AA403314	AA291411	Hs.97247	ESTs
	121324	AA404229	AA404229	Hs.97842	EST
55	444422	AA404260	AI768623	Hs.108264	ESTs
	131074	AA404271	U16125	Hs.181581	glutamate receptor, ionotropic, kainate
	121344	AA405026	AA405026	Hs.193754	ESTs
	121348	AA405182	AA405182	Hs.97973	ESTs
	121350	AA405237	AA405237		gb:zt06e10.s1 NCL_CGAP_GCB1 Homo sapiens
60	121400	AA406061	AA406061	Hs.98001	EST
	121402	AA406063	AA406063	Hs.98003	ESTs
	121403	AA406070	AA406070	Hs.98004	EST
	121408	AA406137	AA406137	Hs.98019	EST
	121431	AA406335	AA035279	Hs.176731	ESTs
65	121471	AA411804	AA411804	Hs.261575	ESTs
	121474	AA411833	AA402335	Hs.188760	ESTs, Highly similar to Trad [H.sapiens]
	121526	AA412219	AW665325	Hs.98120	ESTs
	121530	AA412259	AA778658	Hs.98122	ESTs
	121558	AA412497	AA412497		gb:zt95g12.s1 Soares_testis_NHT Homo sap
70	121559	AA412498	AI192044	Hs.104778	ESTs
	121584	AA416586	AI024471	Hs.98232	ESTs
	121609	AA416867	AA416867	Hs.98185	EST
	121612	AA416874	AA416874	Hs.98168	ESTs
	121737	AA421133	AA421133	Hs.104671	erythrocyte transmembrane protein
75	121740	AA421138	AA421138	Hs.143835	EST
	436032	AA422079	AA150797	Hs.109276	latexin protein
	121784	AA423837	T90789	Hs.94308	RAB35, member RAS oncogene family

	121802	AA424328	AI251870	Hs.188898	ESTs
	121803	AA424339	AI338371	Hs.157173	ESTs
	135286	AA424469	AW023482	Hs.97849	ESTs
5	332778	AA424469	AW023482	Hs.97849	ESTs
	121806	AA424502	AA424313	Hs.98402	ESTs
	129517	AA425004	AW972853	Hs.112237	ESTs
	121845	AA425734	AI732692	Hs.165066	ESTs, Moderately similar to ALU2_HUMAN A
	121853	AA425887	AA425887	Hs.98502	hypothetical protein FLJ14303
10	121891	AA426456	AA426456	Hs.98469	ESTs
	121895	AA427396	AA427396		gb:zw33a02.s1 Soares ovary tumor NbHOT H
	121899	AA427555	R55341	Hs.50421	KIAA0203 gene product
	121917	AA428218	AA406397	Hs.139425	ESTs
	121918	AA428242	BE274689	Hs.184175	chromosome 2 open reading frame 3
	121919	AA428281	AA428281	Hs.98560	EST
15	121941	AA428865	AA428865	Hs.98563	ESTs
	121942	AA428994	AW452701	Hs.293237	ESTs
	121970	AA429666	AA429666	Hs.98617	EST
	121993	AA430181	AW297880	Hs.98661	ESTs
20	418706	AA430184	U73524	Hs.87465	ATP/GTP-binding protein
	122022	AA431293	AA431293	Hs.98716	ESTs, Moderately similar to T42650 hypot
	122050	AA431478	AI453076		ELAV (embryonic lethal, abnormal vision,
	122051	AA431492	AA431492	Hs.98742	EST
	122055	AA431732	AA431732	Hs.98747	EST
	122105	AA432278	AW241685	Hs.98699	ESTs
25	122125	AA434411	AK000492	Hs.98806	hypothetical protein
	135235	AA435512	AW298244	Hs.266195	ESTs
	122162	AA435698	AA628233	Hs.79946	cytochrome P450, subfamily XIX (aromatiz
	422072	AA435711	AB018255	Hs.111138	KIAA0712 gene product
30	415106	AA435815	U40763	Hs.77965	peptidyl-prolyl isomerase G (cyclophilin
	122186	AA435842	AA398811	Hs.104673	ESTs
	122235	AA436475	AA436475	Hs.112227	membrane-associated nucleic acid binding
	412970	AA436489	AB026436	Hs.177534	dual specificity phosphatase 10
	419288	AA442060	AA256106	Hs.87507	ESTs
35	122310	AA442079	AW192803	Hs.98974	ESTs, Weakly similar to S65824 reverse t
	122334	AA443151	BE465894	Hs.98365	ESTs, Weakly similar to LB4D_HUMAN NADP-
	122382	AA446133	AA446440	Hs.98643	ESTs
	122425	AA447145	AB007859	Hs.100955	KIAA0399 protein
	122431	AA447398	AA447398	Hs.99104	ESTs
40	122450	AA447643	AA447643	Hs.112095	hypothetical protein DKFZp434F1819
	426284	AA447742	AJ404468	Hs.284259	dynein, axonemal, heavy polypeptide 9
	122477	AA448226	AA448226	Hs.324123	ESTs
	122500	AA448825	AA448825	Hs.99190	ESTs
	122522	AA449444	AA299607	Hs.98969	ESTs
45	122536	AA450087	AF060877	Hs.99236	regulator of G-protein signalling 20
	122538	AA450211	AA450211	Hs.99239	ESTs
	122540	AA450244	AA476741	Hs.98279	ESTs, Weakly similar to A43932 mucin 2 p
	122560	AA452123	AW392342	Hs.283077	centrosomal P4.1-associated protein; unc
	421919	AA452155	AJ224901	Hs.109526	zinc finger protein 198
50	122562	AA452156	AA452156		gb:zx29c03.s1 Soares_total_fetus_Nb2HF8_
	122585	AA453036	AI681654	Hs.170737	hypothetical protein FLJ23251
	122608	AA453526	AA453525	Hs.143077	ESTs
	122635	AA454085	AA454085		gb:zx33a08.s1 Soares_total_fetus_Nb2HF8_
	122636	AA454103	AW651706	Hs.99519	hypothetical protein FLJ14007
55	122653	AA454642	AW009166	Hs.99376	ESTs
	122660	AA454935	AI816827	Hs.180069	nuclear respiratory factor 1
	122703	AA456323	AA456323	Hs.269369	ESTs
	122724	AA457395	AA457395	Hs.99457	ESTs
	122749	AA458850	AA458850	Hs.293372	ESTs, Weakly similar to B34087 hypothe
60	122772	AA459662	AW117452	Hs.99489	ESTs
	430242	AA459668	U66669	Hs.236642	3-hydroxyisobutyryl-Coenzyme A hydrolase
	429838	AA459679	AW904907	Hs.30732	hypothetical protein FLJ13409; KIAA1711
	122777	AA459702	AK001022	Hs.214397	hypothetical protein FLJ10160 similar to
	135362	AA460017	AA978128	Hs.99513	ESTs, Weakly similar to T17454 diaphanou
65	122798	AA460324	AW366286	Hs.145696	splicing factor (CC1.3)
	122837	AA461509	AA461509	Hs.293565	ESTs, Weakly similar to putative p150 [H
	122860	AA464414	AA464414		gb:zx78g01.s1 Soares ovary tumor NbHOT H
	122861	AA464428	AA335721	Hs.213628	ESTs
	122910	AA470084	AA470084	Hs.98358	ESTs
70	132899	AA476606	AA476606	Hs.59666	SMAD in the antisense orientation
	122967	AA478521	AA806187	Hs.289101	glucose regulated protein, 58kD
	422845	AA478523	AA317841	Hs.7845	hypothetical protein MGC2752
	123009	AA479949	AA535244	Hs.78305	RAB2, member RAS oncogene family
	128917	AA481252	AI365215	Hs.206097	oncogene TC21
75	123081	AA485351	AI815486	Hs.243901	Homo sapiens cDNA FLJ20738 fis, clone HE
	123133	AA487264	AA487264	Hs.154974	Homo sapiens mRNA; cDNA DKFZp667N064 (fr
	123184	AA489072	BE247767	Hs.18166	KIAA0870 protein

	332467	AA489630	NM_014700Hs.119004	KIAA0665 gene product
	123233	AA490225	AW974175 Hs.151875	ESTs, Weakly similar to MAPB_HUMAN MICRO
	123234	AA490227	NM_001938Hs.16697	down-regulator of transcription 1, TBP-b
	123236	AA490255	AW968504 Hs.123073	CDC2-related protein kinase 7
5	123255	AA490890	AA830335 Hs.105273	ESTs
	430015	AA490916	AW768399 Hs.106357	ESTs
	448892	AA490925	AF084535 Hs.22464	epilepsy, progressive myoclonus type 2,
	123259	AA490955	AI744152 Hs.283374	ESTs, Weakly similar to CA15_HUMAN COLLA
10	123284	AA495812	AA488988 Hs.293796	ESTs
	123286	AA495824	AA495824 Hs.188822	ESTs, Weakly similar to A46010 X-linked
	123315	AA496369	AA496369	gbzv37d10.s1 Soares ovary tumor NbHOT H
	457397	AA504125	AW969025 Hs.109154	ESTs
	433049	AA521473	AU076668 Hs.334884	SEC10 (S. cerevisiae)-like 1
	123421	AA598440	AA598440 Hs.291154	EST, Weakly similar to I38022 hypothetical
15	123449	AA598899	AL049325 Hs.112493	Homo sapiens mRNA; cDNA DKFZp564D036 (fr
	426981	AA599244	AL044675 Hs.173081	KIAA0530 protein
	409986	AA599694	NM_014777Hs.57730	KIAA0133 gene product
	123497	AA600037	AA765256 Hs.135191	ESTs, Weakly similar to unnamed protein
	123604	AA609135	AA609135 Hs.293076	ESTs
20	123712	AA609684	AA609684	Homo sapiens cDNA: FLJ21543 fis, clone C
	123731	AA609839	AA609839 Hs.334437	gb:ae62f01.s1 Stratagene lung carcinoma
	123800	AA620423	AA620423 Hs.112862	EST
	123841	AA620747	AA620747 Hs.112896	ESTs
	123929	AA621364	AA621364 Hs.112981	ESTs
25	123978	C20653	T89832 Hs.170278	ESTs
	133184	D20085	AA001021 Hs.6685	thyroid hormone receptor interactor 8
	132835	D20749	Z83844 Hs.5790	hypothetical protein dJ37E16.5
	435147	D51285	AL133731 Hs.4774	Homo sapiens mRNA; cDNA DKFZp761C1712 (f
	128695	D59972	NM_003478Hs.101299	culin 5
30	124029	F04112	F04112 Hs.312553	gb:HSC2JH062 normalized infant brain cDN
	124057	F13604	AA902384 Hs.73853	bone morphogenetic protein 2
	449316	H01662	AI609045 Hs.321775	hypothetical protein DKFZp434D1428
	130973	H05135	AI638418 Hs.1440	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep
35	124106	H12245	H12245	gb:ym17a12.r1 Soares infant brain 1NIB H
	124136	H22842	H22842 Hs.101770	EST
	124165	H30894	H30039 Hs.107674	ESTs
	429627	H43442	NM_015340Hs.2450	leucyl-tRNA synthetase, mitochondrial
	124178	H45996	BE463721 Hs.97101	putative G protein-coupled receptor
	129948	H69281	AI537162 Hs.263988	ESTs
40	452114	H69485	N22687 Hs.8236	ESTs
	124+D826254	H69899	H69899	gb:yu70c12.s1 Weizmann Olfactory Epithel
	129056	H70627	AI769958 Hs.108336	ESTs, Weakly similar to ALUE_HUMAN !!!!
	427580	H73260	AK001507 Hs.44143	Homo sapiens clone FLB6914 PRO1821 mRNA,
	426793	H77531	X89887 Hs.172350	HIR (histone cell cycle regulation defec
45	124274	H80552	H80552 Hs.102249	EST
	129078	H80737	AI351010 Hs.102267	lysosomal
	457658	H93412	AW952124 Hs.13094	presenilins associated rhomboid-like pro
	124315	H94892	NM_005402Hs.288757	v-ral simian leukemia viral oncogene hom
	437712	H95643	X04588 Hs.85844	neurotrophic tyrosine kinase, receptor,
50	124324	H96552	H96552 Hs.159472	Homo sapiens cDNA: FLJ22224 fis, clone H
	452933	H97146	AW391423 Hs.288555	Homo sapiens cDNA: FLJ22425 fis, clone H
	132231	H99131	AA662910 Hs.42635	hypothetical protein DKFZp434K2435
	421877	H99462	AW250380 Hs.109059	mitochondrial ribosomal protein L12
	443123	H99837	AA094538 Hs.272808	putative transcription regulation nuclea
55	132963	N22140	AA099693 Hs.34851	epsilon-tubulin
	420473	N22197	AL118782 Hs.300208	Sec23-interacting protein p125
	417381	N23756	AF164142 Hs.82042	solute carrier family 23 (nucleobase tra
	130365	N24134	W56119 Hs.155103	eukaryotic translation initiation factor
	456610	N24195	AF172066 Hs.106346	retinoic acid repressible protein
60	439311	N26739	BE270668 Hs.151945	mitochondrial ribosomal protein L43
	124383	N27098	N27098 Hs.102463	EST
	124387	N27637	N27637 Hs.109019	ESTs
	129341	N33090	AI193519 Hs.226396	hypothetical protein FLJ11126
	419793	N35967	AI364933 Hs.168913	serine/threonine kinase 24 (Ste20, yeast
65	124433	N39069	AA280319 Hs.288840	PRO1575 protein
	124441	N46441	AW450481 Hs.161333	ESTs
	132338	N48270	AA353868 Hs.182982	golgin-67
	436575	N48365	AI473114	ESTs
	124466	N51316	R10084 Hs.113319	kinesin heavy chain member 2
70	408048	N51499	NM_007203Hs.42322	A kinase (PRKA) anchor protein 2
	124483	N53976	AI821780 Hs.179864	ESTs
	124484	N54157	H66118 Hs.285520	ESTs, Weakly similar to 2109260A B cell
	124485	N54300	AB040933 Hs.15420	KIAA1500 protein
	124494	N54831	N54831 Hs.271381	ESTs, Weakly similar to I38022 hypotheti
75	129200	N59849	N59849 Hs.13565	Sam68-like phosphotyrosine protein, T-ST
	124527	N62132	N79264 Hs.269104	ESTs

	124532	N62375	N62375	Hs.102731	EST
	133213	N63138	AA903424	Hs.6786	ESTs
	124539	N63172	D54120	Hs.146409	cell division cycle 42 (GTP-binding prot
5	129196	N63787	BE296313	Hs.265592	ESTs, Weakly similar to I38022 hypotheti
	124575	N68168	N68168		gb:za11c01.s1 Soares fetal liver spleen
	124576	N68201	N68201		ESTs, Weakly similar to I38022 hypotheti
	124577	N68300	N68300	Hs.138485	gb:za12g07.s1 Soares fetal liver spleen
	124578	N68321	N68321	Hs.231500	EST
10	124593	N69575	N69575	Hs.102788	ESTs
	128501	N75007	AL133572	Hs.199009	protein containing CXXC domain 2
	332434	N75542	AI680737	Hs.289068	Homo sapiens cDNA FLJ11918 fis; clone HE
	128473	N90066	T78277	Hs.100293	O-linked N-acetylglucosamine (GlcNAc) tr
	128639	N91246	AW582962	Hs.102897	CGI-47 protein
15	124652	N92751	W19407	Hs.3862	regulator of nonsense transcripts 2; DKF
	133137	N93214	AB002316	Hs.65746	KIAA0318 protein
	124671	N99148	AK001357	Hs.102951	Homo sapiens cDNA FLJ10495 fis, clone NT
	133054	R07876	AA464836	Hs.291079	ESTs, Weakly similar to T27173 hypotheti
	425266	R10865	J00077	Hs.155421	alpha-fetoprotein
20	124720	R11056	R05283		gb:ye91c08.s1 Soares fetal liver spleen
	124722	R11488	T97733	Hs.185685	ESTs
	128944	R23930	AL137586	Hs.52763	anaphase-promoting complex subunit 7
	132965	R26589	AI248173	Hs.191460	hypothetical protein MGC12936
	426504	R37588	AW162919	Hs.170160	RAB2, member RAS oncogene family-like
25	438828	R37613	AL134275	Hs.6434	hypothetical protein DKFZp761F2014
	124757	R38398	H11368	Hs.141055	Homo sapiens clone 23758 mRNA sequence
	124762	R39179	AA553722	Hs.92096	ESTs, Moderately similar to A46010 X-in
	124773	R40923	R45154	Hs.338439	ESTs
	135266	R41179	R41179	Hs.97393	KIAA0328 protein
30	427961	R41294	AW293165	Hs.143134	ESTs
	414303	R42307	NM_004427	Hs.165263	early development regulator 2 (homolog o
	128540	R43189	AW297929	Hs.328317	EST
	124785	R43306	W38537	Hs.280740	hypothetical protein MGC3040
	124792	R44357	R44357	Hs.48712	hypothetical protein FLJ20736
35	124793	R44519	R44519		gb:yg24h04.s1 Soares infant brain 1NIB H
	124799	R45088	R45088		gb:yg38g04.s1 Soares infant brain 1NIB H
	124812	R47948	R47948	Hs.188732	ESTs
	124821	R51524	H87832	Hs.7388	kelch (Drosophila)-like 3
	424123	R54950	AW966158	Hs.58582	Homo sapiens cDNA FLJ12789 fis, clone NT
40	124835	R55241	R55241	Hs.101214	EST
	124845	R59585	R59585	Hs.101255	ESTs
	124847	R60044	W07701	Hs.304177	Homo sapiens clone FLB8503 PRO2286 mRNA,
	440630	R60872	BE561430	Hs.239388	Human DNA sequence from clone RP1-304B14
	124861	R66690	R67567	Hs.107110	ESTs
45	332503	R67266	NM_004455	Hs.150956	exostoses (multiple)-like 1
	124879	R73588	R73588	Hs.101533	ESTs
	124892	R79403	AI970003	Hs.23756	hypothetical protein similar to swine ac
	124906	R87647	H75964	Hs.107815	ESTs
	124922	R93622	R93622	Hs.12163	eukaryotic translation initiation factor
50	124940	R99599	AF068846	Hs.103804	heterogeneous nuclear ribonucleoprotein
	124941	R99612	AI766661	Hs.27774	ESTs, Highly similar to AF161349 1 HSPC0
	124943	T02888	AW963279	Hs.123373	ESTs, Weakly similar to ALU1_HUMAN ALU S
	124947	T03170	T03170	Hs.100165	ESTs
	124954	T10465	AW964237	Hs.6728	KIAA1548 protein
55	456862	T15418	U55184	Hs.154145	hypothetical protein FLJ11585
	410653	T15597	BE383768	Hs.65238	95 kDa retinoblastoma protein binding pr
	418133	T15652	R43504	Hs.6181	ESTs
	440014	T16898	AW960782	Hs.6856	ash2 (absent, small, or homeotic, Drosop
	131082	T26644	AI091121	Hs.246218	Homo sapiens cDNA: FLJ21781 fis, clone H
60	124980	T40841	T40841	Hs.98681	ESTs
	124984	T47566	BE313210	Hs.334798	eukaryotic translation elongation factor
	124991	T50116	T50116		gb:yb77c10.s1 Stratagene ovary (937217)
	457222	T50145	NM_004477	Hs.203772	FSHD region gene 1
	125000	T58615	T58615	Hs.235887	ESTs
65	132932	T59940	AW118826	Hs.6093	Homo sapiens cDNA: FLJ22783 fis, clone K
	444484	T63595	AK002126	Hs.11260	hypothetical protein FLJ11264
	125008	T64891	T91251		gb:yd60a10.s1 Soares fetal liver spleen
	125009	T64924	T64924	Hs.303046	ESTs
	445384	T64933	T79136	Hs.127243	Homo sapiens mRNA for KIAA1724 protein,
70	125017	T68875	T68875		gb:yc30f05.s1 Stratagene liver (937224)
	125018	T69027	T69027	Hs.269481	sex comb on midleg homolog 1
	125020	T69924	T69981		gb:yc19d03.r1 Stratagene lung (937210) H
	437871	T70353	AI084813	Hs.114088	ESTs
	134204	T79780	AI873257	Hs.7994	hypothetical protein FLJ20551
75	125050	T79951	AW970209	Hs.111805	ESTs
	125052	T80174	T85104	Hs.222779	ESTs, Moderately similar to similar to N
	125054	T80622	T80622	Hs.268601	ESTs, Weakly similar to envelope [H.sapi

	125063	T85352	T85352	gb:yd82d01.s1 Soares fetal liver spleen
	125064	T85373	T85373	gb:yd82f07.s1 Soares fetal liver spleen
	125066	T86284	T86284	gb:yd77b07.s1 Soares fetal liver spleen
5	416507	T89579	AL045364 Hs.79353	transcription factor Dp-1
	125080	T90360	T90360 Hs.268620	ESTs, Highly similar to ALU6_HUMAN ALU S
	125097	T94328	AW576389 Hs.335774	EST, Moderately similar to S65657 alpha-
	125104	T95590	T95590	gb:ye40a03.s1 Soares fetal liver spleen
	135107	T97257	T97257 Hs.94560	ESTs, Moderately similar to I38022 hypot
10	423122	T97599	AA845462 Hs.124024	deltex (Drosophila) homolog 1
	125118	T97620	R10606 Hs.269890	gb:yf35f11.s1 Soares fetal liver spleen
	125120	T97775	T97775 Hs.100717	EST
	134160	T98152	T98152 Hs.79432	fibrillin 2 (congenital contractural ara
	125136	W31479	AW962364 Hs.129051	ESTs
15	125144	W37999	AB037742 Hs.24336	KIAA1321 protein
	125150	W38240	W38240	Empirically selected from AFFX single pr
	450142	W40150	AW207469 Hs.24485	chondroitin sulfate proteoglycan 6 (bama
	131987	W45435	AW453069 Hs.3657	activity-dependent neuroprotective prote
	125178	W58202	W93127 Hs.31845	ESTs
20	125180	W58344	W58469 Hs.103120	ESTs
	125182	W58650	AA451755 Hs.263560	ESTs
	446888	W68736	AL030996 Hs.16411	hypothetical protein LOC57187
	125197	W69106	AF086270 Hs.278554	heterochromatin-like protein 1
	133497	W69111	BE617303 Hs.74266	hypothetical protein MGC4251
	429922	W69399	Z97630 Hs.226117	H1 histone family, member 0
25	129232	W69459	R98881 Hs.109655	sex comb on midleg (Drosophila)-like 1
	422166	W72424	W72424 Hs.112405	S100 calcium-binding protein A9 (calgran
	125209	W72724	W72724 Hs.103174	ESTs, Weakly similar to TSP2_HUMAN THROM
	125212	W72834	AA746225 Hs.103173	ESTs
30	456631	W73955	BE383436 Hs.108847	hypothetical protein MGC2749
	125223	W74701	AI916269 Hs.109057	ESTs, Weakly similar to ALU5_HUMAN ALU S
	125225	W76540	W74169 Hs.16492	DKFZP564G2022 protein
	125228	W79397	AA033982 Hs.110059	ESTs, Weakly similar to I38022 hypotheti
	132393	W85888	AL135094 Hs.47334	hypothetical protein FLJ14495
35	125238	W86038	N99713 Hs.109514	ESTs
	125247	W86881	AA694191 Hs.163914	ESTs
	129296	W87804	AI051967 Hs.110122	ESTs
	125263	W88942	AA098878	gb:zn45g10.r1 Stratagene HeLa cell s3 93
	125266	W90022	W90022 Hs.186809	ESTs, Highly similar to LCT2_HUMAN LEUKO
40	450862	W92272	U91543 Hs.25601	chromodomain helicase DNA binding protei
	452401	W92764	NM_007115Hs.29352	tumor necrosis factor, alpha-induced pro
	428243	W93040	H05317 Hs.283549	ESTs
	125277	W93227	W93227 Hs.103245	EST
	125278	W93523	AI218439 Hs.129998	enhancer of polycomb 1
45	125280	W93659	AI123705 Hs.106932	ESTs
	448205	W94003	W93949 Hs.33245	ESTs
	131844	W94401	AI419294 Hs.324342	ESTs
	125284	W94688	NM_002666Hs.103253	perilipin
50	417111	W94787	AW016321 Hs.82306	destrin (actin depolymerizing factor)
	445424	Z38294	AB028945 Hs.12696	cortactin SH3 domain-binding protein
	125289	Z38311	T34530 Hs.4210	Homo sapiens cDNA FLJ13069 fis, clone NT
	446313	Z38465	H06245 Hs.106801	ESTs, Weakly similar to PC4259 ferritin
	431342	Z38525	AW971018 Hs.21659	ESTs
	433227	Z38538	AB040923 Hs.106808	kelch (Drosophila)-like 1
55	428306	Z38551	AB037715 Hs.183639	hypothetical protein FLJ10210
	424624	Z38783	AB032947 Hs.151301	Ca2+-dependent activator protein for secr
	125295	Z39113	AB022317 Hs.25887	sema domain, immunoglobulin domain (Ig),
	125298	Z39255	AW972542 Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone H
	125300	Z39591	Z39591 Hs.101376	EST
60	448378	Z39783	BE622770 Hs.264915	Homo sapiens cDNA FLJ12908 fis, clone NT
	444582	Z39920	R55344 Hs.22142	cytochrome b5 reductase b5R.2
	130882	Z40166	AA497044 Hs.20887	hypothetical protein FLJ10392
	128888	Z40388	AI760853 Hs.241558	ariadne (Drosophila) homolog 2
	125310	Z40646	R59161 Hs.124953	ESTs
65	125315	Z41697	R38110 Hs.106296	ESTs
	125317	Z99349	Z99348 Hs.112461	ESTs, Weakly similar to I38022 hypotheti
	135096	Z99394	AA081258	zinc finger protein 36 (KOX 18)

TABLE 3A

Table 3A shows the accession numbers for those pkeys lacking unigenelD's for Table 3. The pkeys in Table 7 lacking unigenelD's are represented within Tables 1-6A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
108469	116761_1	AA079487 AA128547 AA128291 AA079587 AA079600
124106	125446_1	H12245 AA094769 R14576
108501	13684_-12	AA083256
108562	36375_1	AA100796 AF020589 AA074629 AA075946 AA100849 AA085347 AA126309 AA079311 AA079323 AA085274
101300	4669_1	BE535511 M62098 AA306787 AW891766 AA348998 AA338869 AA344013 AW956561 AW389343 AW403607 L40391
		AW408435 AA121738 AI568978 H13317 R20373 AW948724 AW948744 AA335023 AA436722 AA448690 C21404
		AW884390 AA345454 AA303292 AA174174 BE092290 T90614 AA035104 R76028 AA126924 AA741086 AW022056
		AW118940 AA121666 AI832409 AA683475 AI140901 AI623576 AW519064 AW474125 AI953923 AI735349 AW150109
		AI436154 AW118130 AW270782 AI804073 N27434 AA876543 AA937815 AI051166 AA505378 AI041975 AI335355
		AI089540 AA662243 AI127912 AI925604 AI250880 AI366874 AI564386 AI815196 AI683526 AI435885 AI160934 H79030
		AI801493 AA448691 AI673767 AI076042 AI804327 AA813438 AA680002 AI274492 T16177 AI287337 AI935050
		AA907805 AA911493 AI589411 AI371358 AW576236 AI078866 AW516168 AA346372 AI560185 AA471009 R75857
		AA296025 AA523155 AA853168 AI696593 AI658482 AI566601 AW072797 AA128047 AA035502 AW243274 AA992517
		R43760
132091	94851_1	AW954243 AA829930 AA412478 AA828434 AA814538 AI927418 AI192435 W52897 AA443666 AA031913 AI683306
		AA918481 AI183314 D83907 AI206832 AA876122 D83836 D83838 D82533 AI761290 AI191125 AI143749 AW771909
		AI241436 AI676267 W56507 AA847787 AA568692 T10502 AI247870 AA715017 AA643304 AA890233 AA811387
		AA897470 AA907729 AI708679 AI078010 AA452830 AW419160 AI783713 N80205 W56778 AA676899 AI888718 N69930
		AI338935 AI217580 AA639508 AA575836 BE046852 AI312651 AI038406 AA628649 AA643838 AI493761 AA032024
		W38849 AA340178 AA447052 AA452969 W19369 AA296364 H44229 W58767 C05751 C05835 AI741989 N98532
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			AW382712 H05665 F07292 N39875 AA089729 H62556 N42842 R12952 AW373735 AW364155 AA056183 W39185	
			AW382708 N32488 AF114096 AW375993 AI133569 W52561 AA603040 AA133710 AI928796 AW176370 AA827519	
			AW338437 AA521142 T29341 AI800461 AW317002 AA703914 AA860830 AI859203 AI445772 AA714334 AI817066	
			AI832027 AW510442 AI635802 AW088306 AW068672 AW408555 AW467542 AA552657 AA152367 W32081 AA582124	
45			AA074040 AA931657 AI051154 AW410203 AI921644 H17434 AI832330 AW404836 AI925038 AA088423 AA954166	
			AA580453 AW021292 AI267215 AW080082 AW383778 AI933053 AI919097 W31557 N90245 AA931591 AA563995	
			F36352 AA056184 AA476294 AA641327 AA533550 AI749630 W58323 AA569119 AA508573 AI809050 AI378996	
			AA411362 AW407505 AA938104 AA074041 AA632876 AW193748 AA507873 AI270128 AI472365 AA411363 AI523216	
			AI719965 AI816302 AA182681 AI707990 AA133588 AI758537 W60253 AI460308 AA135423 AI083904 F04188 N89693	
50			AW408776 AI678595 AI270568 AA722059 W58234 F33650 AA090547 AA285108 AA425981 N85079 D20218 AI273980	
			AA159028 F03226 AW247914 N26918 AW272741 N90109 H05666 N23327 AW247953 R44748 AA962015 F03558	
			AI752394 AW409913 AW248396 AI816463 AI752393 AA325370 AA263089 AI570130 AI971951 AI160658 AI357360	
			AW168686 AL121075 AW050536 N21672 W67748 AA514242 AI127386 H14607 AI185752 W79364 AA088520 AA152476	
			AW351940 AW373683 AI940524 AW374953 T56500 N24329 AI940720 AW374933 AW374947 AW391913 AL138337	
55			AW376241 AW062943 F26666 AW410202 AW062958 F34529 AW381807 AW393315 W17147 AW176359 AA664576	
			AW380424 AA306040 AI745674 AW300951 AI188579 AI438973 AI305271 AA433818 AA612807 AI831809 AI940409	
			AA158663 AI572988	
	124576	genbank_N68201	N68201	
	108931	genbank_AA147186	AA147186	
60	108941	genbank_AA148650	AA148650	
	124720	144582_1	R05283 R11056	
	124793	genbank_R44519	R44519	
	124799	genbank_R45088	R45088	
	103138	entrez_X65965	X65965	
65	117683	genbank_N40180	N40180	
	124991	genbank_T50116	T50116	
	103432	entrez_X97748	X97748	
	119174	genbank_R71234	R71234	
	119239	95573_2	T11483 T11472	
70	133678	11235_1	AW247252 AA346143 NM_000270 AA381085 N91995 X00737 AA381079 AA296473 AA296110 AA315735 AA311617	
			AA326750 AA376804 AW403290 T95231 M13953 T47963 H82039 AA279899 AA627997 N76320 N99527 H37842	
			W20095 AA457308 AW469547 AA724143 H83220 AA319496 W86334 W30892 R89169 R99427 N41854 H47286	
			AA348094 AA045089 R63016 AI922219 AI024906 AI096488 AI885005 AA194872 N90489 AI452544 H72411 AA282427	
			AA430735 R68963 R22453 H70385 AW129369 AW467320 AW519082 AA345018 AA582183 AI961789 R65918 N30611	
			AI979189 AI280889 AW273191 R66531 AI285845 AI675927 AI421990 AW190879 H37794 AA699667 H68427 AA954388	
			AI188757 AI140048 AA430382 AI204151 AW247864 AA559099 AI431420 AA548276 AI149466 AA772669 AA694388	
75			AA724168 AA301651 AA281952 AA779925 AA234760 W86290 AA913603 AW511745 AI500697 AA814922 AA835040	

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T47964 H53998 AA975804 R98710 AI077604 N70252 R98084 AW250171 H69268 AI597614 AA970746 AA972548
 AI377116 R62962 H16737 R89070 AA731329 R66532 N54354 AI818832 H81944 N71567 T95122 W86463 AA437095
 AI431999 AI915724 N63851 AI674743 AA457307 AA211475 N64444 AI799146 H72853 R99335 H60413 AA770367
 AA156105 AI269937 H64029 H89728 R65819 AW470496 AI873318 AI735713 H82987 C02447 AI478666 T27651
 AI699770 AW025156 H69719 AI984717 N69225 AI459856 AA953577 AI424691 H13843 R22404 AI873796 AI336002
 N70898 AI420854 AA541792 AA346142 AI000814 AI828348 AA045090 T51257 N90434 H13890 N73184 AI708083
 AA781606 AA329050 AA339985 R68964 H64795 W04186 H16845

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119416 genbank_T97186 T97186
 119558 NOT_FOUND_entrez_W38194 W38194
 119559 NOT_FOUND_entrez_W38197 W38197
 119654 genbank_W57759W57759
 121350 genbank_AA405237 AA405237
 121558 genbank_AA412497 AA412497
 105985 genbank_AA406610 AA406610
 114648 genbank_AA101056 AA101056
 121895 genbank_AA427396 AA427396
 100327 entrez_D55640 D55640
 123315 714071_1 AA496369 AA496646
 123473 genbank_AA599143 AA599143

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TABLE 4:

Pkey: Unique Eos probeset identifier number
 Accession: Accession number used for previous patent filings
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title

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Pkey	Accession	ExAccn	UniGene	UnigeneTitle
100405	D86425	AW291587	Hs.82733	nidogen 2
100420	D86983	D86983	Hs.118893	Melanoma associated gene
100481	HG1098-HT1098	X70377	Hs.121489	cystatin D
100484	HG1103-HT1103	NM_005402	Hs.288757	v-rat simian leukemia viral oncogene hom
100718	HG3342-HT3519	BE295928	Hs.75424	inhibitor of DNA binding 1, dominant neg
100991	J03764	J03836	Hs.82085	serine (or cysteine) proteinase inhibito
101097	L06797	BE245301	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus
101168	L15388	NM_005308	Hs.211569	G protein-coupled receptor kinase 5
101194	L20971	L20971	Hs.188	phosphodiesterase 4B, cAMP-specific (dun
101261	L35545	D30857	Hs.82353	protein C receptor, endothelial (EPCR)
101345	L76380	NM_005795	Hs.152175	calcitonin receptor-like
101447	M21305	M21305		gb:Human alpha satellite and satellite 3
101485	M24736	AA296520	Hs.89546	selectin E (endothelial adhesion molecul
101543	M31166	M31166	Hs.2050	pentaxin-related gene, rapidly induced b
101550	M31551	Y00630	Hs.75716	serine (or cysteine) proteinase inhibito
101560	M32334	AW958272	Hs.347326	intercellular adhesion molecule 2
101674	M61916	NM_002291	Hs.82124	laminin, beta 1
101714	M68874	M68874	Hs.211587	phospholipase A2, group IVA (cytosolic,
101741	M74719	NM_003199	Hs.326198	transcription factor 4
101838	M92934	BE243845	Hs.75511	connective tissue growth factor
101857	M94856	BE550723	Hs.153179	fatty acid binding protein 5 (psoriasis-s
102012	U03057	BE259035	Hs.118400	singed (Drosophila)-like (sea urchin fas
102024	U03877	AA301867	Hs.76224	EGF-containing fibulin-like extracellular
102164	U18300	NM_000107	Hs.77602	damage-specific DNA binding protein 2 (4
102241	U27109	NM_007351	Hs.268107	multimerin
102283	U31384	AW161552	Hs.83381	guanine nucleotide binding protein 11
102303	U33053	U33053	Hs.2499	protein kinase C-like 1
102564	U59423	U59423	Hs.79067	MAD (mothers against decapentaplegic, Dr
102663	U70322	NM_002270	Hs.168075	karyopherin (importin) beta 2
102759	U81607	NM_005100	Hs.788	A kinase (PRKA) anchor protein (gravin)
102778	U83463	AF000652	Hs.8180	syndecan binding protein (syntenin)
102804	U89942	NM_002318	Hs.83354	lysyl oxidase-like 2
102887	X04729	J03836	Hs.82085	serine (or cysteine) proteinase inhibito
102898	X06256	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,
102915	X07820	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin
103036	X54925	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial
103037	X54936	BE018302	Hs.2894	placental growth factor, vascular endoth
103095	X60957	NM_005424	Hs.78824	tyrosine kinase with immunoglobulin and
103158	X67235	BE242587	Hs.118651	hematopoietically expressed homeobox
103166	X67951	AA159248	Hs.180909	peroxiredoxin 1
103185	X69910	NM_006825	Hs.74368	transmembrane protein (63kD), endoplasm
103280	X79981	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula
103554	Z18951	A1878826	Hs.74034	caveolin 1, caveolae protein, 22kD
103850	AA187101	AA187101	Hs.213194	hypothetical protein MGC10895
104465	N24990	Z44203	Hs.26418	ESTs
104592	R81003	AW630488	Hs.25338	protease, serine, 23
104764	AA025351	A1039243	Hs.278585	ESTs
104786	AA027168	AA027167	Hs.10031	KIAA0955 protein
104850	AA040465	AL133035	Hs.8728	hypothetical protein DKFZp434G171
104865	AA045136	T79340	Hs.22575	B-cell CLL/lymphoma 6, member B (zinc fi
104894	AA054087	AF065214	Hs.18858	phospholipase A2, group IVC (cytosolic,
104952	AA071089	AW076098	Hs.345588	desmoplakin (DPI, DPII)
104974	AA085918	Y12059	Hs.278675	bromodomain-containing 4
105178	AA187490	AA313825	Hs.21941	AD036 protein
105263	AA227926	AW388633	Hs.6682	solute carrier family 7, (cationic amino
105330	AA234743	AW338625	Hs.22120	ESTs
105376	AA236559	AW994032	Hs.8768	hypothetical protein FLJ10849
105729	AA292694	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds
105826	AA398243	AA478756	Hs.194477	E3 ubiquitin ligase SMURF2
105977	AA406363	AK001972	Hs.30822	hypothetical protein FLJ11110
106008	AA411465	AB033888	Hs.8619	SRY (sex determining region Y)-box 18
106031	AA412284	X64116	Hs.171844	Homo sapiens cDNA: FLJ22296 fis, clone H
106124	AA423987	H93366	Hs.7567	Homo sapiens cDNA: FLJ21962 fis, clone H

	106155	AA425309	AA425414	Hs.33287	nuclear factor I/B
	106302	AA435896	AA398859	Hs.18397	hypothetical protein FLJ23221
	106423	AA448238	AB020722	Hs.16714	Rho guanine exchange factor (GEF) 15
5	106793	AA478778	H94997	Hs.16450	ESTs
	107174	AA621714	BE122762	Hs.25338	ESTs
	107216	D51069	D51069	Hs.211579	melanoma cell adhesion molecule
	107295	T34527	AA186629	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp
	107385	U97519	NM_005397	Hs.16426	podocalyxin-like
10	108756	AA127221	AA127221	Hs.117037	ESTs
	108846	AA132983	AL117452	Hs.44155	DKFZP586G1517 protein
	108888	AA135606	AA135606	Hs.189384	gb:zl10a05.s1 Soares_pregnant_uterus_NbH
	109001	AA156125	AI056548	Hs.72116	hypothetical protein FLJ20992 similar to
	109166	AA179845	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines
15	109456	AA232645	AW956580	Hs.42699	ESTs
	109768	F10399	F06838	Hs.14763	ESTs
	110107	H16772	AW151660	Hs.31444	ESTs
	110906	N39584	AA035211	Hs.17404	ESTs
	110984	N52006	AW613287	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp
20	111006	N53375	BE387014	Hs.166146	Homer, neuronal immediate early gene, 3
	111018	N54067	AI287912	Hs.3628	mitogen-activated protein kinase kinase
	111133	N64436	AW580939	Hs.97199	complement component C1q receptor
	111760	R26892	BE551929	Hs.268754	Homo sapiens cDNA FLJ11949 fis, clone HE
	113073	T33637	N39342	Hs.103042	microtubule-associated protein 1B
25	113195	T57112	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom
	113923	W80763	AW953484	Hs.3849	hypothetical protein FLJ22041 similar to
	114521	AA046808	AW139036	Hs.108957	40S ribosomal protein S27 isoform
	115061	AA253217	AI751438	Hs.41271	Homo sapiens mRNA full length insert cDN
	115096	AA255991	AI683069	Hs.175319	ESTs
30	115145	AA258138	AA740907	Hs.88297	ESTs
	115819	AA426573	AA486620	Hs.41135	endomucin-2
	115947	AA443793	R47479	Hs.94761	KIAA1691 protein
	116314	AA490588	AI799104	Hs.178705	Homo sapiens cDNA FLJ11333 fis, clone PL
	116339	AA496257	AK000290	Hs.44033	dipeptidyl peptidase 8
35	116430	AA609717	AK001531	Hs.66048	hypothetical protein FLJ10669
	116589	D59570	AI557212	Hs.17132	ESTs, Moderately similar to I54374 gene
	116733	F13787	AL157424	Hs.61289	synaptojanin 2
	117023	H88157	AW070211	Hs.102415	Homo sapiens mRNA; cDNA DKFZp586N0121 (f
	117186	H98988	H98988	Hs.42612	ESTs, Weakly similar to ALU1_HUMAN ALU S
40	117563	N34287	AF055634	Hs.44553	unc5 (C.elegans homolog) c
	117997	N52090	N52090	Hs.47420	EST
	118475	N66845	N66845		gb:za46c11.s1 Soares fetal liver spleen
	118581	N68905	N68905		gb:za69b09.s1 Soares_fetal_lung_NbHL19W
	119073	R32894	BE245360	Hs.279477	ESTs
45	119155	R61715	R61715	Hs.310598	ESTs, Moderately similar to ALU1_HUMAN A
	119174	R71234	R71234		gb:yi54c08.s1 Soares placenta Nb2HP Homo
	119221	R98105	C14322	Hs.250700	trypsin beta 1
	119416	T97186	T97186		gb:ye50h09.s1 Soares fetal liver spleen
	119866	W80814	AA496205	Hs.193700	Homo sapiens mRNA; cDNA DKFZp586I0324 (f
50	121335	AA404418	AA404418		gb:zw37e02.s1 Soares_total_fetus_Nb2HF8_
	121381	AA405747	AW088642	Hs.97984	hypothetical protein FLJ22252 similar to
	123160	AA488687	AA488687	Hs.284235	ESTs, Weakly similar to I38022 hypotheti
	123473	AA599143	AA599143		gb:ae52d04.s1 Stratagene lung carcinoma
	123523	AA608588	AA608588		gb:ae54e06.s1 Stratagene lung carcinoma
55	123533	AA608751	AA608751		gb:ae56h07.s1 Stratagene lung carcinoma
	123964	C13961	C13961		gb:C13961 Clontech human aorta polyA+ mR
	124006	D60302	AI147155	Hs.270016	ESTs
	124315	H94892	NM_005402	Hs.288757	v-ral simian leukemia viral oncogene hom
	124659	N93521	AI680737	Hs.289068	Homo sapiens cDNA FLJ11918 fis, clone HE
60	124669	N95477	AI571594	Hs.102943	hypothetical protein MGC12916
	124847	R60044	W07701	Hs.304177	Homo sapiens clone FLB8503 PRO2286 mRNA,
	124875	R70506	AI887664	Hs.285814	sprouty (Drosophila) homolog 4
	125091	T91518	T91518		gb:ye20f05.s1 Stratagene lung (937210) H
	125103	T95333	AA570056	Hs.122730	ESTs, Moderately similar to KIAA1215 pro
65	125355	R45630	R60547	Hs.170098	KIAA0372 gene product
	125565	R20839	R20840		gb:yg05c08.r1 Soares infant brain 1N1B H
	125590	R23858	R23858	Hs.143375	Homo sapiens, clone IMAGE:3840937, mRNA,
	423765	R23858	R23858	Hs.143375	Homo sapiens, clone IMAGE:3840937, mRNA,
	126511	AI024874	T92143	Hs.57958	EGF-TM7-latrophilin-related protein
70	100286	W26247	BE247550	Hs.86859	growth factor receptor-bound protein 7
	126563	W26247	AA516391	Hs.181368	U5 snRNP-specific protein (220 kD), orth
	126649	AA856990	AA001860	Hs.279531	ESTs
	449602	AA856990	AA001860	Hs.279531	ESTs
	126872	AA136653	AW450979		gb:UI-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su
75	456000	AA136653	BE180876	Hs.11614	HSPC065 protein
	414221	AA136653	AW450979		gb:UI-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su
	127402	AA358869	AA358869	Hs.227949	SEC13 (S. cerevisiae)-like 1

	127651	AI123976	AA382523	Hs.105689	MSTP031 protein
	424806	AI123976	AA382523	Hs.105689	MSTP031 protein
	128062	AA379500	AA379621	Hs.105547	neural proliferation, differentiation an
	128992	R49693	H04150	Hs.107708	ESTs
5	129046	AA195678	AB029290	Hs.108258	actin binding protein; macrophin (microf
	129188	M30257	NM_001078	Hs.109225	vascular cell adhesion molecule 1
	129314	AA028131	BE622768	Hs.290356	mesoderm development candidate 1
	129371	M10321	X06828	Hs.110802	von Willebrand factor
10	129468	J03040	AW410538	Hs.111779	secreted protein, acidic, cysteine-rich
	129765	M86933	M86933	Hs.1238	amelogenin (Y chromosome)
	129805	AA012933	AA012848	Hs.12570	tubulin-specific chaperone d
	129884	AA286710	AF055581	Hs.13131	lysosomal
	130495	AA243278	AW250380	Hs.109059	mitochondrial ribosomal protein L12
15	130639	D59711	AI557212	Hs.17132	ESTs, Moderately similar to I54374 gene
	130657	T94452	AW337575	Hs.201591	ESTs
	130828	AA053400	AW631469	Hs.203213	ESTs
	130972	AA370302	D81866	Hs.21739	Homo sapiens mRNA; cDNA DKFZp58611518 (f
	131080	J05008	NM_001955	Hs.2271	endothelin 1
	131137	U85193	W27392	Hs.33287	nuclear factor I/B
20	131182	AA256153	AI824144	Hs.23912	ESTs
	131486	X83107	F06972	Hs.27372	BMX non-receptor tyrosine kinase
	131573	AA046593	AA040311	Hs.28959	ESTs
	131647	AA410480	AA359615	Hs.30089	ESTs
	131756	D45304	AA443966	Hs.31595	ESTs
25	131859	M90657	AW960564		transmembrane 4 superfamily member 1
	131881	AA010163	AW361018	Hs.3383	upstream regulatory element binding prot
	132050	AA136353	AI267615	Hs.38022	ESTs
	132083	Y07867	BE386490	Hs.279663	Pirin
30	132164	U84573	AI752235	Hs.41270	procollagen-lysine, 2-oxoglutarate 5-dio
	132358	X60486	NM_003542	Hs.46423	H4 histone family, member G
	132413	AA132969	AW361383	Hs.260116	metalloprotease 1 (pitrilysin family)
	132456	AA114250	AB011084	Hs.48924	KIAA0512 gene product; ALEX2
	132490	F13782	NM_001290	Hs.4980	LIM domain binding 2
35	132676	AA283035	N92589	Hs.261038	ESTs, Weakly similar to I38022 hypotheti
	132687	AB002301	AB002301	Hs.54985	KIAA0303 protein
	132718	AA056731	NM_004600	Hs.554	Sjogren syndrome antigen A2 (60kD, ribon
	132736	U68019	AW081883	Hs.211578	Homo sapiens cDNA: FLJ23037 fis, clone L
	132760	H99198	AA125985	Hs.56145	thymosin, beta, identified in neuroblast
40	132933	AA598702	BE263252	Hs.6101	hypothetical protein MGC3178
	132968	N77151	AF234532	Hs.61638	myosin X
	132994	AA505133	AA112748	Hs.279905	clone HQ0310 PRO0310p1
	133061	AB000584	AI186431	Hs.296638	prostate differentiation factor
	133147	D12763	AA026533	Hs.66	interleukin 1 receptor-like 1
45	133161	AA253193	AW021103	Hs.6631	hypothetical protein FLJ20373
	133200	AA432248	AB037715	Hs.183639	hypothetical protein FLJ10210
	133260	AA083572	AA403045	Hs.6906	Homo sapiens cDNA: FLJ23197 fis, clone R
	133363	AA479713	AI866286	Hs.71962	ESTs, Weakly similar to B36298 proline-r
	133491	L40395	BE619053	Hs.170001	eukaryotic translation initiation factor
50	133517	X52947	NM_000165	Hs.74471	gap junction protein, alpha 1, 43kD (con
	133550	W80846	AI129903	Hs.74669	vesicle-associated membrane protein 5 (m
	133607	M34539	BE273749		FK506-binding protein 1A (12kD)
	133614	D67029	NM_003003	Hs.75232	SEC14 (S. cerevisiae)-like 1
	133627	U09587	NM_002047	Hs.75280	glycyl-tRNA synthetase
55	133691	M85289	M85289	Hs.211573	heparan sulfate proteoglycan 2 (perlecan
	133696	D10522	AI878921	Hs.75607	myristoylated alanine-rich protein kinas
	133913	W84712	AU076964	Hs.7753	calumenin
	133975	D29992	C18356	Hs.295944	tissue factor pathway inhibitor 2
	133985	L34657	L34657	Hs.78146	platelet/endothelial cell adhesion molec
60	134039	S78569	NM_002290	Hs.78672	laminin, alpha 4
	134088	D43636	AI379954	Hs.79025	KIAA0096 protein
	134161	U97188	AA634543	Hs.79440	IGF-II mRNA-binding protein 3
	134299	AA487558	AW580939	Hs.97199	complement component C1q receptor
	134416	M28882	X68264	Hs.211579	melanoma cell adhesion molecule
65	116470	X70683	AI272141	Hs.83484	SRY (sex determining region Y)-box 4
	134656	X14787	AI750878	Hs.87409	thrombospondin 1
	134989	AA236324	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi
	135051	C15324	AI272141	Hs.83484	SRY (sex determining region Y)-box 4
	135073	AA452000	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f
70	135349	D83174	AA114212	Hs.9930	serine (or cysteine) proteinase inhibito
	100114	D00596	X02308	Hs.82962	thymidylate synthetase
	100130	D11428	NM_000304	Hs.103724	peripheral myelin protein 22 ~
	100143	D13640	AU076465	Hs.278441	KIAA0015 gene product
	100168	D14874	H73444	Hs.394	adrenomedullin
	100208	D26129	NM_002933	Hs.78224	ribonuclease, RNase A family, 1 (pancrea
75	100224	D28476	AL121516	Hs.138617	thyroid hormone receptor interactor 12
	100405	D86425	AW291587	Hs.82733	nidogen 2

	100420	D86983	D86983	Hs.118893	Melanoma associated gene
	100455	D87953	AW888941	Hs.75789	N-myc downstream regulated
	100529	HG1862-HT1897	BE313693	Hs.334330	calmodulin 2 (phosphorylase kinase, delt
5	100618	HG2614-HT2710	AI752163	Hs.114599	collagen, type VIII, alpha 1
	100619	HG2639-HT2735	N24433	Hs.241567	RNA binding motif, single stranded inter
	100658	HG2855-HT2995	U56725	Hs.180414	heat shock 70kD protein 2
	100676	HG3044-HT3742	X02761	Hs.287820	fibronectin 1
	100718	HG3342-HT3519	BE295928	Hs.75424	inhibitor of DNA binding 1, dominant neg
10	100752	HG3543-HT3739	T81309		insulin-like growth factor 2 (somatomedi
	100828	HG4069-HT4339	AL048753	Hs.303649	small inducible cytokine A2 (monocyte ch
	100850	HG417-HT417	AA836472	Hs.297939	cathepsin B
	100991	J03764	J03836	Hs.82085	serine (or cysteine) proteinase inhibito
	101097	L06797	BE245301	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus
15	101110	L08246	AI439011	Hs.86386	myeloid cell leukemia sequence 1 (BCL2-r
	101142	L12711	L12711	Hs.89643	transketolase (Wernicke-Korsakoff syndro
	101156	L13977	AA340987	Hs.75693	prolylcarboxypeptidase (angiotensinase C
	101168	L15388	NM_005308	Hs.211569	G protein-coupled receptor kinase 5
	101184	L19871	NM_001674	Hs.460	activating transcription factor 3
	101192	L20859	BE247295	Hs.78452	solute carrier family 20 (phosphate tran
20	101317	L42176	L42176	Hs.8302	four and a half LIM domains 2
	101336	L49169	NM_006732	Hs.75678	FBJ murine osteosarcoma viral oncogene h
	101345	L76380	NM_005795	Hs.152175	calcitonin receptor-like
	101400	M15990	M15990	Hs.194148	v-yes-1 Yamaguchi sarcoma viral oncogene
25	101475	M23254	BE410405	Hs.76288	calpain 2, (m/l) large subunit
	101485	M24736	AA296520	Hs.89546	selectin E (endothelial adhesion molecu
	101496	M26576	X12784	Hs.119129	collagen, type IV, alpha 1
	101505	M27396	AA307680	Hs.75692	asparagine synthetase
	101543	M31166	M31166	Hs.2050	pentaxin-related gene, rapidly induced b
30	101557	M31994	BE293116	Hs.76392	aldehyde dehydrogenase 1 family, member
	101560	M32334	AW958272	Hs.347326	intercellular adhesion molecule 2
	101587	M35878	AI752416	Hs.77326	insulin-like growth factor binding prote
	101592	M36429	AF064853	Hs.91299	guanine nucleotide binding protein (G pr
	101633	M57730	NM_004428	Hs.1624	ephrin-A1
35	101634	M57731	AV650262	Hs.75765	GRO2 oncogene
	101667	M60858	NM_005381		nucleolin
	101682	M62994	AF043045	Hs.81008	filamin B, beta (actin-binding protein-2
	101714	M68874	M68874	Hs.211587	phospholipase A2, group IVA (cytosolic,
	101720	M69043	M69043	Hs.81328	nuclear factor of kappa light polypeptid
40	101741	M74719	NM_003199	Hs.326198	transcription factor 4
	101744	M75126	AI879352	Hs.118625	hexokinase 1
	101793	M84349	W01076	Hs.278573	CD59 antigen p18-20 (antigen identified
	101837	M92843	M92843	Hs.343586	zinc finger protein homologous to Zfp-36
	101838	M92934	BE243845	Hs.75511	connective tissue growth factor
45	101840	M93056	AA236291	Hs.183583	serine (or cysteine) proteinase inhibito
	101857	M94856	BE550723	Hs.153179	fatty acid binding protein 5 (psoriasis-
	101864	M95787	BE392588	Hs.75777	transgelin
	101931	S76965	NM_006823	Hs.75209	protein kinase (cAMP-dependent, catalyti
	101966	S81914	X96438	Hs.76095	immediate early response 3
50	102012	U03057	BE259035	Hs.118400	singed (Drosophila)-like (sea urchin fas
	102013	U03100	BE616287	Hs.178452	catenin (cadherin-associated protein), a
	102024	U03877	AA301867	Hs.76224	EGF-containing fibulin-like extracellula
	102059	U08021	AI752666	Hs.76669	nicotinamide N-methyltransferase
	102121	U14391	NM_004998	Hs.82251	myosin IE
55	102283	U31384	AW161552	Hs.83381	guanine nucleotide binding protein 11
	102300	U32944	AI929721	Hs.5120	dynein, cytoplasmic, light polypeptide
	102378	U40369	AU076887	Hs.28491	spermidine/spermine N1-acetyltransferase
	102395	U41767	AU077005	Hs.92208	a disintegrin and metalloproteinase doma
	102460	U48959	U48959	Hs.211582	myosin, light polypeptide kinase
60	102491	U51010	U51010		gb:Human nicotinamide N-methyltransferas
	102499	U51478	BE243877	Hs.76941	ATPase, Na+/K+ transporting, beta 3 poly
	102523	U53445	U53445	Hs.15432	downregulated in ovarian cancer 1
	102560	U59289	R97457	Hs.63984	cadherin 13, H-cadherin (heart)
	102564	U59423	U59423	Hs.79067	MAD (mothers against decapentaplegic, Dr
65	102589	U62015	AU076728	Hs.8867	cysteine-rich, angiogenic inducer, 61
	102600	U63825	AI984144	Hs.66713	hepatitis delta antigen-interacting prot
	102645	U67963	AL119566	Hs.6721	lysosomal
	102687	U73379	NM_007019	Hs.93002	ubiquitin carrier protein E2-C
	102693	U73824	AA532780	Hs.183684	eukaryotic translation initiation factor
70	102709	U77604	AA122237	Hs.81874	microsomal glutathione S-transferase 2
	102759	U81607	NM_005100	Hs.788	A kinase (PRKA) anchor protein (gravin)
	102804	U89942	NM_002318	Hs.83354	lysyl oxidase-like 2
	102882	X04412	AI767736	Hs.290070	gelsolin (amyloidosis, Finnish type)
	102907	X06985	BE409861	Hs.202833	heme oxygenase (decycling) 1
	102915	X07820	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin
75	102927	X12876	BE512730	Hs.65114	keratin 18
	102960	X15729	AI904738	Hs.76053	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep

	103011	X52541	AJ243425	Hs.326035	early growth response 1
	103020	X53416	X53416	Hs.195464	filamin A, alpha (actin-binding protein-
	103029	X54489	AW800726	Hs.789	GRO1 oncogene (melanoma growth stimulat
5	103036	X54925	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial
	103056	X57206	Y18024	Hs.78877	inositol 1,4,5-trisphosphate 3-kinase B
	103080	X59798	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomatos
	103095	X60957	NM_005424	Hs.78824	tyrosine kinase with immunoglobulin and
	103138	X65965	X65965		gb:H.sapiens SOD-2 gene for manganese su
10	103176	X69111	AL021154	Hs.76884	inhibitor of DNA binding 3, dominant neg
	103195	X70940	AA351647	Hs.2642	eukaryotic translation elongation factor
	103347	X87838	AU077309	Hs.171271	catenin (cadherin-associated protein), b
	103371	X91247	X91247	Hs.13046	thioredoxin reductase 1
	103432	X97748	X97748		gb:H.sapiens PTX3 gene promotor region.
	103471	Y00815	Y00815	Hs.75216	protein tyrosine phosphatase, receptor t
15	103967	AA303711	AL120051	Hs.144700	ephrin-B1
	104447	L44538	AW204145	Hs.156044	ESTs
	104764	AA025351	AI039243	Hs.278585	ESTs
	104783	AA027050	AA533513	Hs.93659	protein disulfide isomerase related prot
20	104798	AA029462	AW952619	Hs.17235	Homo sapiens clone TCCCA00176 mRNA sequ
	104865	AA045136	T79340	Hs.22575	B-cell CLL/lymphoma 6, member B (zinc fi
	104877	AA047437	AI138635	Hs.22968	Homo sapiens clone IMAGE:451939, mRNA se
	104894	AA054087	AF065214	Hs.18858	phospholipase A2, group IVC (cytosolic,
	104952	AA071089	AW076098	Hs.345588	desmoplakin (DPI, DPII)
25	105113	AA156450	AB037816	Hs.8982	Homo sapiens, clone IMAGE:3506202, mRNA,
	105178	AA187490	AA313825	Hs.21941	AD036 protein
	105196	AA195031	W84893	Hs.9305	angiotensin receptor-like 1
	105215	AA205724	AA205759	Hs.10119	hypothetical protein FLJ14957
	105263	AA227926	AW388633	Hs.6682	solute carrier family 7, (cationic amino
30	105271	AA227986	AA807881	Hs.25329	ESTs
	105330	AA234743	AW338625	Hs.22120	ESTs
	105461	AA253216	BE539071	Hs.69388	hypothetical protein FLJ20505
	105492	AA256210	AI805717	Hs.289112	CGI-43 protein
	105493	AA256268	AL047586	Hs.10283	RNA binding motif protein 8B
35	105594	AA279397	AB024334	Hs.25001	tyrosine 3-monooxygenase/tryptophan 5-mo
	105727	AA292379	AL135159	Hs.20340	KIAA1002 protein
	105732	AA292717	AW504170	Hs.274344	hypothetical protein MGC12942
	105767	AA346551	AW370946	Hs.23457	ESTs
	105882	AA400292	W46802	Hs.81988	disabled (Drosophila) homolog 2 (mitogen
40	105936	AA404338	AI678765	Hs.21812	ESTs
	106031	AA412284	X64116	Hs.171844	Homo sapiens cDNA: FLJ22296 fis, clone H
	106124	AA423987	H93366	Hs.7567	Homo sapiens cDNA: FLJ21962 fis, clone H
	106222	AA428594	AA356392	Hs.21321	Homo sapiens clone FLB9213 PRO2474 mRNA,
	106241	AA430108	BE019681	Hs.6019	Homo sapiens cDNA: FLJ21288 fis, clone C
45	106263	AA431462	W21493	Hs.28329	hypothetical protein FLJ14005
	106264	AA431470	AL046859	Hs.3407	protein kinase (cAMP-dependent, catalyti
	106366	AA443756	AA186715	Hs.336429	RIKEN cDNA 9130422N19 gene
	106454	AA449479	NM_014038	Hs.5216	HSPC028 protein
	106634	AA459916	W25491	Hs.288909	hypothetical protein FLJ22471
50	106724	AA465226	N48670	Hs.28631	Homo sapiens cDNA: FLJ22141 fis, clone H
	106793	AA478778	H94997	Hs.16450	ESTs
	106799	AA479037	BE313412	Hs.7961	Homo sapiens clone 25012 mRNA sequence
	106842	AA482597	AF124251	Hs.26054	novel SH2-containing protein 3
	106868	AA487561	BE185536	Hs.301183	molecule possessing ankryrin repeats indu
55	106890	AA489245	AA489245	Hs.88500	mitogen-activated protein kinase 8 inter
	106961	AA504110	AW243614	Hs.18063	Homo sapiens cDNA FLJ10768 fis, clone NT
	106974	AA520989	AI817130	Hs.9195	Homo sapiens cDNA FLJ13698 fis, clone PL
	107030	AA599434	AL117424	Hs.25035	chloride intracellular channel 4
	107061	AA608649	BE147611	Hs.6354	stromal cell derived factor receptor 1
60	107086	AA609519	NM_012331	Hs.26458	methionine sulfoxide reductase A
	107216	D51069	D51069	Hs.211579	melanoma cell adhesion molecule
	107385	U97519	NM_005397	Hs.16426	podocalyxin-like
	107444	W28391	W28391	Hs.343258	proliferation-associated 2G4, 38kD
	107985	AA035638	T40064	Hs.71968	Homo sapiens mRNA; cDNA DKFZp564F053 (fr
65	108507	AA083514	AI554545	Hs.68301	ESTs
	108695	AA121315	AB029000	Hs.70823	KIAA1077 protein
	108931	AA147186	AA147186		gb:zo38d01.s1 Stratagene endothelial cel
	109001	AA156125	AI056548	Hs.72116	hypothetical protein FLJ20992 similar to
	109195	AA188932	AF047033	Hs.132904	solute carrier family 4, sodium bicarbon
70	109390	AA219653	AW007485	Hs.87125	EH-domain containing 3
	109456	AA232645	AW956580	Hs.42699	ESTs
	109737	F10078	AA055415	Hs.13233	ESTs, Moderately similar to A47582 B-cel
	110411	H48032	AW001579	Hs.9645	Homo sapiens mRNA for KIAA1741 protein,
	110660	H82117	AA782114	Hs.28043	ESTs
	110906	N39584	AA035211	Hs.17404	ESTs
75	111018	N54067	AI287912	Hs.3628	mitogen-activated protein kinase kinase
	111091	N59858	AA300067	Hs.33032	hypothetical protein DKFZp434N185

	111356	N90933	BE301871	Hs.4867	mannosyl (alpha-1,3-)-glycoprotein beta-
	111378	N93764	AW160993	Hs.326292	hypothetical gene DKFZp434A1114
	111741	R26124	AB020653	Hs.24024	KIAA0846 protein
5	111769	R27957	AW629414	Hs.24230	ESTs
	112318	R55470	AW083384	Hs.11067	ESTs, Highly similar to T46395 hypotheti
	112951	T16550	AA307634	Hs.6650	vacuolar protein sorting 45B (yeast homo
	113057	T26674	AW194301	Hs.339283	Human DNA sequence from clone RP1-187J11
	113195	T57112	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom
10	113490	T88700	BE178110	Hs.173374	Homo sapiens cDNA FLJ10500 fis, clone NT
	113542	T90527	H43374	Hs.7890	Homo sapiens mRNA for KIAA1671 protein,
	113803	W42789	AW880709	Hs.283683	chromosome 8 open reading frame 4
	113847	W60002	NM_005032	Hs.4114	plastin 3 (T isoform)
	113910	W78175	AA113262	Hs.17901	Homo sapiens, clone IMAGE:3937015, mRNA,
15	113947	W84768	W84768		gb:zh53d03.s1 Soares_fetal_liver_spleen_
	114047	W94427	AL035858	Hs.3807	FXD domain-containing ion transport reg
	115061	AA253217	AI751438	Hs.41271	Homo sapiens mRNA full length insert cDN
	115819	AA426573	AA486620	Hs.41135	endomucin-2
	115870	AA432374	NM_005985	Hs.48029	snail 1 (drosophila homolog), zinc finger
20	115964	AA446622	AA987568	Hs.74313	KIAA1265 protein
	116228	AA478771	AI767947	Hs.50841	ESTs
	116264	AA482594	D51174	Hs.272239	lysosomal
	116314	AA490588	AI799104	Hs.178705	Homo sapiens cDNA FLJ11333 fis, clone PL
	116589	D59570	AI557212	Hs.17132	ESTs, Moderately similar to I54374 gene
25	117023	H88157	AW070211	Hs.102415	Homo sapiens mRNA; cDNA DKFZp586N0121 (f
	117112	H94648	AW969999	Hs.293658	ESTs
	117156	H97538	W73853		ESTs
	117176	H98670	H45100	Hs.49753	uveal autoantigen with coiled coil domai
	117280	N22107	M18217	Hs.172129	Homo sapiens cDNA: FLJ21409 fis, clone C
30	119559	W38197	W38197		Empirically selected from AFFX single pr
	119866	W80814	AA496205	Hs.193700	Homo sapiens mRNA; cDNA DKFZp586I0324 (f
	120655	AA287347	AA305599	Hs.238205	hypothetical protein PRO2013
	121314	AA402799	W07343	Hs.182538	phospholipid scramblase 4
	121335	AA404418	AA404418		gb:zw37e02.s1 Soares_total_fetus_Nb2HF8_
	121822	AA425107	AI743860		metallothionein 1E (functional)
35	121835	AA425435	AB033030	Hs.300670	KIAA1204 protein
	122331	AA442872	AL133437	Hs.110771	Homo sapiens cDNA: FLJ21904 fis, clone H
	122577	AA452860	AA829725	Hs.334437	hypothetical protein MGC4248
	123160	AA488687	AA488687	Hs.284235	ESTs, Weakly similar to I38022 hypotheti
40	123486	AA599674	BE019072	Hs.334802	Homo sapiens cDNA FLJ14680 fis, clone NT
	124059	F13673	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti
	124339	H99093	H99093	Hs.343411	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep
	124358	N22495	AW070211	Hs.102415	Homo sapiens mRNA; cDNA DKFZp586N0121 (f
	124364	N23031	AF265555	Hs.250646	baculoviral IAP repeat-containing 6
45	124726	R15740	NM_003654	Hs.104576	carbohydrate (keratan sulfate Gal-6) sul
	124763	R39610	BE410405	Hs.76288	calpain 2, (mII) large subunit
	125167	W45560	AL137540	Hs.102541	netrin 4
	125304	Z39833	AL359573	Hs.124940	GTP-binding protein
	125307	Z40583	AW580945	Hs.330466	ESTs
50	125329	AA825437	AA825437	Hs.58875	ESTs
	107985	R66613	T40064	Hs.71968	Homo sapiens mRNA; cDNA DKFZp564F053 (fr
	125598	R66613	T40064	Hs.71968	Homo sapiens mRNA; cDNA DKFZp564F053 (fr
	125609	AA868063	AA868063	Hs.104576	carbohydrate (keratan sulfate Gal-6) sul
	116024	AA128075	AA088767	Hs.83883	transmembrane, prostate androgen induced
55	418000	AA128075	AA932794	Hs.83147	guanine nucleotide binding protein-like
	126399	AA128075	AA088767	Hs.83883	transmembrane, prostate androgen induced
	127435	N66570	X69086	Hs.286161	Homo sapiens cDNA FLJ13613 fis, clone PL
	127566	AI051390	AI051390	Hs.116731	ESTs
	127619	AA627122	AA627122	Hs.163787	ESTs
	434190	AA627122	AA627122	Hs.163787	ESTs
60	128453	X02761	X02761	Hs.287820	fibronectin 1
	128495	AF010193	NM_005904	Hs.100602	MAD (mothers against decapentaplegic, Dr
	128515	AA149044	BE395085	Hs.10086	type I transmembrane protein Fn14
	128580	U82108	U82108	Hs.101813	solute carrier family 9 (sodium/hydrogen
65	128623	D78676	BE076608	Hs.105509	CTL2 gene
	128642	L35240	Z28913	Hs.102948	enigma (LIM domain protein)
	128669	AA598737	W28493	Hs.180414	heat shock 70kD protein 8
	128903	R69417	AW150717	Hs.345728	STAT induced STAT inhibitor 3
	128914	AA232837	AW867491	Hs.107125	plasmalemma vesicle associated protein
70	129087	N72695	AI348027	Hs.108557	hypothetical protein PP1057
	129188	M30257	NM_001078	Hs.109225	vascular cell adhesion molecule 1
	129226	M96843	BE222494	Hs.180919	inhibitor of DNA binding 2, dominant neg
	129265	X68277	AA530892	Hs.171695	dual specificity phosphatase 1
	129345	AA292440	R22497	Hs.110571	growth arrest and DNA-damage-inducible,
75	129468	J03040	AW410538	Hs.111779	secreted protein, acidic, cysteine-rich
	129488	AA228107	AW966728	Hs.54642	methionine adenosyltransferase II, beta
	101838	AA449789	BE243845	Hs.75511	connective tissue growth factor

	413731	AA449789	BE243845	Hs.75511	connective tissue growth factor
	129557	W01367	AL045404	Hs.46366	KIAA0948 protein
	129619	AA610116	AA209534	Hs.284243	tetraspan NET-6 protein
	129627	AA258308	T40064	Hs.71968	Homo sapiens mRNA; cDNA DKFZp564F053 (fr
5	129762	AA460273	AA453694	Hs.12372	tripartite motif protein TRIM2
	129884	AA286710	AF055581	Hs.13131	lysosomal
	130018	T68873	AA353093		metallothionein 1L
	130147	D63476	D63476	Hs.172813	PAK-interacting exchange factor beta
10	130178	M62403	U20982	Hs.1516	insulin-like growth factor-binding prote
	130282	X55740	BE245380	Hs.153952	5' nucleotidase (CD73)
	130431	L10284	AW505214	Hs.155560	calnexin
	130495	AA243278	AW250380	Hs.109059	mitochondrial ribosomal protein L12
	130553	AA430032	AF062649	Hs.252587	pituitary tumor-transforming 1
15	130638	H16402	AW021276	Hs.17121	ESTs
	130639	D59711	AI557212	Hs.17132	ESTs, Moderately similar to I54374 gene
	130657	T94452	AW337575	Hs.201591	ESTs
	130686	AA431571	BE548267	Hs.337986	Homo sapiens cDNA FLJ10934 fis, clone OV
	130776	R79356	AF167706	Hs.19280	cysteine-rich motor neuron 1
20	130818	AA280375	AW190920	Hs.19928	hypothetical protein SP329
	130840	Z49269	BE048821	Hs.20144	small inducible cytokine subfamily A (Cy
	130899	Z41740	AI077288	Hs.296323	serum/glucocorticoid regulated kinase
	131002	AA121543	AL050295	Hs.22039	KIAA0758 protein
	131080	J05008	NM_001955	Hs.2271	endothelin 1
25	131084	AA101878	NM_017413	Hs.303084	apelin; peptide ligand for APJ receptor
	131091	T35341	AJ271216	Hs.22880	dipeptidylpeptidase III
	131107	N87590	BE620886	Hs.75354	GCN1 (general control of amino-acid synt
	131182	AA256153	AI824144	Hs.23912	ESTs
	131207	W74533	AF104266	Hs.24212	latrophilin
30	131319	U25997	NM_003155	Hs.25590	stanniocalcin 1
	131328	V01512	AW939251	Hs.25647	v-fos FBJ murine osteosarcoma viral onco
	131509	X56681	X56681	Hs.2780	jun D proto-oncogene
	131555	AA161292	T47364	Hs.278613	interferon, alpha-inducible protein 27
	131564	AA491465	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL
35	131573	AA046593	AA040311	Hs.28959	ESTs
	131692	D50914	BE559681	Hs.30736	KIAA0124 protein
	131756	D45304	AA443966	Hs.31595	ESTs
	131859	M90657	AW960564		transmembrane 4 superfamily member 1
	131909	W69127	NM_016558	Hs.274411	SCAN domain-containing 1
40	131915	AA316186	AI161383	Hs.34549	ESTs, Highly similar to S94541 1 clone 4
	132046	AA384503	AI359214	Hs.179260	chromosome 14 open reading frame 4
	132050	AA136353	AI267615	Hs.38022	ESTs
	132151	AA044755	BE379499	Hs.173705	Homo sapiens cDNA: FLJ22050 fis, clone H
	132164	U84573	AI752235	Hs.41270	procollagen-lysine, 2-oxoglutarate 5-dio
45	132187	AA058911	AA235709	Hs.4193	DKFZP586O1624 protein
	132303	AA620962	BE177330	Hs.325093	Homo sapiens cDNA: FLJ21210 fis, clone C
	132314	AA285290	AF112222	Hs.323806	pinin, desmosome associated protein
	132358	X60486	NM_003542	Hs.46423	H4 histone family, member G
	132398	R31641	AA876616	Hs.16979	ESTs, Weakly similar to A43932 mucin 2 p
50	132421	AA489190	AW163483	Hs.48320	double ring-finger protein, Dorfin
	132490	F13782	NM_001290	Hs.4980	LIM domain binding 2
	132520	AA257993	AA257992	Hs.50651	Janus kinase 1 (a protein tyrosine kinas
	132546	M24283	M24283	Hs.168383	intercellular adhesion molecule 1 (CD54)
	132610	AA443114	AA160511	Hs.5326	amino acid system N transporter 2; porcu
55	132716	T35289	BE379595	Hs.283738	casein kinase 1, alpha 1
	132840	N23817	BE218319	Hs.5807	GTPase Rab14
	132883	AA047151	AA373314	Hs.5897	Homo sapiens mRNA; cDNA DKFZp586P1622 (f
	132968	N77151	AF234532	Hs.61638	myosin X
	132989	AA480074	AA480074	Hs.331328	hypothetical protein FLJ13213
60	132999	Y00787	Y00787	Hs.624	interleukin 8
	133071	T99789	BE384932	Hs.64313	ESTs, Weakly similar to AF257182 1 G-pro
	133076	W84341	AW946276	Hs.6441	Homo sapiens mRNA; cDNA DKFZp586J021 (fr
	133099	L09209	W16518	Hs.279518	amyloid beta (A4) precursor-like protein
	133147	D12763	AA026533	Hs.66	Interleukin 1 receptor-like 1
65	133149	T16484	AA370045	Hs.6607	AXIN1 up-regulated
	133161	AA253193	AW021103	Hs.6631	hypothetical protein FLJ20373
	133200	AA432248	AB037715	Hs.183639	hypothetical protein FLJ10210
	133220	X82200	NM_006074	Hs.318501	Homo sapiens mRNA full length insert cDN
	133260	AA083572	AA403045	Hs.6906	Homo sapiens cDNA: FLJ23197 fis, clone R
70	133295	L00352	AI147861	Hs.213289	low density lipoprotein receptor (famili
	133349	N75791	AW631255	Hs.8110	L-3-hydroxyacyl-Coenzyme A dehydrogenase
	133391	X57579	AW103364	Hs.727	inhibin, beta A (activin A, activin AB a
	133398	X02612	NM_000499	Hs.72912	cytochrome P450, subfamily I (aromatic c
	133436	H44631	BE294068	Hs.737	immediate early protein
	133454	AA090257	BE547647	Hs.177781	hypothetical protein MGC5618
75	133478	X83703	X83703	Hs.31432	cardiac ankyrin repeat protein
	133491	L40395	BE619053	Hs.170001	eukaryotic translation initiation factor

	133510	AA227913	AW880841	Hs.96908	p53-induced protein
	133517	X52947	NM_000165	Hs.74471	gap junction protein, alpha 1, 43kD (con
	133526	M11313	AU077051	Hs.74561	alpha-2-macroglobulin
5	133538	L14837	NM_003257	Hs.74614	tight junction protein 1 (zona occludens
	133562	M60721	M60721	Hs.74870	H2.0 (Drosophila)-like homeo box 1
	133584	D90209	D90209	Hs.181243	activating transcription factor 4 (tax-r
	133590	T67986	T70956	Hs.75106	clusterin (complement lysis inhibitor, S
	133617	AA148318	BE244334	Hs.75249	ADP-ribosylation factor-like 6 interacti
10	133651	U97105	AI301740	Hs.173381	dihydropyrimidinase-like 2
	133671	T25747	AW503116	Hs.301819	zinc finger protein 146
	133678	K02574	AW247252		nucleoside phosphorylase
	133681	D78577	AI352558		tyrosine 3-monooxygenase/tryptophan 5-mo
	133722	X53331	AW969976	Hs.279009	matrix Gla protein
15	133730	S73591	BE242779	Hs.179526	upregulated by 1,25-dihydroxyvitamin D-3
	133750	X95735	BE410769	Hs.75873	zyxin
	133802	L16862	AW239400	Hs.76297	G protein-coupled receptor kinase 6
	133825	U44975	BE616902	Hs.285313	core promoter element binding protein
	133838	M97796	BE222494	Hs.180919	inhibitor of DNA binding 2, dominant neg
20	133859	U86782	U86782	Hs.178761	26S proteasome-associated pad1 homolog
	133889	AA099391	U48959	Hs.211582	myosin, light polypeptide kinase
	133960	M19267	M19267	Hs.77899	tropomyosin 1 (alpha)
	133975	D29992	C18356	Hs.295944	tissue factor pathway inhibitor 2
	133977	L19314	AI125639	Hs.250666	hairy (Drosophila)-homolog
25	134039	S78569	NM_002290	Hs.78672	laminin, alpha 4
	134075	U28811	NM_012201	Hs.78979	Golgi apparatus protein 1
	134081	L77886	AL034349	Hs.79005	protein tyrosine phosphatase, receptor t
	134164	C14407	AW245540	Hs.79516	brain abundant, membrane attached signal
	134203	M60278	AA161219	Hs.799	diphtheria toxin receptor (heparin-bindi
30	134238	R81509	AA102179	Hs.160726	Homo sapiens cDNA FLJ11680 fis, clone HE
	134299	AA487558	AW580939	Hs.97199	complement component C1q receptor
	134332	D86962	D86962	Hs.81875	growth factor receptor-bound protein 10
	134339	AA478971	R70429	Hs.81988	disabled (Drosophila) homolog 2 (mitogen
	134343	D50683	D50683	Hs.82028	transforming growth factor, beta recepto
35	134381	U56637	AI557280	Hs.184270	capping protein (actin filament) muscle
	134403	M61199	AA334551		sperm specific antigen 2
	134416	M28882	X68264	Hs.211579	melanoma cell adhesion molecule
	134493	X15183	M30627	Hs.289088	heat shock 90kD protein 1, alpha
	134558	S53911	NM_001773	Hs.85289	CD34 antigen
40	134817	U20734	AU076592	Hs.198951	jun B proto-oncogene
	134983	D28235	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p
	134989	AA236324	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi
	135052	AA148923	AL136653	Hs.93675	decidual protein induced by progesterone
	135062	AA174183	AK000967	Hs.93872	KIAA1682 protein
45	135069	AA456311	AA876372	Hs.93961	Homo sapiens mRNA; cDNA DKFZp667D095 (fr
	135071	L08069	W27190	Hs.94	DnaJ (Hsp40) homolog, subfamily A, membe
	135073	AA452000	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f
	135170	AA282140	T53169	Hs.9587	Homo sapiens cDNA: FLJ22290 fis, clone H
	135196	J02854	C03577	Hs.9615	myosin regulatory light chain 2, smooth
	135348	AA442054	U80983	Hs.268177	phospholipase C, gamma 1 (formerly subty

TABLE 4A

Table 4A shows the accession numbers for those pkeys lacking unigenelD's for Table 4. The pkeys in Table 7 lacking unigenelD's are represented within Tables 1-6A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

10	Pkey: CAT number: Accession:	Unique Eos probeset identifier number Gene cluster number Genbank accession numbers	
15	Pkey	CAT Number	Accession
20	100752	33207_21	T81309 BE019033 R94181 BE019198 NM_000612 J03242 AW411299 BE300064 BE297544 R94182 AW630108 T53723 D58853 H78073 H80594 BE299560 T48899 H70196 M17426 N77077 S77035 H58384 H61664 H78540 T84527 C17198 H60255 H71980 R92644 W79050 X00910 M29645 R91055 M17863 M17862 T71815 BE299561 BE464561 X06260 R94741 T54216 C18594 BE262015 X06161 AW409889 AA378400 BE263228 BE313278 R88116 BE313457 H43500 T48617 BE313761 H77309 AI207601 X06159 H40413 X03425 T87663 R10627 X03562 M14118 W03982 R97520 H81229 T83157 H83168 H48762 AA669898 BE263054 H47289 AA022807 R11555 H74260 R76968 R28338 H72534 H72464 H62031 N72478 H45355 AW411300 R89113 R69135 H58454 T83281 R93476 H69645 H68015 T82229 H71089 T85121 H59939 W65299 N78176 H53909 N72373 R21788 H04660 H59639 H61874 BE262219 T53614 N73335 N50464 W00943 N77189 R89257 AA570502 R89432 R06366 AA553480 AA776271 AA551359 AA551050 H51670 AA601052 BE299081 H68198 H52276 BE207832 N91192 H70332 X07868 X07868 H69464 H53782 H73710 R80435 AA553384 AW884176 N53475 T71662 AW954036 AW954033 AA552931 H93206 AA430218 AA553476 AI918470 T54124 BE207982 BE300177 N73994 AW882625 N39549 N53838 AA722389 H71878 H58909 H37849 H78435 T47933 R77174 R83814 AA411890 H94199 AA663208 BE205778 AA490137 H70492 R98232 H37800 AA679294 H40341 H74238 H47290 H73231 T48618 AA025428 AI039521 H92969 N59389 H80538 H72933 T90630 AA411891 N55000 H74225 AA340290 AW957061 T54316 AA340437 H57125 H58908 H79027 H63450 N74623 R93425 H68714 H68758 N68396 H48763 N69256 H57320 H53831 H53589 N68833 N52453 H56048 H69870 H78074 R69253 R83375 T53615 H94330 H58455 H90864 T47934 H74261 R89258 R97997 R91056 R28339 R86760 H78235 R97521 H67692 H40358 AA022688 H52513 H59601 T88690 H65256 H63397 W65397 AA553588 R19280 N52645 W73930 R06367 R21743 H72372 N73921 AW883539 AW882639 T40616 H47084 R95723 AA634316 AA862781 H77310 R91389 H93111 R92767 T54512 R89341 H70333 H57817 H82941 H62032 N52638 H58385 T91796 H51086 AA340292 T49918 H81230 R36121 N50411 T87664 N62436 N39340 AA665637 AA340446 H93377 H92973 BE296290 BE269788 H61665 AA340444 N54605 AA454101 R10628 R94200 AI200549 AA342640 BE298855 BE250229 T49916 H82008 N28278 AW880662 H71268 N76791 H47685 H65255 W05198 AW889144 N76677 H71702 H68036 H71915 R91612 R87807 H68059 AI133328 AI247866 AA621443 AW881050 AA700847 AA340413 AW878608 AW881181 AW878249 H71916 N54596 BE161581 AW878082 W04212 AW881040 AW885492 AW880519 AA334887 AW878715 W06882 AW630222 AW885381 H70869 AW381778 H47601 AW889982 H63868 AW884986 AW878713 AW878685 R36391 AW878694 AA368070 C03393 AW878695 AW878705 AW878665 AW878742 AW878620 AW878823 AW878688 R29048 AW878690 AW878686 AW878810 AW878827 AW878733 AW878659 AW878749 AW878681 AW883353 AW883277 AW883300 AW883565 AW883298 AW883143 AW883045 AW883482 AW883352 AW883417 AW883357 AW883231 AW883474 AW883355 AW882620 AW882533 AW883754 AW883139 AW882827 AW883641 AW883567 AW883481 AW882983 AW882982 AW882465 AW883419 AW882466 AW883639 AW883230 AW882981 AW882534 AW882874 AW882619 AW883480 AW882826 AW882831 AW882835 AW882830 AW883563 AW882456 AW627642
25			W73853 AA928112 W77887 AW889237 AA148524 AI749182 AI754442 AI338392 AI253102 AI079403 AI370541 AI697341 H97538 AW188021 AI927669 W72716 AI051402 AI188071 AI335900 N21488 AW770478 W92522 AI691028 AI913512 AI144448 W73819 AA604358 N28900 W95221 AI868132 H98465 AA148793
30			AW960564 AA092457 T55890 D56120 T92525 AI815987 BE182608 BE182595 AW080238 M90657 AA347236 AW961686 AW176446 AA304671 AW583735 T61714 AA316968 AI446615 AA343532 AA083489 AA488005 W52095 W39480 N57402 D82638 W25540 W52847 D82729 D58990 BE619182 AA315188 AA308636 AA112474 W76162 AA088544 H52265 AA301631 H80982 AA113786 BE620997 AW651691 AA343799 BE613669 BE547180 BE546656 F11933 AA376800 AW239185 AA376086 BE544387 BE619041 AA452515 AA001806 AA190873 AA180483 AA159546 F00242 AI940609 AI940602 AI189753 T97663 T66110 AW062896 AW062910 AW062902 AI051622 AI828930 AA102452 AI685095 AI819390 AA557597 AA383220 AI804422 AI633575 AW338147 AW603423 AW606800 AW750567 AW510672 AI250777 AA083510 AW629109 AW513200 AA921353 AI677934 AI148698 AI955858 AA173825 AA453027 AI027865 AW375542 AA454099 AA733014 AI591384 R79300 R80023 AA843108 AA626058 AA844898 AW375550 AA889018 AI474275 AW205937 AI052270 AW388117 AW388111 AA699452 AI242230 N47476 H38178 AA366621 AA113196 AA130023 H39740 T61629 AI885973 AW083671 AA179730 AA305757 AI285455 N83956 AA216013 AA336155 AW999959 T97525 AA345349 T91762 AA771981 AI285092 AI591386 BE392486 BE385852 AA682601 AI682884 AA345840 T85477 AA292949 AA932079 AA098791 D82607 T48574 AW752038 C06300
35			R20840 R20839
40			BE273749 BE397561 BE387189 AL037858 AL037878 AI963094 BE259216 AA011363 AL036189 BE562325 AA251169 BE617431 N98537 AA158093 AL047800 M34539 NM_000801 AA312140 D16971 AA158904 AA307114 AA312803 T09203 AW629686 AL048504 BE388578 AA220957 AA158364 BE267385 AA294971 C18055 BE241757 AA115056 AI936769 BE378435 BE206971 AW674924 BE622060 AA604674 AA115273 AW402159 AA338608 BE568819 M80199 X55741 AA375111 AA376016 BE612671 AA805742 AW405588 N25850 N44580 H06031 AW403549 BE536552 AA056726 BE543239 AA082517 AI201645 AI201642 AI192622 N40104 AA370921 BE547569 AI969602 AA302038 AI197890 AW268354 AI014938 W45448 AI541395 AA037272 BE538826 AL039613 BE536130 AA299355 AW805147 AW974624 H53220 AI471471 AA399303 AA007386 W35106 BE613277 R12739 R12738 AA304342 AA687802 BE409581 AI498844 AV662092 AW904105 AA011375 BE315214 H99302 BE537893 N32299 AW855829 AI291320 BE078322 AI301395 AA303362 N32719 AA358328 AA357877 AI952540 H56279 H02758 H02048 AW805233 R82224 AA10772 AA291352
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75			

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 AI583349 AW183058 AI308085 AI074952 AA437315 AA628161 AW301728 AI150224 AA400137 AA437279 AI223355
 AA639462 AI261373 AI432414 AI984994 AI539335 AA401550 AA358757 AI609976 AA442357 AA359393 AA437046
 AA370301 AA429328 AW272055 AI580502 AI832944 AI038530 AA425107 AI014986 AI148349 AW237721 AW779756
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	125091	genbank_T91518	T91518
	123964	genbank_C13961	C13961
	102491	entrez_U51010	U51010
5	118475	genbank_N66845	N66845
	118581	genbank_N68905	N68905
	113947	genbank_W84768	W84768
	101447	entrez_M21305	M21305
10	101667	13349_1	NM_005381 M60858 AW373732 AW373724 AW373689 AW373629 AW373609 AW373776 AA187806 AW386946 AW374207 T05235 AA216203 AW385556 AA306940 AA306526 AA315461 AL036757 AW373711 AW403124 AW403640 AW377084 T27360 H62638 F06957 AW377051 AA554779 AA378568 AA096007 AW352407 AW302637 F07929 H17433 AW382712 H05665 F07292 N39875 AA089729 H62556 N42842 R12952 AW373735 AW364155 AA056183 W39185 AW382708 N32488 AF114095 AW375993 AI133569 W52561 AA603040 AA133710 AI928796 AW176370 AA827519 AW338437 AA521142 T29341 AI800461 AW317002 AA703914 AA860830 AI859203 AI445772 AA714334 AI817066 AI832027 AW510442 AI635802 AW088306 AW068672 AW408555 AW467542 AA552657 AA152367 W32081 AA582124 AA074040 AA931657 AI051154 AW410203 AI921644 H17434 AI832330 AW404836 AI925038 AA088423 AA954166 AA580453 AW021292 AI267215 AW080082 AW383778 AI933053 AI919097 W31557 N90245 AA931591 AA563995 F36352 AA056184 AA476294 AA641327 AA533550 AI749630 W58323 AA569119 AA508573 AI809050 AI378996 AA411362 AW407505 AA938104 AA074041 AA632876 AW193748 AA507873 AI270128 AI472365 AA411363 AI523216 AI719965 AI816302 AA182681 AI707990 AA133588 AI758537 W60253 AI460308 AA135423 AI083904 F04188 N89693 AW408776 AI678595 AI270568 AA722059 W58234 F33650 AA090547 AA285108 AA425981 N85079 D20218 AI273980 AA159028 F03226 AW247914 N26918 AW272741 N90109 H05666 N23327 AW247953 R44748 AA962015 F03558 AI752394 AW409913 AW248396 AI816463 AI752393 AA325370 AA263089 AI570130 AI971951 AI160658 AI357360 AW168686 AL121075 AW050536 N21672 W67748 AA514242 AI127386 H14607 AI185752 W79364 AA088520 AA152476 AW351940 AW373683 AI940524 AW374953 T56500 N24329 AI940720 AW374933 AW374947 AW391913 AL138337 AW376241 AW062943 F26666 AW410202 AW062958 F34529 AW381807 AW393315 W17147 AW176359 AA664576 AW380424 AA306040 AI745674 AW300951 AI188579 AI438973 AI305271 AA433818 AA612807 AI831809 AI940409 AA158663 AI572988
	108931	genbank_AA147186	AA147186
30	103138	entrez_X65965	X65965
	103432	entrez_X97748	X97748
	119174	genbank_R71234	R71234
	133678	11235_1	AW247252 AA346143 NM_000270 AA381085 N91995 X00737 AA381079 AA296473 AA296110 AA315735 AA311617 AA326750 AA376804 AW403290 T95231 M13953 T47963 H82039 AA279899 AA627997 N76320 N99527 H37842 W20095 AA457308 AW469547 AA724143 H83220 AA319496 W86334 W30892 R89169 R99427 N41854 H47286 AA348094 AA045089 R63016 AI922219 AI024906 AI096488 AI885005 AA194872 N90489 AI452544 H72411 AA282427 AA430735 R68963 R22453 H70385 AW129369 AW467320 AW519082 AA345018 AA582183 AI961789 R65918 N30611 AI979189 AI280889 AW273191 R66531 AI285845 AI675927 AI421990 AW190879 H37794 AA699667 H68427 AA954388 AI188757 AI140048 AA430382 AI204151 AW247864 AA559099 AI431420 AA548276 AI149466 AA772669 AA694388 AA724168 AA301651 AA281952 AA779925 AA234760 W86290 AA913603 AW511745 AI500697 AA814922 AA835040 T47964 H53998 AA975804 R98710 AI077604 N70252 R98084 AW250171 H69268 AI597614 AA970746 AA972548 AI377116 R62962 H16737 R89070 AA731329 R66532 N54354 AI818832 H81944 N71567 T95122 W86463 AA437095 AI431999 AI915724 N63851 AI674743 AA457307 AA211475 N64444 AI799146 H72853 R99335 H60413 AA770367 AA156105 AI269937 H64029 H89728 R65819 AW470496 AI873318 AI735713 H82987 C02447 AI478666 T27651 AI699770 AW025156 H69719 AI984717 N69225 AI459856 AA953577 AI424691 H13843 R22404 AI873796 AI336002 N70898 AI420854 AA541792 AA346142 AI000814 AI828348 AA045090 T51257 N90434 H13890 N73184 AI708083 AA781606 AA329050 AA339985 R68964 H64795 W04186 H16845
	119416	genbank_T97186	T97186
50	119559	NOT_FOUND_entrez_W38197	W38197
	123473	genbank_AA599143	AA599143

TABLE 5:

5	Pkey:	Unique Eos probeset identifier number			
	Accession:	Accession number used for previous patent filings			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
10					
	Pkey	Accession	ExAccn	UniGene	UnigeneTitle
15	115819	AA426573	AA486620	Hs.41135	AA486620
	132837	D58024	AA370362	Hs.57958	AA370362
	101545	M31210	BE246154	Hs.154210	BE246154
	102898	X06256	NM_002205	Hs.149609	NM_002205
	101192	L20859	BE247295	Hs.78452	BE247295
20	102915	X07820	X07820	Hs.2258	X07820
	105330	AA234743	AW338625	Hs.22120	AW338625
	107385	U97519	NM_005397	Hs.16426	NM_005397
	102024	U03877	AA301867	Hs.76224	AA301867
	134416	M28882	X68264	Hs.211579	X68264
25	103036	X54925	M13509	Hs.83169	M13509
	104865	AA045136	T79340	Hs.22575	T79340
	106124	AA423987	H93366	Hs.7567	H93366
	105330	AA234743	AW338625	Hs.22120	AW338625
	109001	AA156125	AI056548	Hs.72116	AI056548
30	104764	AA025351	AI039243	Hs.278585	AI039243
	133200	AA432248	AB037715	Hs.183639	AB037715
	105263	AA227926	AW388633	Hs.6682	AW388633
	105178	AA187490	AA313825	Hs.21941	AA313825
	109456	AA232645	AW956580	Hs.42699	AW956580

TABLE 5A

Table 5A shows the accession numbers for those pkeys lacking unigenelD's for Table 5. The pkeys in Table 7 lacking unigenelD's are represented within Tables 1-6A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey:	Unique Eos probeset identifier number	
CAT number:	Gene cluster number	
Accession:	Genbank accession numbers	
Pkey	CAT Number	Accession
115819	10241_1	AA486620 AF205940 AA297524 AB034695 AA081335 NM_016242 AA188323 AA297537 H88204 AW953081 W31695 AW582203 AA248250 AW681211 AA426230 AA464807 AA426155 N44141 AA347390 AA770661 AI333225 N36136 AW665724 AA431894 AI374976 AI400254 AI338446 AA186695 H88205 W04527 AA487066 AI051414 AA918383 AA426573 AA425620 AW438654 AA090513 BE167284 BE167291 AI301726
102024	14505_1	AA301867 AW957981 R27614 AA155808 AI920990 AI740711 AA301026 AA301015 AI220981 AI857670 AI537140 AW015210 AA030000 W46890 H44021 AI355967 AI651735 AA058479 AA146932 T58265 R85890 AA047810 AA017387 AW026093 AA971133 AI827263 AI056416 AI355994 AI127691 H46603 U03877 NM_004105 AA157357 H42844 AA146824 AA187709 AA187269 AA304348 AA147292 AA361687 AA156041 AA330636 R32929 AA321130 AW950260 AA082157 AA029129 AA303708 AA028155 D31561 T84689 AA302493 BE153057 BE153181 W39408 AA187200 BE153250 AW383337 AW382622 AW382647 AW750072 BE153060 AW382630 AW371865 AW392464 AW382664 AW382658 AW382650 H61647 AW365075 AW365049 AA373397 BE072779 BE072781 Z30254 W24381 BE153254 AA040442 BE072729 BE072731 N94740 AA146945 AW802737 AI826799 AI085395 R34034 H65140 AA082800 H88275 AA147824 R63882 W80899 AA296413 AI765300 AI862426 AW022055 AW300003 AI743784 AI862635 AI985428 AA147764 AW573245 AW190290 AI040898 D57613 N63457 AA148082 AI028458 AA148110 AW814489 N75105 AW629443 AA704122 AW582220 AA181240 AA057495 AI418224 AI261751 AW388595 AI472205 AW470672 AA102546 AA789046 AA182416 AA062668 AW300732 AI288220 AA181982 AA146825 AA028130 AI985522 AA303344 AA081313 N69082 AA182035 AI867128 AA100902 AA605087 N67178 AW020324 AW890446 AI472191 AI335691 AI597837 AI081143 AI335681 AA040443 AI128067 AI678244 AA018303 AA157260 W80792 AI934590 AI096430 T54343 AI446350 AA165196 AA780683 AA603631 AA047787 AA968580 AA912645 AW890504 AW026913 D56983 H52088 AA156121 R30848 AW023036 AI590960 N67345 AI753225 AI753283 AI183768 AA147818 H89101 AI362141 H89205 AI147711 AA321129 AA668622 AA343479 AW069438 AI422376 AW629270 AA013413 AI221948 AA970605 N52335 H38366 T91180 AA657841 AA017386 AA152227 AA187593 AI913340 AI719313 AI969943 AI701271 AI004328 AI868348 N93659 H65093 H25736 D57007 D56957 C00987 D61839 D56661 AI472137 AI971002 D56971 BE048830 D57972 AI589286 AI361055 AI361071 AI292223 AA155898 D57139 D57981 D57345 AI420034 D57332 D57959 AA875933 R33493 N67558 D58353 AA188394 AA147966 AI160640 AI363165 H40638 AA578137 AW950265 AA300943 AI128999 H46584 AA917355 N57820 AA320504 H51959 H25737
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109456	180633_1	AW956580 AA886361 AI147670 AI090115 AI168683 AA232645 H99504 AA374707 AA380875 AW139567 AI735132 BE439385 AW629780 N28322 AA232789 AA232790 N73285
103036	17145_1	M13509 X54925 NM_002421 M16567 X05231 M15996 W39354 AA186634 AA852324 AA187507 AA081149 AA186524 AA187264 AA187361 AA386155 AA186973 AA374217 U78045 AA081230 AA188049 AA186393 W56827 AA852602 AA157468 AA308204 AA186754 AA186808 AA082516 AA304334 AW376428 BE439384 AW376420 AA156273 T18504 AA186521 W49496 AW084608 AA083575 AA372360 AW963590 AA132297 W47445 AA186376 AA157628 AW003999 AI037890 AI858060 AI589010 AI743739 AI452673 AW304188 AW117854 BE439933 AA157416 AW778966 AI038497 AA081006 AA100829 AA181048 C02231 T27821 W23960 AW954802 AI471432 AW801296 AW801289 AW801603 AW801523 AW801292 AW801542 AW801601 AA181134 AI445147 AA191501 AA582862 N94407 AI147810 AA181880 W49497 W52714 AA188249 AI932881 AI082493 AA503656 AA182682 AW801393 AA182830 AA181882 AA182826 AI613182 N94510 W47343 AI085755 AI076956 AI918426 AA081208 AI282835 AA147528 AI081490 AI654536 AA181875 AA081282 AA186389 C06085 AA083542 AI800644 AA157642 AA101069 AA157752 AA158121 AA143331 AA081283 AA852603 AA188296 AI932880 AW449628 AA187348 C02091 AA514656 AA082736 AA308786 AA143201 M16567 AB037715 AI351347 AI375796 AI884765 AI121124 W01068 AI807275 T95240 R42807 AW515645 AI057314 AI033520 AA057671 N70215 AA054215 AW204183 AA552149 T95130 AW796310 AI866520 AW275564 AW796308 AI637901 AW197404 T78406 AA456232 AW206463 AA779800 AI052696 AA026744 AA454623 AW470729 R45490 AW770258 AI038393 AI290170 AA722734 AL121125 R41608 AI862414 AA838611 R45582 AI278083 BE466849 BE219944 AA148030 BE041555 AA578572 T16528 AW006344 Z39782 AI244848 AW137344 AA707400 AI032028 BE540464 AI094265 AI184281 AA931890 AW382744 AW382729 AW020448 AW827237 AA431226 AI672059 AW772345 N70172 AW022003 AI862704 H19344 R61511 AI080204 H16566 AA432248 AI767980 T16688 AI984342 AI217478 AI767095 Z38551 AI359566 AI361437 AI041000 R07033 H16608 H19054 R12874 R61567 N98368 BE221199 Z42320 AA094554 R07078 AW860886 AA418090 R41262
132837	256666_1	AA370362 AA364110 AW959554 AW371737 AW382068 AW604716 AW604713 AA487827 AW371674 AA429137 BE503321 T93570 W72803 AI093076 AA487977 AI241562 BE439445 AW204065 R51635 AI802994 T10362 W68553 AI866215 AW152154 AA700716 AI127443 R15824 AI537587 AA953110 D58024 AI520811 AA693670 AI453280 W76329 AW023955 AW022563
102898	24023_1	NM_002205 X06256 M13918 BE070866 AW239485 AW996127 BE273894 BE272590 BE410252 R25975 T11786 T11787 AA301142 AA301165 AW960506 BE272819 AA386086 T39391 AA285303 AA370580 D58585 T58668 AA156213 W24142 AA343323 AW796067 AA151197 AA376121 R94782 AA302363 H90357 R82621 AA301677 AW796059 W92358 AL046458 AA471198 AA301952 R46287 R82694 H03186 AA187706 R32562 R27094 R25947 R25320 AW949809 H13505 H79049 R32403 H11213 R39710 H49765 H21142 H21006 AA417664 W52075 N56771 AA284240 N98556 N30907

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104865 102037_1

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107385 6976_1

101192 15367_1

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AA419627 H03986 H20963 T56245 AI459715 AW973768 AI334096 AI693020 T63414 R82646 AW167251 H55998
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AA151198 T53400 AI567709 AI185326 AA309205 AW338969 R53903 AA991891 AA301643 AH93337 AI026049 H25514
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AA578313 AW874497 AA181284 AA861947 T29451 D20841 T58618 AA418731 AI282500 AW081407 AA604560
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AA325490 BE006161 AA349269 AA323568 AL042548 AA191148 AA187703 AA322791 AJ297452 T11625 AW366487
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AA182823 AW166205 F27886 R79246 F37329 AA565697 AI075739 AI088654 AI094287 AI204256 AA095203 T93020
AA688298 AA057324 N23442 AA075411 AA305046 AI031688 AI191503 AA111887 AA112264 W27929 AA187509
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AA301986 W74531 AI051747 AA187715 AI888888 AA993017 AI057530 T92954 N80227 AW273595 AI351260 AW170643
AW292979 AA302605 AA302330 BE349495 AA328602 AA302361 AI470984 AA155943 AA155914
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AA187222 AA187207 AW371052 AW449751 AW748803 AW391606 AW371047 AW371057 AW371085 AW362895
AW371092 AW377556 BE010930 AI016882 AA247878 C04398 C05158 F11398 AA188315 H23385 R55086 H15346
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AA100927 AA496988 AA055917 AI089303 AW014967 AW090248 AW338371 AW131066 D62963 D79713 AI583950
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F09065 H14930 AA890693 H23274
AW388633 AW378440 AW388283 AW388339 AW388414 AW388413 AW388607 AW388453 AW388687
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AW023660 AA262892 T26891 AW089917 T26926 R32227
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AI247108 AI371261 AI364987 AI280171 AI269104 AI868756 AA909836 AA983640 AI973271 AI913092 AI868205
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AI611228 AW131922 AA862687 AA902519 C01732 AW796045 AL044660
BE247295 AW068092 AL041313 AI159244 NM_005415 L20859 AL135570 W47073 AW516906 BE388271 BE408629
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109001 146370_3

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AI393465 AW069210 AI743830 AA744243 AA401310 AW439758 AW088152 R93391 AA291379 AA225220 AW009358
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AI174628 AI432042 AI424528 AA909562 T17342 AI783866
AI056548 AW409843 AW263540 AA723669 AA909334 AA156120 AA157141 AA156125 AW409866 W19499 AA157229
AW887435

TABLE 6:

5	Pkey:	Unique Eos probeset identifier number
	ExAccn:	Exemplar Accession number, Genbank accession number
	UnigeneID:	Unigene number
	Unigene Title:	Unigene gene title
	AUC1:	70 th percentile of average intensity (AI) for probeset at each of 2,6,15,24,48, and 96 hour timepoints minus 70 th percentile AI at 0 hrs, summed over 5 experiments.
10	AUC2:	AUC1/90 th percentile of AI for aorta, aortic valve, vein, and artery.

	Pkey	Ex.Accn	UnigeneID	UnigeneTitle	AUC1	AUC2
15	314941	AA515902	Hs.130650	ESTs	1038	9
	327414			predicted exon	303.2	30.3
	321911	AF026944	Hs.293797	ESTs	429.2	42.9
	331578	AI246482	Hs.249989	ESTs	677.4	10.3
	332466	AB018259	Hs.118140	KIAA0716 gene product	395.2	39.5
20	313513	AW298600	Hs.141840	ESTs, Weakly similar to S59501 interfero	324	32.4
	320635	N50617	Hs.80506	small nuclear ribonucleoprotein polypept	394.8	39.5
	326230			predicted exon	357.2	35.7
	313556	AA628517	Hs.118502		433.6	12
	313665	AW751201	Hs.120932	ESTs	-83	0.5
25	324852	AI380792	Hs.135104	ESTs	348.2	34.8
	314372	AL040178	Hs.142003	ESTs, Weakly similar to The KIAA0149 gen	-49.2	0.5
	311877	AA084248	Hs.85339	G protein-coupled receptor 39	-1309	0.2
	322262	AA632012	Hs.188746	ESTs	-247.8	1
	312173	AI821409	Hs.304471	ESTs, Highly similar to AF116865 1 hedge	-1025.8	1
30	319795	AB037821	Hs.146858	protocadherin 10	203.6	5.2
	313350	AW591949	Hs.57958	ETL protein	183.8	18.4
	326759			predicted exon	1654.4	1.2
	300318	AW444502	Hs.256982	ESTs, Highly similar to AF116865 1 hedge	-346	1
	313978	AI870175	Hs.13957	ESTs	576.6	2.3
35	306840	AI077477	Hs.307912	EST	56.4	0.4
	310272	AF216389	Hs.148932	semaphorin Rs, short form	-127.6	0
	315044	BE547674	Hs.204169	ESTs	-102.6	0
	321325	AB033100	Hs.300646	KIAA protein (similar to mouse paladin)	1080.6	4.8
	303251	AF240635	Hs.115897	protocadherin 12	1270.8	5.3
40	302378	AL109712	Hs.296506	Homo sapiens mRNA full length insert cDN	915.8	15.8
	315060	AA551104	Hs.189048	ESTs, Moderately similar to ALUC_HUMAN I	1236.8	4.9
	332048	AW337575	Hs.201591	ESTs	522.6	4.7
	337214			predicted exon	269	26.9
	311598	AW023595	Hs.232048	ESTs	796.4	20.2
45	304782	AA582081		gb:nn32h08.s1 NCI_CGAP_Gas1 Homo sapiens	316.4	10.5
	312802	AA644669	Hs.193042	ESTs	349.6	7.6
	302680	AW192334	Hs.38218	ESTs	638.6	63.9
	317452	AA972965	Hs.135568	ESTs	360.8	36.1
	318558	AW402677	Hs.146381	RNA binding motif protein, X chromosome	700.2	6.6
50	312149	T90309	Hs.269651	ESTs	274.2	7.5
	319267	F11802	Hs.6818	ESTs	238.2	23.8
	321510	H75391	Hs.255748	ESTs	231.8	23.2
	326198			predicted exon	581.6	8.2
	315730	H25899	Hs.201591	ESTs	281.6	9.7
55	310442	AW072215	Hs.208470	ESTs	-213	0.3
	331237	W87874	Hs.25277	hypothetical protein FLJ21065	285	0.5
	300469	BE301708	Hs.233955	hypothetical protein FLJ20401	26.6	0.3
	338316			predicted exon	1494.2	34.7
	330968	R44557	Hs.23748	ESTs	975.8	1.8
60	331019	NM_006033	Hs.65370	lipase, endothelial	201.2	0.9
	331261	BE539976	Hs.103305	Homo sapiens mRNA; cDNA DKFZp434B0425 (f	478.6	1.3
	301822	X17033	Hs.271986	Integrin, alpha 2 (CD49B, alpha 2 subuni	356.2	1.7
	325544			predicted exon	1014.6	9.4
	328700			predicted exon	627.4	62.7
65	322882	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	84.8	5.7
	336034			predicted exon	782.6	78.3
	316580	AA938198	Hs.146123	hypothetical protein FLJ12972	746.4	13.8
	309931	AW341683		gb:hd13d01.x1 Soares_NFL_T_GBC_S1 Homo s	134.8	13.5
	330692	R39288	Hs.6702	ESTs	137	13.7
70	319962	H06350	Hs.135056	Human DNA sequence from clone RP5-850E9	14.6	0.5
	338033			predicted exon	540.6	14
	314943	Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	-494.8	1
	332640	BE568452	Hs.5101	protein regulator of cytokinesis 1	-600	1
	338158			predicted exon	311.2	31.1
75	327036			predicted exon	351.8	35.2

	302655	AJ227892	Hs.146274	ESTs	180.2	18
	327568			predicted exon	229	22.9
	324801	AW770553	Hs.14553	sterol O-acyltransferase (acyl-Coenzyme	161.2	16.1
5	317850	AI681545	Hs.152982	hypothetical protein FLJ13117	-690	1
	322818	AW043782	Hs.293616	ESTs	126.4	4.5
	324626	AI685464	Hs.292638	ESTs	170.2	17
	317224	X73608	Hs.93029	sparc/osteonectin, cwcv and kazal-like d	-80	0
	310955	AI476732	Hs.263912	ESTs	466.8	46.7
10	315240	R38772	Hs.172619	KIAA1106 protein	277	27.7
	338388			predicted exon	267.6	26.8
	338442			predicted exon	256	25.6
	318617	AW247252	Hs.75514	nucleoside phosphorylase	1247.8	24.2
	338645			predicted exon	206	20.6
	313135	N58907	Hs.162430	ESTs	204.8	20.5
15	324716	BE169746	Hs.12504	hypothetical protein DKFZp761D081	203.6	20.4
	330305			predicted exon	199.8	20
	308248	AI560919		gb:taq41g10.x1 NCI_CGAP_Ut1 Homo sapiens	199.4	19.9
	308886	AI833240		gb:at76d10.x1 Barstead colon HPLRB7 Homo	198.2	19.8
20	315622	AI796144	Hs.258188	Homo sapiens cDNA FLJ11674 fis, clone HE	191.2	19.1
	323675	R43240	Hs.272168	tumor differentially expressed 1	189.2	18.9
	312164	T91980	Hs.221074	ESTs	187.6	18.8
	300378	Z45270	Hs.235873	hypothetical protein FLJ22672	271.6	18.7
	317478	AI343569	Hs.107000	Homo sapiens mRNA for WDC146, complete c	187	18.7
25	317559	AW452344	Hs.129977	ESTs	184.2	18.4
	317207	AI873346	Hs.214505	ESTs	182.8	18.3
	334834			predicted exon	178.8	17.9
	320925	D62892		gb:HUM337C07B Clontech human aorta polyA	177.2	17.7
	303289	AL121460	Hs.272673	hypothetical protein FLJ20508	316.4	17.6
30	328548			predicted exon	174.6	17.5
	317108	AA884000	Hs.8173	hypothetical protein FLJ10803	172.4	17.2
	318013	AI188183	Hs.144078	ESTs	326	17.2
	314299	AW382682	Hs.154840	ESTs	170.8	17.1
	317702	AW173339	Hs.135665	ESTs	169.8	17
35	316094	AW975920	Hs.283361	ESTs	169.4	16.9
	323706	AA377578	Hs.65234	hypothetical protein FLJ20596	169.2	16.9
	325843			predicted exon	321.4	16.9
	316012	AA764950	Hs.119898	ESTs	1047.2	16.9
	309687	AW236154	Hs.77385	myosin,lightpolypeptide6,alkali,smoothmu	168.2	16.8
40	323329	AL134744	Hs.10852	ESTs	168	16.8
	312853	W05086	Hs.114256	ESTs	167.4	16.7
	313070	AI422023	Hs.161338	ESTs	298.6	16.6
	314096	AW977642	Hs.291742	ESTs	165.6	16.6
	338728			predicted exon	165.4	16.5
45	316609	AW292520	Hs.122082	ESTs	165	16.5
	305989	AA888220		gb:oj15h01.s1 NCI_CGAP_Kid5 Homo sapiens	164.6	16.5
	312642	AW052128		gb:wx26c02.x1 NCI_CGAP_Kid11 Homo sapien	164	16.4
	339236			predicted exon	163.6	16.4
	317058	AI217713	Hs.147586	ESTs	161.8	16.2
50	311137	AW207582	Hs.196042	ESTs	582.2	16.2
	310178	AI936450	Hs.147482	ESTs	161.2	16.1
	320745	H51696	Hs.89278	hypothetical protein FLJ11186	161	16.1
	317336	AW014637	Hs.130212	ESTs	160	16
	309871	AW300366		gb:xs63b05.x1 NCI_CGAP_Kid11 Homo sapien	159.8	16
55	302038	AC004076	Hs.129709	Homo sapiens chromosome 19, cosmid R3021	159	15.9
	332237	N52883	Hs.102676	EST	159	15.9
	312362	AW015994		gb:UI-H-BI0p-abh-g-09-0-UI.s1 NCI_CGAP_S	158.6	15.9
	331558	N62401	Hs.48531	EST	158.6	15.9
	316215	AI684535	Hs.200811	ESTs	158.4	15.8
60	336059			predicted exon	157.4	15.7
	302790	AJ245245		gb:Homo sapiens mRNA for immunoglobulin	155.8	15.6
	328418			predicted exon	153.8	15.4
	304229	AK000149	Hs.29493	hypothetical protein FLJ20142	153.6	15.4
	331606	AW273285	Hs.50802	ESTs	153	15.3
65	338962			predicted exon	664.4	15.3
	317959	AI204202	Hs.130264	ESTs	152.6	15.3
	336228			predicted exon	152.4	15.2
	313534	AW072916	Hs.78743	zinc finger protein 131 (clone pHZ-10)	152.2	15.2
	317404	AI806867	Hs.126594	ESTs	152.2	15.2
70	311943	AI469911	Hs.26498	hypothetical protein FLJ21657	152	15.2
	314680	AI247425	Hs.152182	ESTs	151.4	15.1
	331484	N29696	Hs.44076	EST	151.2	15.1
	338116			predicted exon	151.2	15.1
	329863			predicted exon	150.6	15.1
75	315555	AW452886	Hs.239107	ESTs	149.6	15
	317039	AA868583	Hs.126153	ESTs	149.6	15
	331138	R63816	Hs.28445	ESTs	149.6	15

	316561	AI917222	Hs.121655	ESTs	149.4	14.9
	328695			predicted exon	149.2	14.9
	302282	BE396283	Hs.173987	eukaryotic translation initiation factor	148.4	14.8
5	318781	F11802	Hs.6818	ESTs	148.2	14.8
	323709	AW297246	Hs.288546	Homo sapiens cDNA FLJ14190 fis, clone NT	148	14.8
	310790	AW192063	Hs.248865	ESTs	147.8	14.8
	316833	AW292614	Hs.124367	ESTs	147.8	14.8
	323176	NM_007350	Hs.82101	pleckstrin homology-like domain, family	229	14.8
10	324188	AW274439	Hs.252709	ESTs	147.6	14.8
	317441	AA922798	Hs.196583	ESTs	147.4	14.7
	317584	AI825890	Hs.220513	ESTs	146.8	14.7
	321798	AI308206	Hs.181959	ESTs	146.8	14.7
	304363	AA206045		gb:zq77f05.s1 Stratagene hNT neuron (937	146.6	14.7
	313952	F20956		gb:HSPD05390 HM3 Homo sapiens cDNA clone	146.6	14.7
15	301909	AI702609	Hs.15713	ESTs	263.8	14.7
	309196	AI904895	Hs.9614	nucleophosmin (nucleolar phosphoprotein	146.2	14.6
	321860	N47474	Hs.212631	ESTs	146.2	14.6
	330187			predicted exon	146	14.6
20	323042	AA463571	Hs.172550	polypyrimidine tract binding protein (he	145.6	14.6
	313636	AA262397	Hs.201366	ESTs	145.2	14.5
	302437	AB024729	Hs.227473	UDP-N-acetylglucosamine:a-1,3-D-mannosid	145	14.5
	318197	AI473096	Hs.133403	ESTs	144.8	14.5
	302749	M16951		gb:Human Ig mu-chain mRNA VDJ4-region, 5	144.6	14.5
25	322357	AI734258	Hs.245367	ESTs, Weakly similar to ALU1_HUMAN ALU S	144.6	14.5
	300391	AI927371	Hs.288839	hypothetical protein FLJ12178	144.4	14.4
	326077			predicted exon	144.4	14.4
	302004	Y18264	Hs.123094	sal (Drosophila)-like 1	144	14.4
	320668	AA805666	Hs.146217	Homo sapiens cDNA: FLJ23077 fis, clone L	144	14.4
30	331212	T88693	Hs.226410	ESTs	144	14.4
	311268	AI969727	Hs.231859	ESTs	143.2	14.3
	305159	AA659166	Hs.275668	EST,Weakly similar to EF1D_HUMAN ELONGATION F	143	14.3
	304510	AA457391	Hs.119122	ribosomal protein L13a	142.8	14.3
	320852	AA772920	Hs.303527	ESTs	142.8	14.3
35	330854	AW291944	Hs.122139	ESTs	142.8	14.3
	318275	AW449952	Hs.190125	basic-helix-loop-helix-PAS protein	142.6	14.3
	314992	AI824879	Hs.211286	ESTs, Weakly similar to 1207289A reverse	142.2	14.2
	322631	AA001697	Hs.293565	ESTs, Weakly similar to putative p150 [H	142.2	14.2
	332283	R40855	Hs.100839	EST	142	14.2
40	302894	AA719572	Hs.274441	Homo sapiens mRNA; cDNA DKFZp434N011 (fr	141.2	14.1
	301808	R35391	Hs.252831	reticulin 3	141	14.1
	318608	AI204491	Hs.151502	ESTs	141	14.1
	316499	AW292947	Hs.122872	ESTs	140.8	14.1
	317011	AI248760	Hs.150276	ESTs	140.8	14.1
45	321840	N45600	Hs.46534	Homo sapiens mRNA; cDNA DKFZp434P0714 (f	140.8	14.1
	327365			predicted exon	140.8	14.1
	331264	AA278898	Hs.225979	hypothetical protein similar to small G	140.8	14.1
	324545	AW501944	Hs.127243	Homo sapiens mRNA for KIAA1724 protein,	140.4	14
	312986	AA211586		gb:zn56d05.s1 Stratagene muscle 937209 H	140.2	14
50	316053	AA825814	Hs.149065	ESTs	140.2	14
	330723	BE247449	Hs.31082	hypothetical protein FLJ10525	140.2	14
	304876	AA595765		gb:nj28g06.s1 NCI_CGAP_AA1 Homo sapiens	139.8	14
	311379	AW134766	Hs.202450	ESTs	139.8	14
	318265	AW019873	Hs.146840	ESTs	139.8	14
55	324137	AA393127	Hs.222762	ESTs	139.8	14
	328262			predicted exon	139.6	14
	322349	AK001279	Hs.180171	Homo sapiens cDNA FLJ10417 fis, clone NT	139.4	13.9
	323504	AA280223	Hs.130865	ESTs	139.4	13.9
	304261	AA059387		gb:zf66d01.s1 Soares retina N2b4HR Homo	139.2	13.9
60	310489	AW451493	Hs.235516	hypothetical protein PRO2955	139.2	13.9
	335946			predicted exon	139.2	13.9
	318155	AI041546	Hs.132133	ESTs	138.8	13.9
	313796	AI797169	Hs.208486	ESTs	138.6	13.9
	333977			predicted exon	138.6	13.9
65	324845	AW969635	Hs.283718	ESTs	138.2	13.8
	331139	R65706		gb:yi16g12.s1 Soares placenta Nb2HP Homo	138.2	13.8
	331131	R54797		gb:yg87b07.s1 Soares infant brain 1NIB H	669.6	13.8
	321250	H58539	Hs.151692	ESTs	138	13.8
	312498	AA668782	Hs.191284	ESTs, Weakly similar to ALU1_HUMAN ALU S	137.8	13.8
70	331252	W52470	Hs.34578	alpha2,3-sialyltransferase	137.8	13.8
	337407			predicted exon	137.8	13.8
	303973	AW512014		gb:xx68a03.x1 NCI_CGAP_Lym12 Homo sapien	137.4	13.7
	314582	AA412258	Hs.188817	ESTs	137.4	13.7
	327373			predicted exon	137.2	13.7
75	323367	AA234591	Hs.304123	ESTs	136.6	13.7
	316207	AA832065	Hs.120260	ESTs	136.4	13.6
	315231	AA705809	Hs.119922	ESTs	136.2	13.6

	318592	T39310	Hs.1139	cold shock domain protein A	136.2	13.6
	320906	AW969706	Hs.293332	ESTs	136.2	13.6
	328937			predicted exon	136.2	13.6
	329073			predicted exon	136.2	13.6
5	318231	AV659082	Hs.134228	ESTs	136	13.6
	311992	AL360200	Hs.114145	ESTs	135.8	13.6
	316497	AA766457	Hs.136849	ESTs	135.8	13.6
	317677	AA968594	Hs.127868	ESTs	135.8	13.6
10	321680	W02848	Hs.93704	ESTs	135.8	13.6
	326080			predicted exon	135.8	13.6
	330938	AF036943	Hs.172619	KIAA1106 protein	135.8	13.6
	306573	AL134878	Hs.119500	ribosomal protein, large P2	135.6	13.6
	307383	AI223207	Hs.147888	EST	135.6	13.6
	311114	AW449382	Hs.195297	ESTs	135.6	13.6
15	320579	R15138	Hs.165570	Homo sapiens clone 25052 mRNA sequence	135	13.5
	301328	AA884104	Hs.125546	ESTs	134.8	13.5
	312063	N58198	Hs.182898	ESTs	134.8	13.5
	323036	H09604	Hs.13268	ESTs	134.6	13.5
20	332776	AF241850	Hs.151428	ret finger protein 2	134.4	13.4
	332494	AA282330	Hs.145668	ESTs	134.2	13.4
	334376			predicted exon	134.2	13.4
	313264	N93416	Hs.118228	ESTs	133.6	13.4
	313669	AA351109	Hs.5437	Tax1 (human T-cell leukemia virus type I	133.2	13.3
	312083	T87398	Hs.205816	ESTs	132.6	13.3
25	319354	AA993807	Hs.167367	ESTs	132.6	13.3
	307414	AI242106		gb:qh92a02.x1 Soares_NFL_T_GBC_S1 Homo s	132.2	13.2
	312771	AA018515	Hs.264482	Apq12 (autophagy 12, S. cerevisiae)-like	131.8	13.2
	313004	AI274963	Hs.145900	ESTs	131.2	13.1
30	300995	AW510641	Hs.258018	ESTs	220.6	13
	319323	F12650	Hs.13287	ESTs	125.4	12.5
	329451			predicted exon	123.4	12.3
	337603			predicted exon	572	12.2
	312480	R68651	Hs.144997	ESTs	121.4	12.1
35	324934	AW452051	Hs.147546	ESTs	119.4	11.9
	320723	BE178025	Hs.7942	hypothetical protein FLJ20080	117	11.7
	318188	AI792566		gb:q74f02.y5 NCI_CGAP_Ov26 Homo sapiens	116.6	11.7
	320873	AF238869	Hs.283955	Homo sapiens clone GLSH-2 similar to gli	112.8	11.3
	331005	BE003191	Hs.119555	ESTs	112.6	11.3
40	304969	AA614406		gb:np46f05.s1 NCI_CGAP_Br11 Homo sapiens	112.4	11.2
	319799	AI139253	Hs.227767	zinc finger protein 41	111.2	11.1
	302610	AA347945	Hs.256024	ESTs	111	11.1
	309485	AW130320	Hs.108124	ribosomal protein S4,X-linked	111	11.1
	311880	AW419225	Hs.256247	ESTs	110.2	11
45	313981	AW452334	Hs.128148	ESTs	110.2	11
	322442	W49701	Hs.29667	ESTs	109.4	10.9
	315099	AA806536	Hs.291841	ESTs	109	10.9
	304793	AA583264	Hs.182979	ribosomal protein L12	108.8	10.9
	330815	AA019211	Hs.236463	KIAA1238 protein	108.8	10.9
50	304044	T81656	Hs.252259	ribosomal protein S3	714.8	10.8
	325222			predicted exon	135	10.8
	325889			predicted exon	814.6	10.8
	321447	AW891130	Hs.38173	ESTs	107.8	10.8
	302990	AA496212	Hs.180182	ESTs	106.2	10.6
55	308106	AI476803		gb:ij77e12.x1 Soares_NSF_F8_9W_OT_PA_P_S	270.6	10.6
	310536	AI301041	Hs.150174	ESTs	106	10.6
	315257	AW157431	Hs.248941	ESTs	233	10.6
	318787	Z42313	Hs.22657	ESTs	105.8	10.6
	312306	AI927226	Hs.175610	ESTs	105.2	10.5
60	326788			predicted exon	104.4	10.4
	312234	AA830640	Hs.206934	ESTs	104	10.4
	314482	AW085525	Hs.134182	ESTs	234	10.4
	323597	AI185693	Hs.135119	ESTs	102.4	10.2
	302623	AW836724	Hs.194110	hypothetical protein PRO2730	162.4	10.2
	323594	AI791531	Hs.129993	ESTs	101	10.1
65	324315	N55761	Hs.194718	zinc finger protein 265	100.2	10
	314217	AA256465	Hs.188725	ESTs	99.2	9.9
	320932	AA554913	Hs.162297	ESTs	98.2	9.8
	327876			predicted exon	98.2	9.8
70	319736	R17424	Hs.6650	vacuolar protein sorting 45B (yeast homo	98	9.8
	327747			predicted exon	97.6	9.8
	327844			predicted exon	97.4	9.7
	318200	AI061192	Hs.166517	ESTs	97.2	9.7
	329414			predicted exon	97.2	9.7
75	318296	AI089667	Hs.270713	ESTs	121.4	9.7
	307010	AI140014		gb:qa68f09.x1 Soares_fetal_heart_NbHH19W295	9.7	9.7
	319792	AI138635	Hs.22968	ESTs	385.4	9.6

	305671	AA811688	Hs.82113	dUTPyrophosphatase	96	9.6
	329440			predicted exon	93.8	9.4
	310381	AI263059	Hs.145594	ESTs	93.4	9.3
5	318824	F06771	Hs.27226	ESTs	93.4	9.3
	328957			predicted exon	92.2	9.2
	318804	Z42549	Hs.160893	ESTs	92	9.2
	330836	AA055611	Hs.226568	ESTs, Moderately similar to ALU4_HUMAN A	92	9.2
	324592	AW752437	Hs.325708	ESTs	91.8	9.2
10	311820	AW274545	Hs.254333	ESTs	91.4	9.1
	321614	H86161		gb:ys94b01.r1 Soares retina N2b5HR Homo	91	9.1
	330306			predicted exon	91	9.1
	303096	AL080276	Hs.268562	regulator of G-protein signalling 17	90	9
	313275	AI027604	Hs.159650	ESTs	110.4	8.8
15	302593	H54855	Hs.36958	ESTs	88	8.8
	321421	BE465115	Hs.171688	ESTs	86.2	8.6
	330832	AI133530	Hs.62930	ESTs	456.4	8.6
	311847	AW301807	Hs.297260	ESTs	86	8.6
	322036	BE002723	Hs.301905	Homo sapiens cDNA FLJ14080 fis, clone HE	145.8	8.6
20	328688			predicted exon	85.6	8.6
	325251			predicted exon	85.4	8.5
	329088			predicted exon	85.4	8.5
	322524	W79027	Hs.271762	ESTs	84	8.4
	337953			predicted exon	451	8.3
25	323529	AA284397	Hs.201485	Homo sapiens clone FLC0664 PRO2866 mRNA,	82.6	8.3
	307041	AI144243		gb:qb85b12.x1 Soares_fetal_heart_NbHH19W	306.8	8.2
	318285	AI332454	Hs.158412	ESTs	81.4	8.1
	312021	AA759263	Hs.14041	ESTs	81	8.1
	329350			predicted exon	81	8.1
30	326169			predicted exon	80.4	8
	338038			predicted exon	1024.2	7.9
	312549	AI214510	Hs.146304	ESTs	77.4	7.7
	312542	D60076		gb:HUM084E10A Clontech human fetal brain	76.8	7.7
	320992	AB026891	Hs.225972	solute carrier family 7, (cationic amino	76	7.6
35	318596	AI470235	Hs.172698	EST	150.6	7.5
	315650	AA649042	Hs.269615	ESTs	73.4	7.3
	324328	AA447276	Hs.292020	ESTs	210.4	7.1
	332622	R10674	Hs.128856	CSR1 protein	70.2	7
	328229			predicted exon	69.4	6.9
40	319110	T75260	Hs.98321	hypothetical protein FLJ14103	68.6	6.9
	316133	AI187742	Hs.125562	ESTs	308.6	6.9
	303992	AW515800		gb:hd88g01.x1 NCI_CGAP_GC6 Homo sapiens	67.8	6.8
	322675	AA017656	Hs.146580	enolase 2, (gamma, neuronal)	377.2	6.7
	325753			predicted exon	105.2	6.6
45	312539	AI004377	Hs.200360	Homo sapiens cDNA FLJ13027 fis, clone NT	92.2	6.4
	302592	AA294921	Hs.250811	v-ral simian leukemia viral oncogene hom	361.6	6.3
	314578	AA410183	Hs.137475	ESTs	201.6	6.1
	335986			predicted exon	108.6	6
	321478	AW402593	Hs.123253	hypothetical protein FLJ22009	528	6
50	305192	AA666019		gb:ag44a04.s1 Jia bone marrow stroma Hom	58.6	5.9
	304275	AA070605		gb:zm53h09.s1 Stratagene fibroblast (937	78.6	5.6
	302779	AJ235667		gb:Homo sapiens mRNA for immunoglobulin	278.8	5.5
	301976	T97905	Hs.77256	enhancer of zeste (Drosophila) homolog 2	479.2	5.4
	316021	AW293399	Hs.144904	nuclear receptor co-repressor 1	792.4	5.3
55	320802	BE336699	Hs.185055	BENE protein	2423.8	5.3
	317282	AI733112	Hs.176101	ESTs	523.2	5.1
	316827	AI380429	Hs.172445	ESTs	578	5.1
	303190	BE280787	Hs.16079	hypothetical protein FLJ10233	223	5.1
	315587	AI268399	Hs.140489	ESTs	136.2	5
60	333122			predicted exon	399	5
	310214	AI220072	Hs.165893	ESTs	234.4	4.9
	320089	D43945	Hs.113274	transcription factor EC	68	4.9
	309328	AW024348	Hs.233191	EST, Weakly similar to A27217 glucose tr	258.8	4.8
	318971	Z44067	Hs.10957	ESTs	376.6	4.8
65	327220			predicted exon	47.4	4.7
	315757	AW014605	Hs.179872	ESTs	177.4	4.7
	320730	R68869	Hs.151072	ESTs	205.2	4.6
	313339	AI682536	Hs.163495	Homo sapiens cDNA FLJ13608 fis, clone PL	260	4.5
	318634	T49598	Hs.156832	ESTs	475.2	4.5
70	320955	AW820035	Hs.278679	a disintegrin and metalloproteinase doma	388.6	4.4
	306605	AI000497	Hs.119500	ribosomalprotein,largeP2	81.6	4.4
	309349	AW051913		gb:wx24a09.x1 NCI_CGAP_Kid11 Homo sapien	102.4	4.3
	306004	AA889992	Hs.2186	eukaryotic translation elongation factor 1ga	451.2	4.2
	330020			predicted exon	61.2	4.1
75	302308	AW327279	Hs.91379	ribosomal protein L26	342	3.9
	314648	AW979268		gb:EST391378 MAGE resequences, MAGP Homo	56.4	3.8
	315131	AI753709	Hs.152484	ESTs	130.4	3.7

	313690	AI493591	Hs.78146	platelet/endothelial cell adhesion molec	3179.6	3.6	
	333585			predicted exon	175.4	3.5	
	312911	H93366	Hs.7567	Homo sapiens cDNA: FLJ21962 fis, clone H	219	3.5	
5	322966	AA633669	Hs.235920	Homo sapiens cell recognition molecule C	350.2	3.4	
	312492	R71072	Hs.191269	ESTs	322.8	3	
	318988	Z44203	Hs.26418	ESTs	25	2.5	
	332363	AI123705	Hs.108932	ESTs	773.4	2.5	
	324181	AI025476	Hs.131628	ESTs	634.8	2.4	
	311717	AW205369	Hs.312830	ESTs	54.2	2.4	
10	321342	AA127984	Hs.222024	transcription factor BMAL2	23.4	2.3	
	308852	AI829848	Hs.182937	peptidylprolylisomeraseA(cyclophilinA)	92	2.3	
	331466	AA373210	Hs.43047	Homo sapiens cDNA FLJ13585 fis, clone PL	494	2.3	
	320279	AB033062	Hs.134970	DKFZP434N178 protein	76.2	2.2	
	322221	N24236	Hs.179662	nucleosome assembly protein 1-like 1	253.2	2.1	
15	302925	AL137449	Hs.126666	homeo box B4	136.6	2.1	
	331384	AB041035	Hs.93847	NADPH oxidase 4	720	1.8	
	300938	AA514416	Hs.152320	ESTs, Weakly similar to 1605244A erythro	27	1.8	
	312695	AW196663	Hs.200242	ESTs	303.8	1.6	
	320223	W35132	Hs.267442	ESTs	189	1.5	
20	332743	AW247977	Hs.87595	translocase of inner mitochondrial membr	14.4	1.4	
	331039	AW378685	Hs.18625	Mitochondrial Acyl-CoA Thioesterase	529.8	1.4	
	333123			predicted exon	396.2	1.4	
	328455			predicted exon	91.8	1.3	
	334458			predicted exon	406.4	1.3	
25	313478	AA643008	Hs.192775	ESTs	413.4	1.1	
	309899	AW338564	Hs.217493	annexinA2	-30.8	1	
	311735	AW294416	Hs.144687	Homo sapiens cDNA FLJ12981 fis, clone NT	-62.8	1	
	312953	NM_001992	Hs.128087	coagulation factor II (thrombin) recepto	-73.6	1	
	313055	AW367295	Hs.241175	ESTs	-43.8	1	
30	313291	AI267970	Hs.150614	ESTs, Weakly similar to ALU4_HUMAN ALU S	-63	1	
	315059	AW275110	Hs.271106	ESTs	-67	1	
	322284	AI792140	Hs.49265	ESTs	-395.2	1	
	322450	AL121278	Hs.25144	ESTs	-1.6	1	
	324803	AW975183	Hs.292663	ESTs	4.4	1	
35	331495	AW970939	Hs.291039	ESTs	-282.8	1	
	333610			predicted exon	-152.6	1	
	335093			predicted exon	-23.2	1	
	339403			predicted exon	-331.2	1	
40	302820	X04588	Hs.85844	neurotrophic tyrosine kinase, receptor,	591.2	1	
	302270	R56151	Hs.93589	Homo sapiens mRNA; cDNA DKFZp564B1162 (f	276.6	1	
	323755	AW300094	Hs.136252	ESTs	135	0.9	
	326946			predicted exon	727.4	0.9	
	315343	BE144306	Hs.179891	ESTs, Weakly similar to P4HA_HUMAN PROLY	122.8	0.9	
45	311168	AK001270	Hs.196086	hypothetical protein FLJ10408	304	0.9	
	329732			predicted exon	109.2	0.9	
	321415	BE621807	Hs.3337	transmembrane 4 superfamily member 1	414.8	0.7	
	333121			predicted exon	87.8	0.7	
	333120			predicted exon	379.8	0.7	
50	330392	AW797956	Hs.75748	proteasome (prosome, macropain) subunit,	589.2	0.7	
	314711	AA769365	Hs.126058	ESTs	-87	0.6	
	330865	BE409857	Hs.69499	hypothetical protein	347.4	0.6	
	333169			predicted exon	-1182	0.6	
	335095			predicted exon	106.4	0.6	
	335815			predicted exon	-156	0.6	
55	330232			predicted exon	102.6	0.6	
	330823	AA031565	Hs.221255	ESTs, Moderately similar to ALU5_HUMAN A	-62	0.5	
	331704	F04225	Hs.66032	ESTs	-14.6	0.5	
	302642	NM_016428	Hs.130719	NESH protein	267.6	0.5	
60	304484	AA432067	Hs.258373	ESTs	85	0.5	
	310230	AK000377	Hs.144840	homolog of mouse C2PA	-70	0.4	
	301531	AI077462	Hs.134084	ESTs	-195.4	0.4	
	306337	AA954221	Hs.73742	ribosomal protein, large, P0	-33.4	0.4	
	331327	N46436	Hs.109221	ESTs	-392	0.4	
	332961			predicted exon	-5.6	0.4	
65	322796	W31178	Hs.154140	Homo sapiens ovary-specific acidic prote	-880.6	0.3	
	328857			predicted exon	55.2	0.3	
	316342	AA743935	Hs.202329	ESTs	43.4	0.3	
	331263	AW780192	Hs.267596	ESTs	-180.4	0.3	
	335987			predicted exon	-134	0.3	
70	311923	T60843	Hs.189679	ESTs	12.2	0.3	
	310522	AW134529	Hs.244647	ESTs	-187.8	0.3	
	315363	AA759190	Hs.121454	ESTs, Weakly similar to olfactory recept	80	0.3	
	302032	NM_001992	Hs.128087	coagulation factor II (thrombin) recepto	-877	0.3	
	313140	BE265133	Hs.217493	annexin A2	95.4	0.3	
75	310860	AW015920	Hs.161359	ESTs	-239	0.3	
	317899	AI952430	Hs.150614	ESTs, Weakly similar to ALU4_HUMAN ALU S	-715.2	0.3	

	328520		predicted exon	-109.2	0.2
	302406	NM_012099Hs.211956	CD3-epsilon-associated protein; antisens	10	0.2
	311804	AI866921 Hs.203349	Homo sapiens cDNA FLJ12149 fis, clone MA	-252.6	0.2
5	315065	AK001122 Hs.105859	hypothetical protein FLJ10260	-46.2	0.2
	314129	AA228366 Hs.115122	ESTs	-308.8	0.2
	335697		predicted exon	-47.2	0.2
	335989		predicted exon	89	0.2
	320606	AW867943 Hs.127216	hypothetical protein FLJ13465	-205.6	0.2
10	329745		predicted exon	103	0.2
	313628	AW419069 Hs.209670	ESTs	-177.8	0.2
	334616		predicted exon	-936.6	0.2
	308820	AI821267 Hs.207243	EST	-7.2	0.2
	320416	AI026984 Hs.293662	ESTs	-18.4	0.2
	335211		predicted exon	-142	0.2
15	323629	AA375957 Hs.6682	ESTs	-100	0.1
	331420	AW452904	gb:U1-H-BI3-aly-h-11-0-UI.s1 NCI_CGAP_Su	83	0.1
	315984	AI015862 Hs.131793	ESTs	-250.6	0.1
	332833		predicted exon	-374.2	0.1
20	332607	NM_002314Hs.36566	LIM domain kinase 1	-27.6	0.1
	313467	AA004879 Hs.187820	ESTs	-288.2	0.1
	323333	AV651680 Hs.208558	ESTs	-735.6	0.1
	330775	AW247020 Hs.250747	SUMO-1 activating enzyme subunit 1	53.6	0.1
	333168		predicted exon	-1041.8	0.1
25	332079	AI308876 Hs.103849	ESTs	19.4	0.1
	322724	AF161442 Hs.191591	Homo sapiens HSPC324 mRNA, partial cds	-123.6	0.1
	303652	AI799111 Hs.64341	ESTs	-46.4	0.1
	303131	AW081061 Hs.103180	DC2 protein	-156.4	0.1
	320716	AI479439 Hs.171532	ESTs	-146.6	0.1
30	300454	AA659037 Hs.163780	ESTs	-304	0.1
	312757	AI285970 Hs.183817	ESTs	-445	0.1
	312391	R43707 Hs.133159	ESTs, Weakly similar to PIHUSD salivary	-111.8	0.1
	308877	AI832519	gb:at69h03.x1 Barstead colon HPLRB7 Homo	-149.6	0
	311275	AI659166 Hs.207144	ESTs	-62.6	0
35	302363	AW163799 Hs.198365	2,3-bisphosphoglycerate mutase	-15	0
	321717	AW956580 Hs.42699	ESTs	-1059.6	0
	302638	AA463798 Hs.102696	MCT-1 protein	-332.2	0
	306352	AA961367	gb:orf52a05.s1 NCI_CGAP_GC3 Homo sapiens	21.8	0
	313798	AI292148 Hs.71622	SWI/SNF related, matrix associated, acti	-97.2	0
40	320807	AA135370 Hs.188536	Homo sapiens cDNA: FLJ21635 fis, clone C	-2222	0
	320931	AW262836 Hs.252844	ESTs	-881.6	0
	332450	AW288085 Hs.11156	hypothetical protein	28.4	0
	332535	AF167706 Hs.19280	cysteine-rich motor neuron 1	-722	0
	335990		predicted exon	-421	0
45	330746	AB033888 Hs.8619	SRY (sex determining region Y)-box 18	35.4	0
	316820	AI627912 Hs.130783	Forssman synthetase	-373.6	0
	337429		predicted exon	-257	0
	331192	BE622021 Hs.152571	ESTs, Highly similar to IGF-II mRNA-bind	-33	0
	330609	AI346201 Hs.76118	ubiquitin carboxyl-terminal esterase L1	-280	0
50	323593	AI739435 Hs.39168	ESTs	-3627.6	0
	302704	AA531133 Hs.4253	hypothetical protein MGC2574	-278.6	0
	330534	NM_004579Hs.82979	mitogen-activating protein kinase kinase	-244	0
	332374	X91195 Hs.100623	phospholipase C, beta 3, neighbor pseudo	-1204.2	0
	333221		predicted exon	-189.6	0
55	335988		predicted exon	-122.6	0
	330574	AI984144 Hs.66713	hepatitis delta antigen-interacting prot	-2257.4	0
	312052	BE621697 Hs.14317	nucleolar protein family A, member 3 (H/	-359.2	0
	319568	AF131781 Hs.84753	hypothetical protein FLJ12442	-874.6	0
	337113		predicted exon	-24.6	0
	335149		predicted exon	-191.8	0

TABLE 6A

Table 6A shows the accession numbers for those pkeys lacking unigenelD's for Table 6. The pkeys in Table 7 lacking unigenelD's are represented within Tables 1-6A. For each probeset we have listed the gene cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
320925	1525201_1	D62892 D79755 D62760
321614	87866_1	H86161 AA054308 AA018955
313952	136885_1	F20956 AA129374 AA133740 AW819878
314648	293660_1	AW979268 AA878419 AA431342 AA431628
302749	458_107	M16951 M16952 M16948 M16949 M16950
312362	764066_1	AW015994 R39898 AW000978 AI598202 AI521706
312542	1522649_1	D60076 D60259 D61037
312642	1005225_1	AW052128 H51439 H51481
312986	171879_1	AA211586 F35799 AA211641 F29720 AW937387 AW937408
329350	c_x_hs	
329414	c_y_hs	
329440	c_y_hs	
329451	c_y_hs	
338033	CH22_6528FG_LINK_EM:AC00	
338038	CH22_6535FG_LINK_EM:AC00	
338116	CH22_6650FG_LINK_EM:AC00	
338158	CH22_6700FG_LINK_EM:AC00	
329732	c14_p2	
329745	c14_p2	
308106	AI476803	
329863	c14_p2	
338316	CH22_6944FG_LINK_EM:AC00	
308248	AI560919	
338388	CH22_7034FG_LINK_EM:AC00	
338442	CH22_7109FG_LINK_EM:AC00	
338645	CH22_7410FG_LINK_EM:AC00	
338728	CH22_7527FG_LINK_EM:AC00	
308877	AI832519	
338962	CH22_7838FG_LINK_DJ32110	
308886	AI833240	
333120	CH22_349FG_81_3_LINK_EM:A	
333121	CH22_350FG_81_4_LINK_EM:A	
333122	CH22_351FG_81_6_LINK_EM:A	
333123	CH22_352FG_81_7_LINK_EM:A	
333168	CH22_400FG_94_1_LINK_EM:A	
333169	CH22_401FG_94_2_LINK_EM:A	
333221	CH22_458FG_105_1_LINK_EM:	
326077	c17_hs	
326080	c17_hs	
326169	c17_hs	
326198	c17_hs	
326230	c17_hs	
333585	CH22_846FG_203_4_LINK_EM:	
333610	CH22_871FG_217_5_LINK_EM:	
335093	CH22_2423FG_492_3_LINK_EM	
335095	CH22_2425FG_492_5_LINK_EM	
335149	CH22_2484FG_499_5_LINK_EM	
326759	c20_hs	
333977	CH22_1254FG_309_6_LINK_EM	
326788	c20_hs	
335211	CH22_2550FG_511_2_LINK_EM	
305192	AA666019	
303973	AW512014	
303992	AW515800	
326946	c21_hs	
328229	c_6_hs	
328262	c_6_hs	

328418 c_7_hs
 328455 c_7_hs
 335697 CH22_3058FG_596_12_LINK_E
 5 328520 c_7_hs
 328548 c_7_hs
 335815 CH22_3187FG_618_3_LINK_EM
 328688 c_7_hs
 328695 c_7_hs
 10 307010 AI140014
 337113 CH22_5058FG_493_1_
 307041 AI144243
 328700 c_7_hs
 335946 CH22_3324FG_646_20_LINK_D
 335986 CH22_3366FG_654_10_LINK_D
 15 335987 CH22_3367FG_654_11_LINK_D
 335988 CH22_3368FG_654_12_LINK_D
 335989 CH22_3369FG_655_2_LINK_DJ
 335990 CH22_3370FG_655_4_LINK_DJ
 20 337214 CH22_5288FG_613_7_
 330020 c16_p2
 305989 AA888220
 328857 c_7_hs
 328937 c_8_hs
 25 328957 c_8_hs
 330187 c_4_p2
 337407 CH22_5607FG_755_1_
 337429 CH22_5633FG_762_3_
 330232 c_5_p2
 307414 AI242106
 30 330305 c_7_p2
 330306 c_7_p2
 337603 CH22_5896FG_LINK_C20H12.
 337953 CH22_6395FG_LINK_EM:AC00
 339236 CH22_8181FG_LINK_BA354I1
 35 339403 CH22_8384FG_LINK_BA232E1
 309349 AW051913
 325222 c10_hs
 325251 c10_hs
 40 318188 956161_1 AI792566 AI053836 AI054127 AI792489 AI288324
 309871 AW300366
 325544 c12_hs
 309931 AW341683
 332833 CH22_50FG_17_7_LINK_C20H1
 45 302779 33837_1 AJ235667 AJ235666 AJ235664 AJ235665 AJ235668 AJ235669 AJ235670
 302790 34168_1 AJ245245 AJ245247 AJ245257 AJ245248 AJ245254 AJ245256 AJ245253 AJ245203 AJ245250 AJ245252 AJ245243 AJ245204
 AJ245201 AJ245206 AJ245246 AJ245255 AJ245205 AJ245202 AJ245251 AJ245249 AJ245207 AJ245244
 332961 CH22_185FG_48_18_LINK_EM:
 325753 c14_hs
 50 327036 c21_hs
 325843 c16_hs
 325889 c16_hs
 304261 AA059387
 304275 AA070605
 55 334376 CH22_1670FG_379_8_LINK_EM
 327220 c_1_hs
 304363 AA206045
 334458 CH22_1757FG_391_2_LINK_EM
 327365 c_1_hs
 327373 c_2_hs
 60 334616 CH22_1923FG_411_15_LINK_E
 327414 c_2_hs
 327568 c_3_hs
 336034 CH22_3419FG_678_5_LINK_DJ
 336059 CH22_3445FG_684_2_LINK_DJ
 65 334834 CH22_2148FG_439_3_LINK_EM
 304782 AA582081
 304876 AA595765
 327747 c_5_hs
 70 336228 CH22_3626FG_730_4_LINK_DA
 329073 c_x_hs
 329088 c_x_hs
 304969 AA614406
 327844 c_5_hs
 327876 c_6_hs
 75 306352 AA961367
 331131 genbank_R54797 R54797

WO 02/079492

PCT/US02/04915

331139 genbank_R65706 R65706
331420 675963_1 AW452904 AW449414 BE467906 AI298565 BE549932 BE326357 F04362

TABLE 6B

Table 6B shows the genomic positioning for those pkeys lacking unigene ID's and accession numbers in Table 6. The pkeys in Table 7 lacking unigenelD's are represented within Tables 1-6B. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
332961	Dunham, I. et.al.	Plus	2521424-2521555
333221	Dunham, I. et.al.	Plus	3978070-3978187
333585	Dunham, I. et.al.	Plus	6234778-6234894
333610	Dunham, I. et.al.	Plus	6547007-6547116
334376	Dunham, I. et.al.	Plus	13902218-13902331
334458	Dunham, I. et.al.	Plus	14353496-14353572
334616	Dunham, I. et.al.	Plus	15176123-15176470
335149	Dunham, I. et.al.	Plus	21497441-21497587
335211	Dunham, I. et.al.	Plus	21774611-21774680
335697	Dunham, I. et.al.	Plus	25481456-25481649
335986	Dunham, I. et.al.	Plus	27967791-27967852
335987	Dunham, I. et.al.	Plus	27971413-27971481
335988	Dunham, I. et.al.	Plus	27977912-27978013
335989	Dunham, I. et.al.	Plus	27983788-27983860
335990	Dunham, I. et.al.	Plus	27988532-27988608
336034	Dunham, I. et.al.	Plus	29014404-29014590
337953	Dunham, I. et.al.	Plus	6827029-6827125
338033	Dunham, I. et.al.	Plus	8092128-8092271
338038	Dunham, I. et.al.	Plus	8138219-8138392
338316	Dunham, I. et.al.	Plus	17089711-17089988
338442	Dunham, I. et.al.	Plus	19980640-19980698
338962	Dunham, I. et.al.	Plus	29581892-29582020
332833	Dunham, I. et.al.	Minus	1119848-1119705
333120	Dunham, I. et.al.	Minus	3307508-3307427
333121	Dunham, I. et.al.	Minus	3308446-3308358
333122	Dunham, I. et.al.	Minus	3309596-3309531
333123	Dunham, I. et.al.	Minus	3310817-3310749
333168	Dunham, I. et.al.	Minus	3729896-3729788
333169	Dunham, I. et.al.	Minus	3730864-3730767
333977	Dunham, I. et.al.	Minus	8722928-8722725
334834	Dunham, I. et.al.	Minus	17182681-17182535
335093	Dunham, I. et.al.	Minus	21297367-21297214
335095	Dunham, I. et.al.	Minus	21292546-21292381
335815	Dunham, I. et.al.	Minus	26320518-26320421
335946	Dunham, I. et.al.	Minus	27487203-27487035
336059	Dunham, I. et.al.	Minus	29184079-29183969
336228	Dunham, I. et.al.	Minus	30904602-30904497
337113	Dunham, I. et.al.	Minus	21233344-21233237
337214	Dunham, I. et.al.	Minus	26095902-26095502
337407	Dunham, I. et.al.	Minus	31886652-31886567
337429	Dunham, I. et.al.	Minus	32086238-32086079
337603	Dunham, I. et.al.	Minus	1299296-1299194
338116	Dunham, I. et.al.	Minus	10614071-10613814
338158	Dunham, I. et.al.	Minus	11794465-11794343
338388	Dunham, I. et.al.	Minus	18662403-18662305
338645	Dunham, I. et.al.	Minus	24063839-24063775
338728	Dunham, I. et.al.	Minus	25949039-25948927
339236	Dunham, I. et.al.	Minus	32773355-32773202
339403	Dunham, I. et.al.	Minus	34050728-34050625
325222	6525287	Minus	22332-22473
325251	6682448	Minus	411693-411751
325544	6682452	Plus	171228-171286
325753	6682474	Plus	398512-398621
329745	6065779	Plus	174774-175142
329732	6065783	Plus	161252-161322
329863	6691797	Plus	196801-196971
325889	5867087	Plus	223829-223891

	325843	6552453	Minus	7126-7232
	330020	6671887	Plus	172397-172491
	326198	5867215	Minus	80295-80674
5	326230	5867230	Minus	301868-301972
	326169	5867255	Minus	128321-128388
	326077	6682495	Minus	312108-312168
	326080	6682495	Plus	478644-478847
	326759	6249610	Plus	97216-97311
10	326788	6682503	Plus	277132-277335
	326946	6004446	Minus	116677-116967
	327036	6531965	Plus	319951-320040
	327220	5867525	Minus	65701-65781
	327365	6552412	Minus	118133-118198
15	327414	5867750	Plus	102461-102586
	327373	5867792	Minus	8186-8742
	327568	5867811	Minus	46152-46287
	330187	6706138	Plus	212923-213020
	327747	5867947	Plus	115322-115498
20	327844	6249582	Minus	18895-18958
	330232	6013526	Plus	113655-113830
	328229	5868105	Minus	120936-121053
	327876	5868140	Plus	103882-104034
	328262	6381906	Plus	11867-12027
25	328688	5868262	Plus	626030-626094
	328700	5868264	Plus	764089-764203
	328695	5868264	Plus	318632-318695
	328418	5868409	Minus	258811-258894
	328455	5868431	Plus	385576-385633
30	328520	5868477	Plus	1942075-1942246
	328548	5868487	Plus	72301-72397
	328857	6381927	Minus	80557-81051
	330305	4877982	Minus	52269-52365
	330306	4877982	Plus	96161-96233
35	328937	5868500	Minus	1448241-1448333
	328957	6456773	Plus	219195-219297
	329073	5868596	Plus	37838-37956
	329088	5868608	Plus	116738-116950
	329350	6456785	Plus	98911-98969
40	329414	5868874	Plus	942555-942643
	329440	5868885	Plus	21943-22063
	329451	5868887	Plus	25974-26048

TABLE 7:

Table 7 depicts Seq ID No., UnigeneID, UnigeneTitle, Pkey, and ExAccn for all of the sequences in Table 8. Seq ID No links the nucleic acid and protein sequence information in Table 8 to Table 7.

Pkey:		Unique Eos probeset identifier number		
ExAccn:		Exemplar Accession number, Genbank accession number		
UnigeneID:		Unigene number		
Unigene Title:		Unigene gene title		
Seq.ID.No.:		Sequence Identification Number found in Table 8		
PKey	ExAccn	Unigene ID	Unigene Title	SEQ ID NO
101545	BE246154	Hs.154210	endothelial differentiation, sphingolipi	Seq ID 1 & 2
115819	AA486620	Hs.41135	endomucin-2	Seq ID 3 & 4
424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	Seq ID 5 & 6
102917	AI016712	Hs.287797	integrin, beta 1 (fibronectin receptor,	Seq ID 7 & 8
102915	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	Seq ID 9 & 10
105330	AW338625	Hs.22120	ESTs	Seq ID 11 & 12
107385	NM_005397	Hs.16426	podocalyxin-like	Seq ID 13 & 14
102024	AA301867	Hs.76224	EGF-containing fibulin-like extracellula	Seq ID 15 & 16
102024	AA301867	Hs.76224	EGF-containing fibulin-like extracellula	Seq ID 17 & 18
134416	X68264	Hs.211579	melanoma cell adhesion molecule	Seq ID 19 & 20
103036	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	Seq ID 21 & 22
104865	T79340	Hs.22575	B-cell CLL/lymphoma 6, member B (zinc fi	Seq ID 23 & 24
106124	H93366	Hs.7567	Homo sapiens cDNA: FLJ21962 fis, clone H	Seq ID 25 & 26
109001	AI056548	Hs.72116	hypothetical protein FLJ20992 similar to	Seq ID 27 & 28
104764	AI039243	Hs.278585	ESTs	Seq ID 29 & 30
133200	AB037715	Hs.183639	hypothetical protein FLJ10210	Seq ID 31 & 32
105263	AW388633	Hs.6682	solute carrier family 7, (cationic amino	Seq ID 33 & 34
102892	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	Seq ID 35 & 36
109456	AW956580	Hs.42699	ESTs	Seq ID 37 & 38
110906	AA035211	Hs.17404	ESTs	Seq ID 39 & 40
119073	BE245360	Hs.279477	ESTs	Seq ID 41 & 42
132050	AI267615	Hs.38022	ESTs	Seq ID 43 & 44
132490	NM_001290	Hs.4980	LIM domain binding 2	Seq ID 45 & 46
102283	AW161552	Hs.83381	guanine nucleotide binding protein 11	Seq ID 47 & 48
101714	M68874	Hs.211587	phospholipase A2, group IVA (cytosolic,	Seq ID 49 & 50
133975	C18356	Hs.295944	tissue factor pathway inhibitor 2	Seq ID 51 & 52
106793	H94997	Hs.16450	ESTs	Seq ID 53 & 54
118511	N75620	Hs.43157	ESTs	Seq ID 54 & 55
101447	M21305		gb:Human alpha satellite and satellite 3	Seq ID 56 & 57
314941	AA515902	Hs.130650	ESTs	Seq ID 58 & 59
332466	AB018259	Hs.118140	KIAA0716 gene product	Seq ID 60 & 61
313513	AW298600	Hs.141840	ESTs, Weakly similar to S59501 interfero	Seq ID 62 & 63
313556	AA628517	Hs.118502	ESTs	Seq ID 64 & 65
313665	AW751201	Hs.51233	ESTs	Seq ID 66 & 67
314372	AL040178	Hs.142003	ESTs	Seq ID 68 & 69
429276	AF056085	Hs.198612	G protein-coupled receptor 51	Seq ID 70 & 71
101345	NM_005795	Hs.152175	calcitonin receptor-like	Seq ID 72 & 73
418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecu	Seq ID 74 & 75
103850	AA187101	Hs.213194	hypothetical protein MGC10895	Seq ID 76 & 77
133260	AA403045	Hs.6906	Homo sapiens cDNA: FLJ23197 fis, clone R	Seq ID 78 & 79
101097	BE245301	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus	Seq ID 80 & 81
104786	AA027167	Hs.10031	KIAA0955 protein	Seq ID 82 & 83
132173	X89426	Hs.41716	endothelial cell-specific molecule 1	Seq ID 84 & 85
100420	D86983	Hs.118893	Melanoma associated gene	Seq ID 86 & 87
111018	AI287912	Hs.3628	mitogen-activated protein kinase kinase	Seq ID 88 & 89
108507	AI554545	Hs.68301	ESTs	Seq ID 90 & 91
104894	AF065214	Hs.18858	phospholipase A2, group IVC (cytosolic,	Seq ID 92 & 93
118511	N75620	Hs.43157	ESTs	Seq ID 94 & 95
125609	AA868063	Hs.104576	carbohydrate (keratan sulfate Gal-6) sul	Seq ID 96 & 97
101543	M31166	Hs.2050	pentaxin-related gene, rapidly induced b	Seq ID 98 & 99
102241	NM_007351	Hs.268107	multimerin	Seq ID 100 & 101
101560	AW958272	Hs.347326	intercellular adhesion molecule 2	Seq ID 102 & 103
103280	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula	Seq ID 104 & 105
105826	AA478756	Hs.194477	E3 ubiquitin ligase SMURF2	Seq ID 106 & 107
102804	NM_002318	Hs.83354	lysyl oxidase-like 2	Seq ID 108 & 109
131647	AA359615	Hs.30089	ESTs	Seq ID 110 & 111
103095	NM_005424	Hs.78824	tyrosine kinase with immunoglobulin and	Seq ID 112 & 113
103037	BE018302	Hs.2894	placental growth factor, vascular endoth	Seq ID 114 & 115
100405	AW291587	Hs.82733	nidogen 2	Seq ID 116 & 117
102012	BE259035	Hs.118400	singed (Drosophila)-like (sea urchin fas	Seq ID 118 & 119

	101261	D30857	Hs.82353	protein C receptor, endothelial (EPCR)	Seq ID 120 & 121
	105729	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds	Seq ID 122 & 123
	107216	D51069	Hs.211579	melanoma cell adhesion molecule	Seq ID 124 & 125
	131080	NM_001955	Hs.2271	endothelin 1	Seq ID 126 & 127
5	131486	F06972	Hs.27372	BMX non-receptor tyrosine kinase	Seq ID 128 & 129
	134299	AW580939	Hs.97199	complement component C1q receptor	Seq ID 130 & 131
	134983	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	Seq ID 132 & 133
	115827	AA428000	Hs.283072	actin related protein 2/3 complex, subun	Seq ID 134 & 135
10	133614	NM_003003	Hs.75232	SEC14 (S. cerevisiae)-like 1	Seq ID 136 & 137
	116483	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	Seq ID 138 & 139
	132546	M24283	Hs.168383	intercellular adhesion molecule 1 (CD54)	Seq ID 140 & 141
	133678	AW247252	NA	nucleoside phosphorylase	Seq ID 142 & 143
	130184	H58306	Hs.15165	retinoic acid induced 14	Seq ID 144 & 145
	134786	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous	Seq ID 146 & 147
15	129371	X06828	Hs.110802	von Willebrand factor	Seq ID 148 & 149
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	Seq ID 150 & 151
	322262	AA632012	Hs.188746	ESTs	Seq ID 152 & 153
	312173	AI821409	Hs.304471	EST	Seq ID 154 & 155
20	319795	AB037821	Hs.146858	protocadherin 10	Seq ID 156 & 157
	313978	AI870175	Hs.13957	ESTs	Seq ID 158 & 159
	306840	AI077477	Hs.307912	ESTs	Seq ID 160 & 161
	310272	AF216389	Hs.148932	sema domain, transmembrane domain (TM),	Seq ID 162 & 163
	310272	AF216389	Hs.148932	sema domain, transmembrane domain (TM),	Seq ID 164 & 165
25	315044	BE547674	Hs.204169	ESTs, Weakly similar to S65657 alpha-1C-	Seq ID 166 & 167
	321325	AB033100	Hs.300646	KIAA1274 protein (similar to mouse palad	Seq ID 168 & 169
	321325	AB033100	Hs.300646	KIAA1274 protein (similar to mouse palad	Seq ID 170 & 171
	303251	AF240635	Hs.115897	protocadherin 12	Seq ID 172 & 173
	302378	AL109712	Hs.296506	Homo sapiens mRNA full length insert cDN	Seq ID 174 & 175
30	319267	F11802	Hs.6818	ESTs	Seq ID 176 & 177
	310442	AW072215	Hs.208470	ESTs	Seq ID 178 & 179
	300469	BE301708	Hs.233955	hypothetical protein FLJ20401	Seq ID 180 & 181
	331237	W87874	Hs.25277	Homo sapiens cDNA FLJ10717 fis; clone NT	Seq ID 182 & 183
	330968	R44557	Hs.23748	ESTs	Seq ID 184 & 185
35	301822	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subuni	Seq ID 186 & 187
	422573	AW297985	Hs.295726	integrin, alpha V (vitronectin receptor	Seq ID 188 & 189
	133061	AI186431	Hs.296638	prostate differentiation factor	Seq ID 190 & 191
	135235	AW298244	Hs.266195	ESTs	Seq ID 192 & 193
	101192	BE247295	Hs.78452	solute carrier family 20 (phosphate tran	Seq ID 194 & 195
40	113195	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom	Seq ID 196 & 197
	101741	NM_003199	Hs.326198	transcription factor 4	Seq ID 198 & 199
	321911	AF026944	Hs.293797	ESTs	Seq ID 200 & 201
	320635	N50617	Hs.80506	small nuclear ribonucleoprotein polypept	Seq ID 202 & 203
	326230			NM_017643:Homo sapiens hypothetical prot	Seq ID 204 & 205
45	132968	AF234532	Hs.61638	myosin X	Seq ID 206 & 207
	135073	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f	Seq ID 208 & 209
	108937	AL050107	Hs.24341	transcriptional co-activator with PDZ-bi	Seq ID 210 & 211
	116430	AK001531	Hs.66048	hypothetical protein FLJ10669	Seq ID 212 & 213
	104877	AI138635	Hs.22968	Homo sapiens clone IMAGE:451939, mRNA se	Seq ID 214 & 215
50	122697	AA420683	Hs.98321	hypothetical protein FLJ14103	Seq ID 216 & 217
	112522	R68857	Hs.265499	ESTs	Seq ID 218 & 219
	304782	AA582081		gb:nn32h08.s1 NCI_CGAP_Gas1 Homo sapiens	Seq ID 220 & 221
	312802	AA644669	Hs.193042	ESTs	Seq ID 222 & 223
	302680	AW192334	Hs.38218	ESTs	Seq ID 224 & 225
55	326198			Phase 2 & 3 Exons	Seq ID 226 & 227
	331019	NM_006033	Hs.65370	lipase; endothelial	Seq ID 228 & 229

TABLE 8

Seq ID NO: 1 DNA sequence

Nucleic Acid Accession #: NM_001400

Coding sequence: 244-2208 (underlined sequences correspond to start and stop codons))

10	1	11	21	31	41	51	
	GTCTGGGGGCA	GCAGCAAGAT	GCGAAGCGAG	CCGTACAGAT	CCCCGGGCTCT	CCGAACGCAA	60
	CTTCGCCCTG	CTTGAGCGAG	GCTGCGGTTT	CCGAGGCCCT	CTCCAGCCAA	GGAAAAAGCTA	120
	CACAAAAAGC	CTGGATCACT	CATCGAACCA	CCCCTGAAGC	CAGTGAAGGC	TCTCTCGCCT	180
15	CGCCCTCTAG	CGTTCGTCTG	GAGTAGCGCC	ACCCCGGCTT	CCTGGGGACA	CAGGGTTGGC	240
	ACCATGGGGC	CCACCAGCGT	CCCCTGGTTC	AAGGCCCAAC	GCAGCTCGGT	CTCTGACTAC	300
	GTCAACTATG	ATATCATCGT	CCGGCATTAC	AACTACACGG	GAAAGCTGAA	TATCAGCGCG	360
	GACAAGGAGA	ACAGCATTAA	ACTGACCTCG	GTGGTGTTCA	TTCTCATCTG	CTGCTTTATC	420
	ATCCTGGAGA	ACATCTTTGT	CTTGCTGACC	ATTTGGAAAA	CCAAGAAATT	CCACCGACCC	480
20	ATGTACTATT	TTATTGGCAA	TCTGGCCCTC	TCAGACCTGT	TGGCAGGAGT	AGCCTACACA	540
	GCTAACCTGC	TCTGTCTGCG	GGCCACCACC	TACAAGCTCA	CTCCCGCCCA	GTGGTTTCTG	600
	CGGGAAGGGA	GTATGTTTGT	GGCCCTGTCA	GCCTCCGTGT	TCAGTCTCCT	CGCCATCGCC	660
	ATTGAGCGCT	ATATCACAA	CTGTGAAATG	AAACTCCACA	ACGGGAGCAA	TAACCTCCGC	720
	CTCTTCCTGC	TAATCAGCGC	CTGCTGGGTC	ATCTCCCTCA	TCCTGGGTGG	CCTGCCTATC	780
25	ATGGGCTGGA	ACTGCATCAG	TGCGCTGTCC	AGCTGCTCCA	CCGTGCTGCC	GCTCTACCAC	840
	AAGCACTATA	TCTCTTCTG	CACCACGGTC	TTCACCTGTC	TTCTGCTCTC	CATCGTCATT	900
	CTGTACTGCA	GAATCTACTC	CTTGGTCAGG	ACTCGGAGCC	GCCGCTGAC	GTTCCGCAAG	960
	AACATTTCCA	AGGCCAGCCG	CAGCTCTGAG	AAGTCGCTGG	CGCTGCTCAA	GACCGTAATT	1020
	ATCGTCTCGA	CGCTCTTCAT	CGCCTGCTGG	GCACCGCTCT	TCATCTGCT	CCTGCTGGAT	1080
30	GTGGGCTGCA	AGGTGAAGAC	CTGTGACATC	CTCTTCAGAG	CGGAGTACTT	CCTGGTGTTA	1140
	GCTGTGCTCA	ACTCCGGCAC	CAACCCCATC	ATTTACACTC	TGACCAACAA	GGAGATGCGT	1200
	CGGGCCTTCA	TCCGGATCAT	GTCTGTCTGC	AAGTGCCCGA	GCGGAGACTC	TGCTGGCAAA	1260
	TTCAAGCGAC	CCATCATCGC	CGGCATGGAA	TTCAAGCCGA	GCAAAATCGGA	CAATTCTCTC	1320
	CACCCCCAGA	AAGACGAAGG	GGACAACCCA	GAGACCATTG	TGTCTTCTGG	AAACGTCAAC	1380
35	TCTTCTTCTC	AGAACTGGAA	GCTGTCCACC	CACCGGAAGC	GCTCTTACT	TGGTCGCTGG	1440
	CCACCCAGT	GTTTGGAAAA	AAATCTCTGG	GCTTCGACTG	CTGCCAGGGA	GGAGCTGCTG	1500
	CAAGCCAGAG	GGAGGAAGGG	GGAGAATACG	AACAGCCTGG	TGGTGTGCGG	TGTTGGTGGG	1560
	TAGAGTTAGT	TCCTGTGAAC	AATGCACTGG	GAAGGGTGGA	GATCAGGTCC	CGGCCTGGAA	1620
	TATATATTCT	ACCCCCCTGG	AGCTTTGATT	TTGCACTGAG	CCAAAGGTCT	AGCATTGTCA	1680
40	AGCTCCTAAA	GGGTTTCATT	GGCCCTCCT	CAAAGACTAA	TGTCCCCTATG	TGAAAGCGTC	1740
	TCTTTGTCTG	GAGCTTTGAG	GAGATGTTTT	CCTTCACTTT	AGTTTCAAAC	CCAAGTGAGT	1800
	GTGTGCACTT	CTGCTTCTTT	AGGGATGCCC	TGTACATCCC	ACACCCACC	CTCCCTTCCC	1860
	TTCATACCCC	TCCTCAACGT	TCTTTACTTT	TATACTTTAA	CTACCTGAGA	GTTATCAGAG	1920
	CTGGGGTTGT	GGAAATGATG	ATCATCTATA	GCAATAGGC	TATGTTGAGT	ACGTAGGCTG	1980
45	TGGGAAGATG	AAGATGGTTT	GGAGGTGTAA	AACAATGTCC	TTGCTGAGG	CCAAAGTTTC	2040
	CATGTAAGCG	GGATCCGTTT	TTTGGAAATT	GGTTGAAGTC	ACTTTGATTT	CTTTAAAAAA	2100
	CATCTTTTCA	ATGAAATGAT	TTACCATTTG	ATATCCATTG	AAGCCGAAAT	CTGCATAAGG	2160
	AAGCCCACTT	TATCTAAATG	ATATTAGCCA	GGATCCTTGG	TGTCTTAGGA	GAAACAGACA	2220
	AGCAAAACAA	AGTGAAGAAC	GAATGGATTA	ACTTTTGCAA	ACCAAGGGAG	ATTTCTTAGC	2280
50	AAATGAGTCT	AACAAATATG	ACATCCGTCT	TTCCCACTTT	TGTTGATGTT	TATTTAGAAA	2340
	TCTTGTGTGA	TTCAATTTCA	GCAACAACAT	GTTGTATTTT	GTTGTGTTAA	AAGTACTTTT	2400
	CTTGATTTT	GAATGTATTT	GTTTCAGGAA	GAAGTCATTT	TATGGATTTT	TCTAACCCGT	2460
	GTTAACTTTT	CTAGAATCCA	CCCTCTTGTG	CCCTTAAGCA	TTACTTTAAC	TGGTAGGGAA	2520
	CGCCAGAACT	TTTAAGTCCA	GCTATTTCAT	AGATAGTAAT	TGAAGATATG	TATAAATATT	2580
55	ACAAAGAAATA	AAAATATATT	ACTGTCTCTT	TAGTATGGTT	TTCAAGTGCAA	TTAAACCGAG	2640
	AGATGTCTTG	TTTTTTTAAA	AAGAATAGTA	TTTAATAGGT	TTCTGACTTT	TGTGGATCAT	2700
	TTTGCACATA	GCTTTATCAA	CTTTTAAACA	TTAATAAACT	GATTTTTTTTA	AAG	

Seq ID NO: 2 Protein sequence:

Protein Accession #: NP_001391

65	1	11	21	31	41	51	
	MGPTSVPLVK	AHRSSVSDYV	NYDIIVRHYN	YTGKLNISAD	KENSIKLTSV	VFILICCFII	60
	LENIFVLLTI	WTKTKFHRPM	YYFIGNLALS	DLLAGVAYTA	NLLLSGATTY	KLTPAQWFLR	120
	EGSMFVALSA	SVPSLLAIAI	ERYITMLKMK	LHNGSNNFRL	FLLISACWVI	SLILGLPIM	180
70	GWNCISALSS	CSTVLPLYHK	HYILFCTTVF	TLLLLSIVIL	YCRYISLVRT	RSRRLTFRKN	240
	ISKASRSSEK	SLALLKTVII	VLSVFIACWA	PLFILLLLDV	GCKVKTDIL	FRAEYFLVLA	300
	VLSNGTNPII	YTLTNKEMRR	AFIRIMSCCK	CPSGDSAGKF	KRPPIAGMEF	SRSKSDNSSH	360
	PQKDEGDNPE	TIMSSGNVNS	SS				

5

10 Seq ID NO: 3 Nucleotide sequence:
Nucleic Acid Accession #: NM_016242
Coding sequence: 79-864 (underlined sequences correspond to start and stop codons))

15	1	11	21	31	41	51	
	AAGGCCCTGC	CAGCTTGGGA	GGGAATTGTC	CCTGCCTGCT	TCTGGAGAAA	GAAGATATTG	60
	ACACCATCTA	CGGGCACCAT	GGAACTGCTT	CAAGTGACCA	TTCTTTTCT	TCTGCCAGT	120
	ATTTGCAGCA	GTAACAGCAC	AGGTGTTTTA	GAGGCAGCTA	ATAATTCCT	TGTTGTACT	180
	ACAACAAAAC	CATCTATAAC	AACACCAAAC	ACAGAATCAT	TACAGAAAAA	TGTTGTCACA	240
20	CCAACAAC	GAACAACTCC	TAAAGGAACA	ATCACCAGT	AATTACTTAA	AATGTCTCTG	300
	ATGTCAACAG	CTACTTTT	AACAAGTAAA	GATGAAGGAT	TGAAAGCCAC	AACCACTGAT	360
	GTCAGGAAGA	ATGACTCCAT	CATTTCAAAC	GTAACAGTAA	CAAGTGTTAC	ACTTCCCAAT	420
	GCTGTTTCAA	CATTACAAAG	TTCCAAACCC	AAGACTGAAA	CTCAGAGTTC	AATTAAACA	480
	ACAGAAATAC	CAGGTAGTGT	TCTACAACCA	GATGCATCAC	CTTCTAAAAC	TGGTACATTA	540
25	ACCTCAATAC	CAGTTACAAT	TCCAGAAAC	ACCTCACAGT	CTCAAGTAAT	AGACACTGAG	600
	GGTGGAAAAA	ATGCAAGCAC	TTCAAGCAAC	AGCCGGTCTT	ATTCCAGTAT	TATTTTGCCG	660
	GTGGTTATTG	CTTTGATTGT	AATAACACTT	TCAGTATTG	TTCTGGTGGG	TTTGTACCGA	720
	ATGTCTGGA	AGGCAGATCC	GGGCACACCA	GAAAATGGAA	ATGATCAACC	TCAGTCTGAT	780
	AAAGAGAGCG	TGAAGCTTCT	TACCGTTAAG	ACAATTTCTC	ATGAGTCTGG	TGAGCACTCT	840
30	GCACAAGGAA	AAACCAAGAA	CTGACAGCTT	GAGGAATTCT	CTCCACACCT	AGGCAATAAT	900
	TACGCTTAAT	CTTCAGCTTC	TATGCACCAA	GCGTGGAAAA	GGAGAAAGTC	CTGCAGAATC	960
	AATCCCGACT	TCCATACCTG	CTGCTGG				

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Seq ID NO: 4 Protein sequence:
Protein Accession #: NP_057326

40	1	11	21	31	41	51	
	MELLQVTILF	LLPSICSSNS	TGVLEAANNS	LVVTTTKPSI	TPNTESLQK	NVVTPTTGTT	60
	PKGTTITNELL	KMSLMSTATF	LTSKDEGLKA	TTTDVRKNDS	IISNVTVTSV	TLPNAVSTLQ	120
	SSKPKTETQS	SIKTTEIPGS	VLQPDASPSK	TGTLTSIPVT	IPENTSQSQV	IDTEGGKNAS	180
45	TSATRSYSS	IILPVVIALI	VITLSVFLV	GLYRMCWKAD	PSTPENGNDQ	PQSDKESVKL	240
	LTVKTIISHES	GEHSAQGTKK	N				

Seq ID NO: 5 Nucleotide sequence:
Nucleic Acid Accession #: NM_002205
Coding sequence: 24..3173 (underlined sequences correspond to start and stop codons)

55	1	11	21	31	41	51	
	CAGGACAGGG	AAGAGCGGGC	GCTATGGGGA	GCCGGACGCC	AGAGTCCCT	CTCCACGCCG	60
	TGCAGCTGCG	CTGGGGCCCC	CGGCGCCGAC	CCCCGCTCGT	GCCGCTGCTG	TGCTGCTCG	120
	TGCCGCCGCC	ACCCAGGGTC	GGGGGCTTCA	ACTTAGACGC	GGAGGCCCA	GCAGTACTCT	180
	CGGGGCCCCC	GGGCTCCTTC	TTCGGATTCT	CAGTGGAGTT	TTACCGGCCG	GGAACAGACG	240
	GGGTCACTGT	GCTGGTGGGA	GCACCAAGG	CTAATACCAG	CCAGCCAGGA	GTGCTGCAGG	300
60	GTGGTGCTGT	CTACCTCTGT	CCTTGGGGTG	CCAGCCCCAC	ACAGTGACAC	CCCATTGAAT	360
	TTGACAGCAA	AGGCTCTCGG	CTCCTGGAGT	CCTCACTGTC	CAGCTCAGAG	GGAGAGGAGC	420
	CTGTGGAGTA	CAAGTCCTTG	CAGTGGTTCG	GGGCAACAGT	TCGAGCCCAT	GGCTCCTCCA	480
	TCTTGGCATG	CGCTCCACTG	TACAGCTGGC	GCACAGAGAA	GGAGCCACTG	AGCGACCCCG	540
	TGGGCACCTG	CTACCTCTCC	ACAGATAACT	TCACCCGAAT	TCTGGAGTAT	GCACCTTGCC	600
65	GCTCAGATTT	CAGCTGGGCA	GCAGGACAGG	GTTACTGCCA	AGGAGGCTTC	AGTGCCGAGT	660
	TCACCAAGAC	TGGCCGTGTG	GTTTTAGGTG	GACCAGGAAG	CTATTCTTGG	CAAGGCCAGA	720
	TCCTGTCTGC	CACTCAGGAG	CAGATTGCAG	AATCTTATTA	CCCCGAGTAC	CTGATCAACC	780
	TGGTTCAGGG	GCAGCTGCAG	ACTCGCCAGG	CCAGTTCCAT	CTATGATGAC	AGCTACCTAG	840
70	GATACTCTGT	GGCTGTTGGT	GAATTCAGTG	GTGATGACAC	AGAAGACTTT	GTTGCTGGTG	900
	TGCCCAAAGG	GAACCTCACT	TACGGCTATG	TCACCATCCT	TAATGGCTCA	GACATTCGAT	960
	CCCTCTACAA	CTTCTCAGGG	GAACAGATGG	CCTCCTACTT	TGGCTATGCA	GTGGCCGCCA	1020
	CAGACGTCAA	TGGGGACGGG	CTGGGATGACT	TGCTGGTGGG	GGCACCCCTG	CTCATGGATC	1080
	GGACCCCTGA	CGGGCGGCCT	CAGGAGGTGG	GCAGGTGCTA	CGTCTACCTG	CAGCACCCAG	1140
75	CCGGCATAGA	GCCCCACGCC	ACCCCTTACC	TCATGGGCCA	TGATGAGTTT	GGCCGATTGG	1200
	GCAGCTCCTT	GACCCCTCG	GGGGACCTGG	ACCAGGATGG	CTACAATGAT	GTGGCCATCG	1260
	GGGCTCCCTT	TGGTGGGGAG	ACCCAGCAGG	GAGTAGTGTT	TGTATTTCCT	GGGGGCCCAG	1320

	GAGGGCTGGG	CTCTAAGCCT	TCCCAGGTTC	TGCAGCCCCT	GTGGGCAGCC	AGCCACACCC	1380
	CAGACTTCTT	TGGCTCTGCC	CTTCGAGGAG	GCCGAGACCT	GGATGGCAAT	GGATATCCTG	1440
	ATCTGATTGT	GGGGTCTTTT	GGTGTGGACA	AGGCTGTGGT	ATACAGGGGC	CGCCCCATCG	1500
	TGTCCGCTAG	TGCCTCCCTC	ACCATCTTCC	CCGCCATGTT	CAACCCAGAG	GAGCGGAGCT	1560
5	GCAGCTTAGA	GGGGAACCTT	GTGGCCTGCA	TCAACCTTAG	CTTCTGCCTC	AATGCTTCTG	1620
	GAAAACACGT	TGCTGACTCC	ATTGCTTTCA	CAGTGGAACCT	TCAGCTGGAC	TGGCAGAAGC	1680
	AGAAGGGAGG	GGTACGGCGG	GCACTGTTCC	TGGCCTCCAG	GCAGGCAACC	CTGACCCAGA	1740
	CCCTGCTCAT	CCAGAATGGG	GCTCGAGAGG	ATTGAGAGAG	GATGAAGATC	TACCTCAGGA	1800
10	ACGAGTCAGA	ATTTGAGAGC	AAACTCTCGC	CGATTACACAT	CGCTCTCAAC	TTCTCCTTGG	1860
	ACCCCCAAGC	CCCAGTGGAC	AGCCACGGCC	TCAGGCCAGC	CCTACATTAT	CAGAGCAAGA	1920
	GCCGGATAGA	GGACAAGGCT	CAGATCTTGC	TGGACTGTGG	AGAAGACAAC	ATCTGTGTGC	1980
	CTGACCTGCA	GCTGGAAGTG	TTTGGGGAGC	AGAACCATGT	GTACCTGGGT	GACAAGAATG	2040
	CCCTGAACCT	CACCTTCCAT	GCCGAGAATG	TGGGTGAGGG	TGGCGCCTAT	GAGGCTGAGC	2100
	TTCCGGTTCAC	CGCCCCCTCA	GAGGCTGAGT	ACTCAGGACT	CGTCAGACAC	CCAGGGAACT	2160
15	TCTCCAGCCT	GAGCTGTGAC	TACTTTGCCG	TGAACCAGAG	CCGCCTGCTG	GTGTGTGACC	2220
	TGGGCAACCC	CATGAAGGCA	GGAGCCAGTC	TGTGGGGTGG	CCTTCGGTTT	ACAGTCCCTC	2280
	ATCTCCGGGA	CACCTAAGAAA	ACCATCCAGT	TTGACTTCCA	GATCCTCAGC	AAGAATCTCA	2340
	ACAACCTCGCA	AAGCGACGTG	GTTTCCTTTT	GGCTCTCCGT	GGAGGCTCAG	GCCCAGGTCA	2400
	CCCTGAACGG	TGTCTCCAAG	CCTGAGGCGC	TGCTATTCCC	AGTAAGCGAC	TGGCATCCCC	2460
20	GAGACCAGCC	TCAGAAGGAG	GAGGACCTGG	GACCTGCTGT	CCACCATGTC	TATGAGCTCA	2520
	TCAACCAAGG	CCCCAGCTCC	ATTAGCCAGG	GTGTGCTGGA	ACTCAGCTGT	CCCCAGGCTC	2580
	TGGAAGGTCA	GCAGCTCCTA	TATGTGACCA	GAGTTACGGG	ACTCAACTGC	ACCACCAATC	2640
	ACCCCATTA	CCCAAAGGGC	CTGGAGTTGG	ATCCCGAGGG	TCCCTGCGAC	CACCAGCAAA	2700
	AACGGGAAGC	TCCAAGCCGC	AGCTCTGCTT	CCTCGGGACC	TCAGATCCTG	AAATGCCCCG	2760
25	AGGCTGAGTG	TTTCAGGCTG	CGCTGTGAGC	TCGGGGCCCT	GCACCAACAA	GAGAGCCAAA	2820
	GTCTGCAGTT	GCATTTCCGA	GTCTGGGCCA	AGACTTTCTT	GCAGCGGGAG	CACCAGCCAT	2880
	TTAGCCTGCA	GTGTGAGGCT	GTGTACAAAG	CCCTGAAGAT	GCCCTACCGA	ATCCTGCCTC	2940
	GGCAGCTGCC	CCAAAAGAG	CGTCAGGTGG	CCACAGCTGT	GCAATGGACC	AAGGCAGAAG	3000
	GCAGCTATGG	CGTCCCACCT	TGGATCATCA	TCCTAGCCAT	CCTGTTTGGC	CTCCTGCTCC	3060
30	TAGGTCTACT	CATCTACATC	CTCTACAAGC	TTGGATTCTT	CAAACGCTCC	CTCCCATATG	3120
	GCACCGCCAT	GGAAAAAGCT	CAGCTCAAGC	CTCCAGCCAC	CTCTGATGCC	TGAGTCTCTC	3180
	CAATTTTCTA	CTCCCATTTCC	TGAAGAACCA	GTCCCCCACC	CCTCATTCTA	CTGAAAAGGA	3240
	GGGGTCTGGG	TACTTCTTGA	AGGTGCTGAC	GGCCAGGGAG	AAGCTCCTCT	CCCCAGCCCA	3300
	GAGACATAGT	TGAAGGGCCA	GAGCCAGGGG	GGTGAGGAGC	TGGGGATCCC	TCCCCCCCAT	3360
35	GCACTGTGAA	GGACCCTTGT	TTACACATAC	CCTCTTTCATG	GATGGGGGAA	CTCAGATCCA	3420
	GGGACAGAGG	CCAGCCTCTC	CTGAAGCCTT	TGCATTTTGG	AGAGTTTCTT	GAAACAACCTG	3480
	GAAAGATAAC	TAGGAATATC	ATTCACAGTT	CTTTGGGCCA	GACATGCCAC	AAGGACTTCC	3540
	TGTCCAGCTC	CAACCTGCAA	AGATCTGTCC	TCAGCCTTGC	CAGAGATCCA	AAAGAAGCCC	3600
40	CCAGTAAGAA	CCTGGAACCT	GGGGAGTTAA	GACCTGGCAG	CTCTGGACAG	CCCCACCCCTG	3660
	GTGGGCCAAC	AAAGAACAAT	AACTATGCAT	GGTGCCCCAG	GACCAGCTCA	GGACAGATGC	3720
	CACAAGGATA	GATGCTGGCC	CAGGGCCAGA	GCCCAGCTCC	AAGGGGAATC	AGAACTCAAA	3780
	TGGGGCCAGA	TCCAGCCTGG	GGTCTGGAGT	TGATCTGGAA	CCAGACTCA	GACATTGGCA	3840
	CCAATCCAGG	CAGATCCAGG	ACTATATTTG	GGCCTGCTCC	AGACCTGATC	CTGGAGGCC	3900
	AGTTTACCCT	GATTTAGGAG	AAGCCAGGAA	TTTCCCAGGA	CCTGAAGGGG	CCATGATGGC	3960
45	AACAGATCTG	GAACCTCAGC	CTGGCCAGAC	ACAGGCCCTC	CCTGTTCCCC	AGAGAAAGGG	4020
	GAGCCCACTG	TCCTGGGCCT	GCAGAAATTTG	GGTCTGCGCT	GCCAGCTGCA	CTGATGCTGC	4080
	CCCTCATCTC	TCTGCCCAAC	CCTTCCCTCA	CCTTGGCACC	AGACACCCAG	GACTTATTTA	4140
	AACTCTGTTG	CAAGTGCAAT	AAATCTGACC	CAGTGCCCCC	ACTGACCAGA	ACTAGAAAAA	4200
50	AAAA						

Seq ID NO: 6 Protein sequence:
Protein Accession #: NP_002196.1

55	1	11	21	31	41	51	
	MGSRTPEPESPL	HAVQLRWGPR	RRPPLVPLLL	LLVPPPPRVG	GFNLDAAEAPA	VLSGPPGSGFF	60
	GFSVEFYRPG	TDGVSVLVGA	PKANTSQPGV	LQGGAVYLCF	WGASPTQCTP	IEFDSKGSRL	120
	LESSLSSESG	EBPVEYKSLQ	WFGATVRAHG	SSILACAPLY	SWRTEKEPLS	DPVGTCTYLS	180
60	DNFTRILEYA	PCRSDFSWAA	GQGYCQGGFS	AEFTKTGRV	LGGPGSYFWQ	GQILSATQEQ	240
	IAESYYPEYL	INLVQGQLQT	RQASSIYDDS	YLGYSVAVGE	FSGDDTEDFV	AGVPKGNLTY	300
	GYVTILNGSD	IRSLYNFSGE	QMASYFGYAV	AATDVNGDGL	DDLLVGAPLL	MDRTPDGRPQ	360
	EVGRVYVYLQ	HPAGIEPTPT	LTLTGHDEFG	RFGSSLTPLG	DLDDQDGYNDV	AIGAPFGGET	420
	QQGVVVFVFP	GPGLGSKSPS	QVLQPLWAAS	HTPDFFGSAL	RGRDRDLGNG	YPDILVGSFG	480
65	VDKAVVYRGR	PIVSASASLT	IFPAMFNPEE	RSCSLBGNPV	ACINLSFCLN	ASGKHVADSI	540
	GFTVELQLDW	QKQKGGVRR	LFLASRQATL	TQTLLIQNGA	REDCREMKIY	LRNESEFRDK	600
	LSPIHIALNF	SLDPQAPVDS	HGLRPAALHYQ	SKSRIEDKAQ	ILDCGEDNI	CVPDLQLEVF	660
	GEQNHVYLG	KNALNLTFA	QNVGEGGAYE	AELRVTAPE	AEYSGLVVRH	GNFSSLSCDY	720
	FAVNQSRLLV	CDLGNPMKAG	ASLWGLRFT	VPHLRDTKKT	IQDFDQILSK	NLNNSQSDVV	780
70	SPRLSVEAQA	QVTLNGVSKP	EAVLFPVSDW	HPRDQPQKEE	DLGPAVHHVY	ELINQGPSSI	840
	SQGVLELSCP	QALEGQQLLY	VTRVTGLNCT	TNHPINPKGL	ELDPEGSLHH	QQKREAPSR	900
	SASSGPQILK	CPBAECFRLR	CELGPLHQQE	SQSLQLHFRV	WAKTFLLQREH	QPFSLQCEAV	960
	YKALKMPYRI	LPRQLPQKER	QVATAVQWTK	AEGSYGVPLW	IIILAILFGL	LLLGLLLIYL	1020
75	YKLGFFKRSL	PYGTAMEKAQ	LKPPATSDA				

Seq ID NO: 7 Nucleotide sequence:

Nucleic Acid Accession #: NM_002211

Coding sequence: 104..2500 (underlined sequences correspond to start and stop codons)

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15
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45
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55
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70

1	11	21	31	41	51	
GTCCGCCAAA	ACCTGCGCGG	ATAGGGAAGA	ACAGCACCCC	GGCGCCGATT	GCCGTACCAA	60
ACAAGCCTAA	CGTCCGCTGG	GCCCGGACG	CCGCGCGGAA	AAGATGAATT	TACAACCAAT	120
TTTCTGGATT	GGACTGATCA	GTTTCAGTTG	CTGTGTGTTT	GCTCAAACAG	ATGAAAATAG	180
ATGTTTAAAA	GCAATAGCCA	AATCATGTGG	AGAATGTATA	CAAGCAGGGC	CAAATTGTGG	240
GTGGTGCACA	AATTCAACAT	TTTTACAGGA	AGGAATGCCT	ACTTCTGCAC	GATGTGATGA	300
TTTAGAAGCC	TTAAAAAAGA	AGGGTTGCC	TCCAGATGAC	ATAGAAAATC	CCAGAGGCTC	360
CAAAGATATA	AAGAAAAATA	AAAATGTAAC	CAACCGTAGC	AAAGGAACAG	CAGAGAAGCT	420
CAAGCCAGAG	GATATTACTC	AGATCCAACC	ACAGCAGTTG	GTTTTGCGAT	TAAGATCAGG	480
GGAGCCACAG	ACATTTACAT	TAAAATTCAA	GAGAGCTGAA	GACTATCCCA	TTGACCTCTA	540
CTACCTTATG	GACCTGTCTT	ATTCAATGAA	AGACGATTTG	GAGAATGTAA	AAAGTCTTGG	600
AACAGATCTG	ATGAATGAAA	TGAGGAGGAT	TACTTCGGAC	TTCAGAATTG	GATTTGGCTC	660
ATTTGTGGAA	AAGACTGTGA	TGCCTTACAT	TAGCACAACA	CCAGCTAAGC	TCAGGAACCC	720
TTGCACAAGT	GAACAGAACT	GCACCACCCC	ATTTAGCTAC	AAAAATGTGC	TCAGTCTTAC	780
TAATAAAGGA	GAAGTATTTA	ATGAACTTGT	TGGAAGACAG	CGCATATCTG	GAAATTGGGA	840
TTCTCCAGAA	GGTGGTTTCG	ATGCCATCAT	GCAAGTTGCA	GTTTGTGGAT	CACTGATTGG	900
CTGGAGGAAT	GTTACACGGC	TGCTGGTGT	TTCCACAGAT	GCCGGGTTTC	ACTTTGCTGG	960
AGATGGGAAA	CTTGGTGGCA	TTGTTTACC	AAATGATGGA	CAATGTCACC	TGGAATAATA	1020
TATGTACACA	ATGAGCCATT	ATTATGATTA	TCCTTCTATT	GCTCACCTTG	TCCAGAAACT	1080
GAGTGAATAA	AATATTTCAG	CAATTTTTCG	AGTTACTGAA	GAATTTTCAGC	CTGTTTACAA	1140
GGAGCTGAAA	AACCTTGATCC	CTAAGTCAGC	AGTAGGAACA	TTATCTGCAA	ATTCTAGCAA	1200
TGTAATTCAG	TTGATCATTG	ATGCATACAA	TTCCCTTTCC	TCAGAAGTCA	TTTTGGAAAA	1260
CGGCAAAATG	TCAGAAGGAG	TAACAATAAG	TTACAAATCT	TACTGCAAGA	ACGGGGTGAA	1320
TGGAACAGGG	GAAAATGGAA	GAAAATGTTT	CAATATTTCC	ATTGGAGATG	AGGTTCAATT	1380
TGAAATTAGC	ATAACTTCAA	ATAAGTGTC	AAAAAAGGAT	TCTGACAGCT	TTAAAATTAG	1440
GCCTCTGGGC	TTTACGGAGG	AAGTAGAGGT	TATTCTTCAG	TACATCTGTG	AATGTGAATG	1500
CCAAAGCGAA	GGCATCCCTG	AAAGTCCCAA	GTGTCATGAA	GGAAATGGGA	CATTGTAGTG	1560
TGGCGCGTGC	AGGTGCAATG	AAGGGCGTGT	TGGTAGACAT	TGTGAATGCA	GCACAGATGA	1620
AGTTAACAGT	GAAGACATGG	ATGCTTACTG	CAGGAAAGAA	AACAGTTCAG	AAATCTGCAG	1680
TAACAATGGA	GAGTGCCTCT	GCGGACAGTG	TGTTTGTAGG	AAGAGGGATA	ATACAAATGA	1740
AATTTATTTCT	GGCAAAATCT	GCGAGTGTGA	TAATTTCAAC	TGTGATAGAT	CCAATGGCTT	1800
AATTTGTGGA	GGAAATGGTG	TTTGCAAGTG	TCGTGTGTGT	GAGTGCAACC	CCAAGTACAC	1860
TGGCAGTGCA	TGTGACTGTT	CTTTGGATAC	TAGTACTTGT	GAAGCCAGCA	ACGGACAGAT	1920
CTGCAATGGC	CGGGGCATCT	GCGAGTGTGG	TGCTGTGAAG	TGTACAGATC	CGAAGTTTCA	1980
AGGGCAAACG	TGTGAGATGT	GTCAGACCTG	CCTTGGTGTG	TGTGCTGAGC	ATAAAGAATG	2040
TGTTTCAAGT	AGAGCCTTCA	ATAAAGGAGA	AAAGAAAGAC	ACATGCACAC	AGGAATGTTT	2100
CTATTTTAAAC	ATTACCAAGG	TAGAAAGTCG	GGACAAATTA	CCCCAGCCCG	TCCAACCTGA	2160
TCCTGTGTCC	CATTGTAAAG	AGAAGGATGT	TGACGACTGT	TGTTTCTATT	TTACGTATTC	2220
AGTGAATGGG	AACAACGAGG	TCATGTTTCA	TGTTGTGGAG	AATCCAGAGT	GTCCCACTGG	2280
TCCAGACATC	ATTCCAATTG	TAGCTGGTGT	GGTTGCTGGA	ATTGTTCTTA	TTGGCCTTGC	2340
ATTACTGCTG	ATATGGAAGC	TTTAAATGAT	AATTCATGAC	AGAAGGGAGT	TTGCTAAATT	2400
TGAAAAGGAG	AAAATGAATG	CCAAATGGGA	CACGGGTGAA	AATCCTATT	ATAAGAGTGC	2460
CGTAACAAC	GTGGTCAATC	CGAAGTATGA	GGGAAAATGA	GTACTGCCCG	TGCAATCCC	2520
ACAACACTGA	ATGCAAAGTA	GCAATTTCCA	TAGTCACAGT	TAGGTAGCTT	TAGGGCAATA	2580
TTGCCATGGT	TTTACTCATG	TGCAGGTTT	GAAAATGTAC	AATATGTATA	ATTTTAAAA	2640
TGTTTATTAT	TTTTGAAAAT	AATGTTGTAA	TTCATGCCAG	GGACTGACAA	AAGACTTGAG	2700
ACAGGATGGT	TATTCTTGTC	AGCTAAGGTC	ACATTGTGCC	TTTTTGACCT	TTTCTTCTG	2760
GACTATTGAA	ATCAAGCTTA	TTGGATTAA	TGATATTCT	ATAGCGATTG	AAAGGGCAAT	2820
AGTTAAAGTA	ATGAGCATGA	TGAGAGTTTC	TGTTAATCAT	GTATTAAAAC	TGATTTTATG	2880
CTTTACATAT	GTCAGTTTGC	AGTTATGCAG	AATCCAAAGT	AAATGTCCTG	CTAGCTAGTT	2940
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CTGAAAGACA	AGTATGTTGA	GAGTTGCTGG	TGTAAAATAC	GTTTGAAATA	GTTGATCTAC	3060
AAAGGCCATG	GGAAAATTC	AGAGAGTTAG	GAAGGAAAAA	CCAATAGCTT	TAAAACCTGT	3120
GTGCCATTTT	AAGAGTTACT	TAATGTTTGG	TAACCTTTAT	GCCTTCACTT	TACAAATTCA	3180
AGCCTTAGAT	AAAAGAACCG	AGCAATTTTC	TGCTAAAAAG	TCCTTGATTT	AGCACTATTT	3240
ACATACAGGC	CATACTTTAC	AAAGTATTTG	CTGAATGGGG	ACCTTTTGAG	TGAATTTAT	3300
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TGTATTGTTT	TGCAATTTTG	GGGTAAGACT	TTTTTATGAG	TACTTTTCT	TGAAGTTT	3420
AGCGGTCAAT	TTGCCTTTT	AATGAACATG	TGAAGTTATA	CTGTGGCTAT	GCAACAGCTC	3480
TCACCTACGC	GAGTCTTACT	TTGAGTTAGT	GCCATAACAG	ACCACTGTAT	GTTTACTTCT	3540
CACCATTTGA	GTTGCCATC	TTGTTTCA	CTAGTCACAT	TCTTGTTTTA	AGTGCCTTTA	3600
GTTTTAACAG	TTCA					

Seq ID NO: 8 Protein sequence:

Protein Accession #: NP_002202

75
1 11 21 31 41 51
| | | | | |
MNLQPIFWIG LISSVCCVFA QTDENRCLKA NAKSCGECIQ AGPNCGWCTN STFLQEGMPT 60

SARCDLEAL KKKGCPPDDI ENPRGSKDIK KNKNVTNRSK GTAEKLPED ITQIQPQQLV 120
 LRLRSGEPT FTLKFKRAED YPIDLYLMD LSYSMKDDLE NVKSLGTDLM NEMRRITSDF 180
 RIGFGSFVEK TVMPYISTTP AKLRNPCTSE QNCTSPFSYK NVLSLTNKGE VFNELVGKQR 240
 ISGNLDSPEG GFDAMQVAV CGSLIGWRNV TRLLVFSSTA GFHFAGDGKL GGIVLPNDGQ 300
 5 CHLENNMYTM SHYDYPSIA HLVQKLSENN IQTIFAVTEE FQPVYKELKN LIPKSAVGTL 360
 SANSSNVIQL IIDAYNSLSS EVILENGKLS EGVITISYKSY CKNGVNGTGE NGRKCSNISI 420
 GDEVQFEISI TSNKCPKKDS DSFKIRPLGF TEEVEVILQY ICECECQSEG IPESPKCHEG 480
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 10 ASNGQICNGR GICECGVCKC TDFKFQGGTC EMCQTCLGVC AEHKECVQCR AFNKGEKDT 660
 CTQECSEYFNI TKVESRDKLP QPVQDPVSH CKEKDVDDCW FYFTYSVNGN NEVMVHVVEN 720
 PECPTGPDII PIVAGVVAGI VLIGLALLLI WKLLMIHHR REFAKFEKEK MNAKWDGTGEN 780
 PIYKSAVTTV VNPKYEGK

15 Seq ID NO: 9 Nucleotide sequence:
 Nucleic Acid Accession #: NM_002425
 Coding sequence: 23..1453 (underlined sequences correspond to start and stop codons)

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 AAAGAAGGTA AGGGCAGTGA GAATGATGCA TCTTGCAATC CTTGTGCTGT TGTGTCTGCC 60
 AGTCTGCTCT GCCTATCCTC TGAGTGGGGC AGCAAAAGAG GAGGACTCCA ACAAGGATCT 120
 TGCCAGCAA TACCTAGAAA AGTACTACAA CCTCGAAAAG GATGTGAAAC AGTTTAGAAG 180
 25 AAAGGACAGT AATCTCATTT TTAATAAAT CCAAGGAATG CAGAAGTTCC TTGGGTTGGA 240
 GGTGACAGGG AAGCTAGACA CTGACACTCT GGAGGTGATG CGCAAGCCCA GGTGTGGAGT 300
 TCCTGACGTT GGTCACTTCA GCTCCTTTCC TGGCATGCCG AAGTGGAGGA AAACCCACCT 360
 TACATACAGG ATTGTGAATT ATACACCAGA TTTGCCAAGA GATGCTGTTG ATTCTGCCAT 420
 TGAGAAAGCT CTGAAAGTCT GGGAAGAGGT GACTCCAATC ACATCTCTCA GGCTGTATGA 480
 30 AGGAGAGGCT GATATAATGA TCTCTTTCGC AGTTAAAGAA CATGGAGACT TTTACTCTTT 540
 TGATGGCCCA GGACACAGTT TGGCTCATGC CTACCCACCT GGACCTGGGC TTTATGGAGA 600
 TATTCACCTT GATGATGATG AAAAATGGAC AGAAGATGCA TCAGGCACCA ATTTATTCCT 660
 CGTTGCTGCT CATGAAGTTC GCCACTCCCT GGGGCTCTTT CACTCAGCCA AACTGAAGC 720
 TTTGATGTAC CCACTCTACA ACTCATTAC AGAGCTCGCC CAGTCCGCC TTTGCAAGA 780
 35 TGATGTGAAT GGCATTCACT TCTCTACGG ACCTCCCCCT GCCTCTACTG AGGAACCCCT 840
 GGTGCCCCA AAATCTGTTC CTTCGGGATC TGAGATGCCA GCCAAGTGTG ATCCTGCTTT 900
 GTCTCTCGAT GCCATCAGCA CTCTGAGGGG AGAATATCTG TTCTTTAAAG ACAGATATTT 960
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 CTCTCTTCCA TCATATTTGG ATGCTGCATA TGAAGTTAAG AGCAGGGACA CCGTTTTTAT 1080
 40 TTTTAAAGGA AATGAGTTCT GGGCCATCAG AGGAAATGAG GTACAAGCAG GTTATCCAAG 1140
 AGGCATCCAT ACCCTGGGTT TTCCTCCAAC AGCGGACAAA TACTGGAGAT TTGATGAAAA 1200
 CAAGGAAAAAG AAGAAAAACAT ACTTCTTTCG AGCGGACAAA TACTGGAGAT TTGATGAAAA 1260
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 45 ACAGTTTGAG TTTGACCCCA ATGCCAGGAT GGTGACACAC ATATTAAAGA GTAACAGCTG 1440
 GTTACATTGC TAGGCGAGAT AGGGGGAAGA CAGATATGGG TGTTTTAAAT AAATCTAATA 1500
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 CTT

55 Seq ID NO: 10 Protein sequence:
 Protein Accession #: NP_002416

1 11 21 31 41 51
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 TPDLPRDAVD SAIEKALKVW EEVTPLTFSR LYEGEADIMI SFAVKEHGDF YSFDGPGHSL 180
 AHAYPPGPGY YGDIHFDDDE KWTEASGTN LFLVAAHELK HSLGLFHSAN TEALMYPLYN 240
 SFTELAQFRL SQDDVNGIQS LYGPPPASTE EPLVPTKSVS SGSEMPAKCD PALSFDAIST 300
 LRGEYLFFKD RYFWRRSHWN PEPEFHLISA FWPSLPSYLD AAYEVNSRDT VFIFKNEFW 360
 65 AIRGNEVQAG YPRGIHTLGF PPTIRKIDAA VSDKEKKKTY FFAADKYWRF DENSQSMQEQ 420
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70 Seq ID NO: 11 Nucleotide sequence:
 Nucleic Acid Accession #: XM_058189
 Coding sequence: 169..774 (underlined sequences correspond to start and stop codons)

75 1 11 21 31 41 51
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 5 AACTACGTGT GGTATTTTGA AGGAATCTGT TTCTCAGGCA TCATGATGCT TATAGTAACA 360
 ACAGTTCTTC TGGTACTGGA GAATAATAAC AACTATAAAT GTTGCCAGAG TGA AAACTGC 420
 AGCAAAAAAT ATGTGACACT GCTGTCAATT ATCTTTTCTT CCCTCGGAAT TGCTTTTCT 480
 GGATACTGCC TGGTCATCTC TGCCTTGGGT CTGTGCCAAG GGCCATATTG CCGCACCCTT 540
 10 GATGGCTGGG AGTATGCTTT TGAAGGCACT GCTGGACGTT TCCTTACAGA TTCTAGCATA 600
 TGGATTCACT GCCTGGAACC TGCACATGTT GTGGAGTGGA ACATCATTTT ATTTTCCATT 660
 CTCATAACCC TCAGTGGGCT TCAAGTGATC ATCTGCCTCA TCAGAGTAGT CATGCAACTA 720
 TCCAAGATAC TGTGTGGAAG CTATTCAGTG ATCTTCCAGC CTGGAATCAT TGAATAAGG 780
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 15 GACTTGAGGG CAATATTGAA ATGATGGTGC TTTCTGCATT TGGTGTITAT TTGTA AAAAA 900
 TTTGCACTCC TCACCTGCACA TGCAAGTATA CCACCTTCC ATTTAGTATG TTTTAAAGT 960
 AATATGCATC AGAAACTTCA GAAATACTTC TGCCCTTTGA TCAACAAAT CCATTTCCAA 1020
 GAATCTGTAC TAGGGAAGTA AATAAGAATA TGAGAGAAAC CTTTATGCAA ATATGTATAT 1080
 TGCAACATTA TTTAATATTC TGGAAAATG GAAACACCCC AAAATTCTAA ACTCAGAGGA 1140
 20 AGGATTAAGT AAAGAGTGGT ACATACTGTA AATGTTTTCT GATATTA AAAA AATTA 1200
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Seq ID NO: 12 Protein sequence:

Protein Accession #: XP_058189

25
 1 11 21 31 41 51
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 30 LIVTTVLLVL ENNNYKCCQ SENCSKKVYT LLSIIFSSLG IAFSGYCLVI SALGLVQGPY 120
 CRTLDGWEYA FEGTAGRFLT DSSIWIQCLB PAHVVEWNII LFSILITLSG LQVIICLIRV 180
 VMQLSKILCG SYSVIFQPGI I

Seq ID NO: 13 Nucleotide sequence:

Nucleic Acid Accession #: NM_005397

Coding sequence: 251..1837 (underlined sequences correspond to start and stop codons)

35
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 CGGGCCACAG CCTGGCCTCC GGAGCCACCC ACAGGCCTCC CCGGGCGGCG CCCACGCTCC 180
 TACCGCCCGG ACGCGCGGAT CCTCCGCGCG CACCGCAGCC ACCTGCTCCC GGGCCAGAGG 240
 45 CGACGACACG ATGCGCTGCG CGCTGGCGCT CTCGGCGCTG CTGCTACTGT TGTCAACGCC 300
 GCCGCTGCTG CCGTCGTCGC CGTCGCGGTC GCCGTCGCGC TCGCCCTCCC AGAATGCAAC 360
 CCAGACTACT ACGGACTCAT CTAACAAAAC AGCACCAGCT CCAGCATCCA GTGTCAACCAT 420
 CATGGCTACA GATACAGCCC AGCAGAGCAC AGTCCCCACT TCCAAGGCCA ACGAAATCTT 480
 GGCCTCGGTC AAGGCGACCA CCGTTGGTGT ATCCAGTGAC TCACCGGGGA CTACAACCTT 540
 50 GGCTCAGCAA GTCTCAGGCC CAGTCAACAC TACCGTGGCT AGAGGAGGCG GCTCAGGCAA 600
 CCCTACTACC ACCATCGAGA GCCCAAGAG CACAAAAGT GCAGACACCA CTACAGTTGC 660
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 AGAACATCTG ACGACCCCTC ACCCTACAAG TCCACTTAGC CCCCACAAC CCACTTTGAC 840
 55 GCATCCTGTG GCCACCCCAA CAAGCTCGGG ACATGACCAT CTTATGAAAA TTTCAAGCAG 900
 TTCAAGCACT GTGGCTATCC CTGGCTACAC CTTCAACAGC CCGGGGATGA CCACCACCCT 960
 ACCGTCATCG GTTATCTCGC AAAGAACTCA ACAGACCTCC AGTCAGATGC CAGCCAGCTC 1020
 TACGGCCCCT TCCTCCCAGG AGACAGTGCA GCCCAGGAGC CCGGCAACGG CATTGAGAAC 1080
 ACCTACCCTG CCAGAGACCA TGAGCTCCAG CCCCACAGCA GCATCAACTA CCCACCGATA 1140
 60 CCCCAAAACA CCTTCTCCCA CTGTGGCTCA TGAGAGTAAC TGGGCAAAGT GTGAGGATCT 1200
 TGAGACACAG ACACAGAGTG AGAAGCAGCT CGTCTGAAC CTCACAGGAA ACACCCTCTG 1260
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 CTTCAACCCG GCCCAAGATA AGTGCGGCAT ACGGCTGGCA TCTGTTCCAG GAAGTCAGAC 1380
 CGTGGTCGTC AAAGAAATCA CTATTCAAC TAAGTCCCT GCCAAGGATG TGTACGAGCG 1440
 65 CGTGAAGGAC AAATGGGATG AACTAAAGG GGCAGGGGTC AGTGACATGA AGCTAGGGGA 1500
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 CTCCCAGAGG AAGGACCAGC AGCGGCTAAC AGAGGAGCTG CAGACAGTGG AGAATGGTTA 1680
 CCATGACAAC CCAACACTGG AAGTGATGGA GACCTCTTCT GAGATGCAGG AGAAGAAGGT 1740
 70 GGTCAAGCCT AACGGGGAGC TGGGGGACAG CTGGATCGTC GGTCTGCCGG TGGCCTCCAG 1800
 GGACGACCTG GATGAGGAGG AAGACACACA CCTCTAGTCC GGTCTGCCGG TGGCCTCCAG 1860
 CAGCACCAAG GAGCTCCAGA CCAACCACCC CAAGTGCCGT TTGGATGGGG AAGGGAAAGA 1920
 CTGGGGAGGG AGAGTGAAC TCCCTCCCCA ATCCCCCAG GGCCTTAATT 1980
 TTTCCCTTTT CAACCTGAAC AAATCACATT CTGTCCAGAT TCCTCTTGTA AAATAACCCA 2040
 75 CTAGTGCCTG AGCTCAGTGC TGCTGGATGA TGAGGGAGAT CAAGAAAAAG CCACGTAAGG 2100
 GACTTTATAG ATGAAC TAGT GGAATCCCTT CATCTGCAG TGAGATTGCC GAGACCTGAA 2160
 GAGGGTAAGT GACTTGCCCA AGGTCAGAGC CACTTGGTGA CAGAGCCAGG ATGAGAACAA 2220

	AGATTCCATT	TGCACCATGC	CACACTGCTG	TGTTCCACATG	TGCCTTCCGT	CCAGAGCAGT	2280
	CCCCGGCAGG	GGTGAACACT	CAGCAGGTGG	CTGGGCTGGA	AAGGAGGGCA	GGGCTACATC	2340
	CTGGCTCGGT	GGGATCTGAC	GACCTGAAAG	TCCAGCTCCC	AAGTTTTCTT	TCTCCTACCC	2400
5	CAGCCTCGTG	TACCCATCTT	CCCACCTCT	ATGTTCTTAC	CCCTCCCTAC	ACTCAGTGTT	2460
	TGTTCCCACT	TACTCTGTCC	TGGGGCCTCT	GGGATTAGCA	CAGGTTATTC	ATAACCTTGA	2520
	ACCCCTTGTT	CTGGATTCCG	ATTTTCTCAC	ATTTGCTTCG	TGAGATGGGG	GCTTAACCCA	2580
	CACAGGTCTC	CGTGCCTGAA	CCAGGTCTGC	TTAGGGGACC	TGCGTGCAGG	TGAGGAGAGA	2640
	AGGGGACACT	CGAGTCCAGG	CTGGTATCTC	AGGGCAGCTG	ATGAGGGGTC	AGCAGGAACA	2700
	CTGGCCCAT	GCCCCTGGA	CTCCTTGCG	AGGCCACCCA	CGATCTTCTT	TGGGCTTCCA	2760
10	TTTCCACCAG	GGACTAAAAAT	CTGCTGTAGC	TAGTGAGAGC	AGCGTGTTC	TTTGTGTGTT	2820
	CACTGCTCAG	CTGATGGGAG	TGATTCCCTG	AGACCCAGTA	TGAAAGAGCA	GTGGCTGCAG	2880
	GAGAGGCCTT	CCCCGGGCCC	CCCATCAGCG	ATGTGTCTTC	AGAGACAATC	CATTAAAGCA	2940
	GCCAGGAAGG	ACAGGCTTTC	CCCTGTATAT	CATAGGAAAC	TCAGGGACAT	TTCAAGTTGC	3000
15	TGAGAGTTTT	GTTATAGTTG	TTTTCTAACC	CAGCCCTCCA	CTGCCAAAGG	CCAAAAGCTC	3060
	AGACAGTTGG	CAGACGTCCA	GTTAGCTCAT	CTCACTCACT	CTGATTCTCC	TGTGCCACAG	3120
	GAAAAGAGGG	CCTGGAAAGC	GCAGTGCATG	CTGGGTGCAT	GAAGGGCAGC	CTGGGGGACA	3180
	GACTGTTGTG	GGAACGTCCC	ACTGTCCTGG	CCTGGAGCTA	GGCCTTGCTG	TTCTCTTCT	3240
	CTGTGAGCCT	AGTGGGGCTG	CTGCGGTTCT	CTTGCAGTTT	CTGGTGGCAT	CTCAGGGGAA	3300
	CACAAAAGCT	ATGTCTATTG	CCCAATATAG	GACTTTTATG	GGCTCGGCAG	TTAGCTGCCA	3360
20	TGTAGAAGGC	TCCTAAGCAG	TGGGCATGGT	GAGGTTTCAT	CTGATTGAGA	AGGGGGAATC	3420
	CTGTGTGGAA	TGTTGAACCT	TGCCATGGT	CTCCATCGTT	CTGGGCGTAA	ATTCCCTGGG	3480
	ATCAAGTAGG	AAAATGGGCA	GAAGTCTTAA	GGGGAATGAA	ATTGCCATT	TTCCGGTGAA	3540
	ACGCCACACC	TCCAGGGTCT	TAAGAGTCAG	GCTCCGGCTG	TAGTAGCTCT	GATGAAATAG	3600
25	CGGTATCCACT	CGGGATGGCT	TACTTTTTAA	AAGGGTAGGG	GGAGGGGCTG	GGGAAGATCT	3660
	GTCCTGCACC	ATCTGCCTAA	TTCTTCTCT	ACAGTCTGTA	GCCATCTGAT	ATCCTAGGGG	3720
	GAAAAGGAAG	GCCAGGGGTT	CACATAGGGC	CCCAGCGAGT	TTCCAGGAG	TTAGAGGGAT	3780
	GCGAGGCTAA	CAAGTTCCAA	AAACATCTGC	CCGATGCTC	TAGTGTTTGG	AGGTGGGCAG	3840
	GATGGAGAAC	AGTGCCTGTT	TGGGGGAAAA	CAGGAAATCT	TGTTAGGCTT	GAGTGAGGTG	3900
30	TTTGCTTCTT	TCTTGCCGAG	CGCTGGGTTC	TCTCCACCCA	GTAGGTTTTT	TGTTGTGGTC	3960
	CCGTGGGAGA	GGCCAGACTG	GATTATTCCT	CCTTTGCTGA	TCCTGGGTCA	CACTTCAACA	4020
	GCCAGGGCTT	TTGACGGAGA	CAGCAAATAG	GCCTCTGCAA	ATCAATCAAA	GGCTGCAACC	4080
	CTATGGCCTC	TTGGAGACAG	ATGATGACTG	GCAAGGACTA	GAGAGCAGGA	GTGCCTGGCC	4140
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35	CTGGGCTGAT	TCAGAGGTTA	CTGCTTTATA	TTCTGCTCAA	CTGTGTTAGT	CTAGGCTTAG	4260
	GACAGCTTCA	GAATCTGACA	CCTTGCCTTG	CTCTTGCCAC	CAGGACACCT	ATGTCAACAG	4320
	GCCAAACAGC	CATGCATCTA	TAAAGGTTCAT	CATCTTCTGC	CACCTTTACT	GGGTTCTAAA	4380
	TGCTCTCTGA	TAATTCAGAG	AGCATTGGGT	CTGGGAAGAG	GTAAGAGGAA	CACTAGAAGC	4440
	TCAGCATGAC	TTAAACAGGT	TGTAGCAAAG	ACAGTTTATC	ATCAACTCTT	TCAGTGGTAA	4500
40	ACTGTGGTTT	CCCCAAGCTG	CACAGGAGGC	CAGAAACCAC	AAGTATGATG	ACTAGGAAGC	4560
	CTACTGTGAT	GAGAGTGGGG	AGACAGGCAG	CAAAGCTTAT	GAAGGAGGTA	CAGAATATTC	4620
	TTTGCGTTGT	AAGACAGAAAT	ACGGGTTTAA	TCTAGTCTAG	GCRCAGATT	TTTTTCCCGC	4680
	TTGATAAGGA	AAGCTAGCAG	AAAGTTTATT	TAAACCATT	CTTGAGCTTT	ATCTTTTTTG	4740
	ACAATATACT	GGAGAAACTT	TGAAGAACAA	GTTCAAACCT	ATACATATAC	ACATATTTTT	4800
45	TTGATAATGT	AAATACAGTG	ACCATGTTAA	CCTACCCTGC	ACTGCTTTAA	GTGAACATAC	4860
	TTTGAAAAG	CATTATGTTA	GCTGAGTGAT	GGCCAAGTTT	TTTCTCTGGA	CAGGAATGTA	4920
	AATGTCTTAC	TGGAAATGAC	AAGTTTTTGC	TTGATTTTTT	TTTTTAAACA	AAAAATGAAA	4980
	TATAACAAGA	CAAACCTATG	ATAAAGTATT	TGCTTGTAG	ATCAGGTGTT	TTGTTTGTGTT	5040
50	TTTTTAAATT	TAAAATGCAA	CCCTGCCCTC	TCCCCAGCAA	AGTCACAGCT	CCATTTCAGT	5100
	AAAGGTTGGA	GTCAATATGC	TCTGGTTGGC	AGGCAACCCT	GTAGTCATGG	AGAAAGGTAT	5160
	TTCAAGATCT	AGTCCAATCT	TTTTCTAGAG	AAAAAGATAA	TCTGAAGCTC	ACAAAGATGA	5220
	AGTGACTTCC	CTCAAAATCAC	ATGGTTCAGG	ACAGAAACAA	GATTAAACC	TGGATCCACA	5280
	GACTGTGCGC	CTCAGAAGGA	ATAATCGGTA	AATTAAGAAT	TGCTACTCGA	AGGTGCCAGA	5340
	ATGACACAAA	GGACAGAATT	CCTTCCCAG	TTGTTACCCT	AGCAAGGCTA	GGGAGGGCAT	5400
55	GAACACAAAC	ATAAGAACTG	GTCTTCTCAC	ACTTTCTCTG	AATCATTTAG	GTTTAAGATG	5460
	TAAAGTGAACA	ATTCTTTCTT	TCTGCCAAGA	AACAAAGTTT	TGGATGAGCT	TTTATATATG	5520
	GAACCTACTC	CAACAGGACT	GAGGGACCAA	GGAAACATGA	TGGGGGAGGC	AAGAGAGGGC	5580
	AAAGAGTAAA	ACTGTAGCAT	AGCTTTTGTC	ACGGTCACTA	GCTGATCCCT	CAGGTCTGCT	5640
	GCAACACAG	CATGGAGGAC	ACAGATGACT	CTTTGGTGTT	GGTCTTTTGG	TCTGCAGTGA	5700
60	ATGTTCAACA	GTTTGCCGAG	GAACCTGGGG	ATCATATATG	TCTTAGTGGA	CAGGGGTCTG	5760
	AAGTACACTG	GAATTTACTG	AGAAACTTGT	TTGTAACAAAC	TATAGTTAAT	AATTATTGCA	5820
	TTTTCTTACA	AAAATATATT	TTGGAAATTT	GTATACTGTC	AATTAAAGT		

Seq ID NO: 14 Protein sequence:
Protein Accession #: NP_005388

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	DTAQQSTVPT	SKANEILASV	KATTLGVSSD	SPGTTTLAQQ	VSGPVNNTVA	RGGGSGNPTT	120
70	TIESPKSTKS	ADTTTVAATST	ATAKPNTTSS	QNGAEDTTNS	GGKSSHSVTT	DLTSTKAEHL	180
	TTPHPTSPLS	SRQPTLTHPV	ATPTSSGHDH	LMKISSSSST	VAIPGYTFTS	PGMTTTLPS	240
	VISQRTQTS	SQMPASSTAP	SSQETVQPTS	PATALRPTL	PETMSSSPTA	ASTHRYPKT	300
	PSPTVAHESN	WAKCEDLETQ	TQSEKQLVLN	LTGNTLCAGG	ASDEKLISLI	CRAVKATFNP	360
	AQDKCGIRLA	SVPGSQTVVV	KEITIHTKLP	AKDVYERLKD	KWDELKEAGV	SDMKLGDQGP	420
75	PEEAEDRFMS	PLIITIVCMA	SFLLLVAALY	GCCHQRLSQR	KDQORLTEL	QTVENGYHDN	480
	PTLEVMEISS	EMQEKVVSL	NGELGDSWIV	PLDNLTKDDL	DEEEDTHL		

Seq ID NO: 15 Nucleotide sequence:

Nucleic Acid Accession #: NM_004105

Coding sequence: 150..1631 (underlined sequences correspond to start and stop codons)

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CAAGGTAAGT	CTGCTAGCTA	AGATTACAA	<u>TGTTGAAAGC</u>	CCTTTTCCTA	ACTATGCTGA	180
CTCTGGCGCT	GGTCAAGTCA	CAGGACACCG	AAGAAACCAT	CACGTACACG	CAATGCACTG	240
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TCCCAGACGC	TTGTAAAGGT	GGAATGAAGT	GTGTCAACCA	CTATGGAGGA	TACCTCTGCC	360
TTCCGAAAAC	AGCCCAGATT	ATTGTCAATA	ATGAACAGCC	TCAGCAGGAA	ACACAACCAG	420
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GAGTGTTGCC	CGGGGTGGT	TTGTGGCCA	GTGCTGCTGC	AGTCGCAGGC	CCTGAAATGC	540
AGACTGGCCG	AAATAACTTT	GTCATCCGGC	GGAAACCCAGC	TGACCTTCAG	CGCATTCCTT	600
CCAACCTTTC	CCACCGTATC	CAGTGTGCAG	CAGGCTACGA	GCAAAGTGAA	CACAACGTGT	660
GCCAAGACAT	AGACGAGTGC	ACTGCAGGGA	CGCACAACTG	TAGAGCAGAC	CAAGTGTGCA	720
TCAATTTACG	GGGATCCTTT	GCAATGTCAGT	GCCCTCCTGG	ATATCAGAAG	CGAGGGGAGC	780
AGTGCCTAGA	CATAGATGAA	TGTACCATCC	CTCCATATTG	CCACCAAAGA	TGCGTGAATA	840
CACCAGGCTC	ATTTTATGTC	CAGTGCAGTC	CTGGGTTTCA	ATTGGCAGCA	AACAACCTATA	900
CCTGCGTAGA	TATAAATGAA	TGTGATGCCA	GCAATCAATG	TGCTCAGCAG	TGCTACAACA	960
TTCTTGGTTC	ATTCATCTGT	CAGTGCATTC	AAGGATATGA	GCTAAGCAGT	GACAGGCTCA	1020
ACTGTGAAGA	CATTGATGAA	TGCAGAACCT	CAAGCTACCT	GTGTCAATAT	CAATGTGTCA	1080
ATGAACCTGG	GAAATTTCTA	TGTATGTGCC	CCCAGGGGATA	CCAAGTGGTG	AGAAGTAGAA	1140
CATGTCAAGA	TATAAATGAG	TGTGAGACCA	CAATGAATG	CCGGGAGGAT	GAAATGTGTT	1200
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TAACACCAGA	GAACCGATGT	GTTTGCCCGC	TCTCAAATGC	CATGTGCCGA	GAAGTCCCCC	1320
AGTCAATAGT	CTACAAATAC	ATGAGCATCC	GATCTGATAG	GTCTGTGCCA	TCAGACATCT	1380
TCCAGATACA	GGCCACAAC	ATTTATGCCA	ACACCATCAA	TACTTTTCGG	ATTAAATCTG	1440
GAAATGAAAA	TGGAGAGTTC	TACCTACGAC	AAACAAGTCC	TGTAAGTGCA	ATGCTTGTGC	1500
TCGTGAAGTC	ATTATCAGGA	CCAAGAGAAC	ATATCGTGGA	CCTGGAGATG	CTGACAGTCA	1560
GCAGTATAGG	GACCTTCCGC	ACAAGCTCTG	TGTTAAGATT	GACAATAATA	GTGGGGCCAT	1620
TTTCATTTTA	<u>GTCTTTTCTA</u>	AGAGTCAACC	ACAGGCATTT	AAGTCAGCCA	AAGAATATTG	1680
TTACCTTAAA	GCACTATTTT	ATTTATAGAT	ATATCTAGTG	CATCTACATC	TCTATACTGT	1740
ACACTCACCC	ATAACAACA	ATTACACCAT	GGTATAAAGT	GGGCATTTAA	TATGTAAAGA	1800
TTCAAAGTTT	GTCTTTTATTA	CTATATGTAA	ATTAGACATT	AATCCACTAA	ACTGGTCTTC	1860
TTCAAGAGAG	CTAAGTATAC	ACTATCTGGT	GAAACTTGGA	TTCTTTCCTA	TAAAAGTGGG	1920
ACCAAGCAAT	GATGATCTTC	TGTGGTGCTT	AAGGAACTT	ACTAGAGCTC	CACTAACAGT	1980
CTCATAGGA	GGCAGCCATC	ATAACCATTG	AATAGCATCG	AAGGGTAAGA	ATGAGTTTTT	2040
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TCTGCCATAT	TTGTGTTGGT	TTTTATTTTC	ATATCCAGCC	TAAAGGTGGT	TGTTTATTAT	2160
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AAAATGAACC	AGATACCCCC	TAGAAAATTA	TACTATTGAG	AAATCTATGG	GGAGGATATG	2340
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TATTCCTGGC	ATCCAGATTC	ACAGTGAATC	TAAAGCAAAT	ACCCTCCTAC	CCAATTCTAT	2640
GGAATATTTT	ATACGTCTCC	TTGTTTAAAA	TCTGACTGCT	TTACTTTGAT	GTATCATATT	2700
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Seq ID NO: 16 Protein sequence:

Protein Accession #: NP_004096

60

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CVNHYGGYLC	LPKTAQIIVN	NEQPQQTQP	AEGTSGATTG	VVAASSMATs	GVLPGGGFVA	120
SAAAVAGPEM	QTGRNPFVIR	RNPADPQRIP	SNPSHRIQCA	AGYEQSEHNV	CQDIDECTAG	180
THNCRADQVC	INLRGSFACQ	CPPGYQKRGE	QCVDIDECTI	PPYCHQRCVN	TPGSFYCQCS	240
PGFQLAANNY	TCVDINECDM	SNQCAQQCYN	ILGSFICQCN	QGYELSSDRL	NCEIDIECRT	300
SSYLCQYQCV	NEPGKFSCMC	PQGYQVVRSR	TCQDINECET	TNECREDEMC	WNYHGGFRCY	360
PRNPCQDPYI	LTPENRCVCP	VSNAMCRELP	QSIVYKYMSI	RSDRSVPSDI	FQIQATTIYA	420
NTINTFRIKS	GNENGEFYLR	QTSPVSAMLV	LVKSLSGPRE	HIVDLEMLTV	SSIGTFRTSS	480
VLRLTIIVGP	FSF					

Seq ID NO: 17 Nucleotide sequence:

Nucleic Acid Accession #: NM_018894

Coding sequence: 27..1967 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
5	AAAACATTCA	ACAAATTAAT	GGGTGTAAGG	AAC TGGA AAA	CCTGGACTCC	TACCACATGC	60
	AGATAAAACC	AATAGAGTGC	AGAATAAGAC	TCAAGTCAAG	TAAGTAACGT	TAAACACCAT	120
	AAAGACACAT	GGCCTTCTTT	GTGTACATGA	CATGCATTCT	CAACAATGCA	CTGACGGATA	180
	TGAGTGGGAT	CCTGTGAGAC	AGCAATGCAA	AGATATTGAT	GAATGTGACA	TTGTCCCAGA	240
	CGCTTGTA AA	GGTGGAATGA	AGTGTGTCAA	CCACTATGGA	GGATACCTCT	GCCTTCCGAA	300
	AACAGCCCCAG	ATTATTGTCA	ATAATGAACA	GCCTCAGCAG	GAAACACAAC	CAGCAGAAGG	360
10	AACCTCAGGG	GCAACCAACG	GGGTGTAGC	TGCCAGCAGC	ATGGCAACCA	GTGGAGTGT	420
	GCCCCGGGGT	GGTTTTGTGG	CCAGTGTCTG	TGCAGTCGCA	GGCCCTGAAA	TGCAGACTGG	480
	CCGAAATAAC	TTTGTCTATC	GGCGGAACCC	AGCTGACCCT	CAGCGCATT	CCTCCAACCC	540
	TTCCCAACCGT	ATCCAGTGTG	CAGCAGGCTA	CGAGCAAAGT	GAACACAACG	TGTGCCAAGA	600
	CATAGACGAG	TGCACCTGAG	GGACGCACAA	CTGTAGAGCA	GACCAAGTGT	GCATCAATTT	660
15	ACGGGGATCC	TTTGCATGTC	AGTGCCTTCC	TGGATATCAG	AAGCGAGGGG	AGCAGTGCCT	720
	AGACATAGAT	GAATGTACCA	TCCTTCCATA	TTGCCACCAA	AGATGCGTGA	ATACACCAGG	780
	CTCATTTTAT	TGCCAGTGCA	GTCTTGGGTT	TCAATTGGCA	GCAAACAAC	ATACCTGCGT	840
	AGATATAAAT	GAATGTGATG	CCAGCAATCA	ATGTGCTCAG	CAGTGTCTACA	ACATTCTTGG	900
	TTCATTTCATC	TGTCAGTGCA	ATCAAGGATA	TGAGCTAAGC	AGTGACAGGC	TCAACTGTGA	960
20	AGACATTGAT	GAATGCAGAA	CCTCAAGCTA	CCTGTGTCAA	TATCAATGTG	TCAATGAACC	1020
	TGGGAAATTC	TCATGTATGT	GCCCCCAGGG	ATACCAAGTG	GTGAGAAAGT	GAACATGTCA	1080
	AGATATAAAT	GAGTGTGAGA	CCACAAATGA	ATGCCGGGAG	GATGAAATGT	GTTTGAATTA	1140
	TCATGGCGGC	TTCCGTTGTT	ATCCACGAAA	TCCTTGTCAA	GATCCCTACA	TTCTAACACC	1200
	AGAGAACCGA	TGTGTTTGCC	CAGTCTCAAA	TGCCATGTGC	CGAGAACTGC	CCCAGTCAAT	1260
25	AGTCTACAAA	TACATGAGCA	TCCGATCTGA	TAGGTCTGTG	CCATCAGACA	TCTTCCAGAT	1320
	ACAGGCCACA	ACTATTTATG	CCAACACCAT	CAATACTTTT	CGGATTAAAT	CTGGAAATGA	1380
	AAATGGAGAG	TTCTACCTAC	GACAAACAAG	TCCTGTAAGT	GCAATGCTTG	TGCTCGTGAA	1440
	GTCATTATCA	GGACCAAGAG	AACATATCGT	GGACCTGGAG	ATGCTGACAG	TCAGCAGTAT	1500
	AGGGACCTTC	CGCACAAGCT	CTGTGTTAAG	ATTGACAATA	ATAGTGGGGC	CATTTTCATT	1560
30	TTAGTCTTTT	CTAAGAGTCA	ACCACAGGCA	TTTAAGTCAG	CCAAAGAATA	TTGTTACCTT	1620
	AAAGCACTAT	TTTATTTTATA	GATATATCTA	GTGCATCTAC	ATCTCTATAC	TGTACACTCA	1680
	CCCATAACAA	ACAATTACAC	CATGGTATAA	AGTGGGCATT	TAATATGTAA	AGATTCAAAG	1740
	TTTGTCTTTA	TTACTATATG	TAAATTAGAC	ATTAATCCAC	TAAACTGGTC	TTCTTCAAGA	1800
	GAGCTAAGTA	TACATATCTG	GGTGAAACTT	GGATTCTTTT	CTATAAAAGT	GGGACCAAGC	1860
35	AATGATGATC	TTCTGTGGTG	CTTAAGGAAA	CTTACTAGAG	CTCCACTAAC	AGTCTCATAA	1920
	GGAGGCAGCC	ATCATAACCA	TTGAATAGCA	TGCAAGGGTA	AGAATGAGTT	TTTAACTGCT	1980
	TTGTAAAGAA	ATGGAAAAGG	TCAATAAAGA	TATATTTCTT	TAGAAAATGG	GGATCTGCCA	2040
	TATTTGTGTT	GGTTTTTATT	TTTCATATCCA	GCCTAAAGGT	GGTTGTTTAT	TATATAGTAA	2100
	TAAATCATTG	CTGTACAACA	TGCTGGTTTC	TGTAGGGTAT	TTTTAATTTT	GTCAGAAATT	2160
40	TTAGATTGTT	AATATTTTGT	AAAAAACAGT	AAGCAAAATT	TTCCAGAATT	CCCAAAATGA	2220
	ACCAGATACC	CCCTAGAAAA	TTTACTATAT	GAGAAATCTA	TGGGGAGGAT	ATGAGAAAAAT	2280
	AAATTCCTTC	TAAACCACAT	TGGAACGTAC	CTGAAGAAGC	AAACTCGGAA	AATATAATAA	2340
	CATCCCTGAA	TTCAGGCATT	CACAAGATGC	AGAACAAAAT	GGATAAAAGG	TATTTCACTG	2400
	GAGAAGTTT	AATTTCTAAG	TAAAATTTAA	ATCCTAACAC	TTCACTAATT	TATAACTAAA	2460
45	ATTTCTCATC	ATGCTACTTG	ATGCTCACAG	AGGAAGAAAA	TGATGATGGT	TTTTATTCTT	2520
	GGCATCCAGA	GTGACAGTGA	ACTTAAGCAA	ATTACCCTCC	TACCCAATTC	TATGGAATAT	2580
	TTTATACGTC	TCCTTGTTTA	AAATCTGACT	GCTTTACTTT	GATGTATCAT	ATTTTAAAT	2640
	AAAAATAAAT	ATTCCTTTAG	AAGATCACTC	TAAAA			

Seq ID NO: 18 Protein sequence:
Protein Accession #: NP_061489.1

	1	11	21	31	41	51	
55	MHSQQCTDGY	EWDPVRQCKK	DIDECDIVPD	ACKGGMKCVN	HYGGYLCPLK	TAQIIVNNEQ	60
	PQGETQPAEG	TSGATTGVVA	ASSMATSGVL	PGGGFVASAA	AVAGPEMQTG	RNNFVIRRN	120
	ADPQRIPSNP	SHRIQCAAGY	EQSEHNVCQD	IDECTAGTHN	CRADQVCINL	RGSFACQCPP	180
	GYQKRGEQCV	DIDECTIPPY	CHQRCVNTPG	SFYCQCSPGF	QLAANNYTCV	DINECDASNQ	240
	CAQQCYNILG	SFICQCNQGY	ELSSDRLNCE	DIDECRTSSY	LCQYQCVNEP	GKFSKCMCPQG	300
60	YQVVRSTCTQ	DINECETTNE	CREDEMWNYY	HGGFRCYPRN	PCQDPYILTP	ENRCVCPVSN	360
	AMCRELPQSI	VLKYSIRSIRSD	RSVPSDIFQI	QATTIYANTI	NTFRIKSGNE	NGEFYLRQTS	420
	PVSAMLVLVK	SLSGPREHIV	DLEMLTVSSI	GTFRTSSVLR	LTIIVGPFSF		

Seq ID NO: 19 Nucleotide sequence:
Nucleic Acid Accession #: NM_006500
Coding sequence: 27..1967 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
70	ACTTGCCTCT	CGCCCTCCGG	CCAAGCATGG	GGCTTCCCAG	GCTGGTCTGC	GCCTTCTTGC	60
	TCGCCGCCTG	CTGCTGCTGT	CCTCGCTCG	CGGGTGTGCC	CGGAGAGGCT	GAGCAGCCTG	120
	CGCCTGAGCT	GGTGGAGGTG	GAAGTGGGCA	GCACAGCCCT	TCTGAAGTGC	GGCCTCTCCC	180
	AGTCCCAAGG	CAACCTCAGC	CATGTGCGAT	GGTTTTCTGT	CCACAAGGAG	AAGCGGACGC	240
75	TCATCTTCCG	TGTGCGCCAG	GGCCAGGGCC	AGAGCGAACC	TGGGGAGTAC	GAGCAGCGGC	300
	TCAGCCTCCA	GTGACAGAGG	GCTACTCTGG	CCCTGACTCA	AGTCACCCCC	CAAGACGAGC	360

GCATCTTCTT GTGCCAGGGC AAGCGCCCTC GGTCCCAGGA GTACCGCATC CAGCTCCGCG 420
 TCTACAAAGC TCCGGAGGAG CCAAACATCC AGGTCAACCC CTGGGGCATC CCTGTGAACA 480
 GTAAGGAGCC TGAGGAGGTC GCTACCTGTG TAGGGAGGAA CGGGTACCCC ATTCTCAAG 540
 5 TCATCTGGTA CAAGAATGGC CGGCCTCTGA AGGAGGAGAA GAACCGGGTC CACATTCAGT 600
 CGTCCCAGAC TGTGGAGTCG AGTGGTTTGT ACACCTTGCA GAGTATTCTG AAGGCACAGC 660
 TGGTTAAAGA AGACAAAGAT GCCCAGTTT ACCTGTAGCT CAACTACCGG CTGCCCAGTG 720
 GGAACCATAT GAAGGAGTCC AGGGAAGTCA CCGTCCCTGT TTCTACCCG ACAGAAAAAG 780
 TGTGGCTGGA AGTGGAGCCC GTGGGAATGC TGAAGGAAGG GGACCGCGTG GAAATCAGGT 840
 10 GTTTGGCTGA TGGCAACCCT CCACCACACT TCAGCATCAG CAAGCAGAAC CCCAGCACCA 900
 GGGAGGCAGA GGAAGAGACA ACCAACGACA ACGGGGTCTT GGTGCTGGAG CCTGCCCGGA 960
 AGGAACACAG TGGGCGCTAT GAATGTCAGG CCTGGAACCT GGACACCATG ATATCGCTGC 1020
 TGAGTGAACC ACAGGAACCTA CTGGTGAACT ATGTGTCTGA CGTCCGAGTG AGTCCCGCAG 1080
 CCGCTGAGAG ACAGGAAGGC AGCAGCCTCA CCCTGACCTG TGAGGCAGAG AGTAGCCAGG 1140
 15 ACCTCGAGTT CCAGTGGCTG AGAGAAGAGA CAGACCAGGT GCTGGAAAGG GGGCCTGTGC 1200
 TTCAGTTGCA TGACCTGAAA CGGGAGGCAG GAGGCGGCTA TCGCTGCGTG GCGTCTGTGC 1260
 CCAGCATACC CGGCCTGAAC CGCACACAGC TGGTCAAGCT GGCCATTTT GGCCCCCTT 1320
 GGTGGCATT CAAGGAGAGG AAGGTGTGGG TGAAAGAGAA TATGGTGTG AATCTGTCTT 1380
 GTGAAGCGTC AGGGCACCCC CGGCCACCA TCTCCTGGAA CGTCAACGGC ACGGCAAGTG 1440
 20 AACAGACCA AGATCCACAG CGAGTCTCTA GCACCTGAA TGTCTCTGTG ACCCGGAGC 1500
 TGTGGAGAC AGGTGTTGAA TGCACGCTT CCAACGACCT GGGCAAAAAC ACCAGCATCC 1560
 TCTTCTGGA GCTGGTCAAT TTAACCAACC TCACACCAGA CTCAAACACA ACCACTGGCC 1620
 TCAGCACTTC CACTGCCAGT CCTCATACCA GAGCCAAACAG CACCTCCACA GAGAGAAAGC 1680
 TGCCGGAGCC GGAGAGCCGG GGGCTGGTCA TCGTGGCTGT GATTGTGTGC ATCTGGTCC 1740
 25 TGGCGGTGCT GGGCGCTGTC CTCTATTTCC TCTATAAGAA GGGCAAGCTG CCGTGCAGGC 1800
 GCTCAGGGAA GCAGGAGATC ACGTGCCTCC CGTCTCGTAA GACCGAAGCT GTAGTTGAAG 1860
 TTAGTTCAGA TAAGTCCCA GAAGAGATGG GCCTCCTGCA GGGCAGCAGC GGTGACAAGA 1920
 GGGCTCCGGG AGACCAGGGA GAGAAATACA TCGATCTGAG GCATTAGCCC CGAATCACTT 1980
 CAGTCCCTT CCCTGCCTGG ACCATTCCCA GCTCCCTGCT CACTCTTCTC TCAGCCAAAG 2040
 30 CCTCCAAAGG GACTAGAGAG AAGCCTCCTG CTCCCTCAC CTGCACACCC CCTTTCAGAG 2100
 GGCCACTGGG TTAGGACCTG AGGACCTCAC TTGGCCCTGC AAGCCGCTTT TCAGGGACCA 2160
 GTCCACCACC ATCTCCTCCA CGTTGAGTGA AGCTCATCCC AAGCAAGGAG CCCCAGTCTC 2220
 CCGAGCGGGT AGGAGAGTTT CTTGCAGAAC GTGTTTTTTC TTTACACACA TTATGGCTGT 2280
 AAATACCTGG CTCTGCCAG CAGCTGAGCT GGGTAGCCTC TCTGAGCTGG TTCTCTGCC 2340
 35 CAAAGGCTGG TCTCCACCAT CCAGGTGCAC CACTGAAGTG AGGACACACC GGAGCCAGGC 2400
 GCCTGCTCAT GTTGAAGTGC GCTGTTTACA CCCGCTCCGG AGAGCACCCC AGCGGCATCC 2460
 AGAAGCAGCT GCAGTGTTCG TGCCACCACC CTCCTGCTCG CCTCTCAAAA GTCTCTGTG 2520
 ACATTTTTTC TTTGGTCAGA AGCCAGGAAC TGGTGTCACT CCTTAAAGA TACGTGCCGG 2580
 40 GGCAGGTGT GTGGGCTCAC GCCTGTAATC CCAGCACTTT GGGAGGCCGA GCGGGCGGA 2640
 TCACAAAGTC AGGACGAGAC CATCTGGCT AACACGGTGA AACCCTGTCT CTAATAAAA 2700
 TACAAAAA AATTAGCTAG GCGTAGTGGT TGGCACCCTAT AGTCCAGCT ACTCGGAAGG 2760
 CTGAAGCAGG AGAATGGTAT GAATCCAGGA GGTGGAGCTT GCAGTGAGC GAGACCGTGC 2820
 CACTGCACTC CAGCCTGGGC AACACAGCGA GACTCCGTCT CGAGGAAAAA AAAAGAAAAG 2880
 45 ACGCGTACCT GCGGTGAGGA AGCTGGGCGC TGTTTTCGAG TTCAGGTGAA TTAGCCTCAA 2940
 TCCCGTGT CACTGTCTCC CATAGCCCTC TTGATGGATC ACGTAAACT GAAAGGCAGC 3000
 GGGAGCAGA CAAAGATGAG GTCTACACTG TCCTTCATGG GGATTAAGC TATGTTATA 3060
 TTAGCACCAA ACTTCTACAA ACCAAGCTCA GGGCCCCAAC CCTAGAAGGG CCCAAATGAG 3120
 AGAATGGTAC TTAGGGATGG AAAACGGGGC CTGGCTAGAG CTTCGGGTGT GTGTGTCTGT 3180
 50 CTGTGTGTAT GCATACATAT GTGTGTATAT ATGGTTTTGT CAGGTGTGTA AATTTGCAA 3240
 TTGTTTCTT TATATATGTA TGTATATATA TATATGAAA TATATATATA TATGAAAAAT 3300
 AAAGCTTAAT TGTCCAGAA AATCATACAT TGCTTTTTTA TTCTACATGG GTACCACAGG 3360
 AAACCTGGGG CCGTGAAAC TACAACCAA AGGCACACAA AACCCTTTCC AGTTGGCAGC 3420
 AGAGATCAGG GGTACCTCT GCTTCTGAGC AAATGGCTCA AGCTCTACCA GAGCAGACAG 3480
 55 CTACCCTACT TTTCAGCAGC AAAACGTCCC GTATGACGCA GCACGAAGGG CCTGGCAGGC 3540
 TGTTAGCAGG AGCTATGTCC CTTCCTATCG TTTCCGTCCA CTT

Seq ID NO: 20 Protein sequence:
 Protein Accession #: NP_006491

60
 1 11 21 31 41 51
 MGLPRLVCAF LLAACCCPR VAGVPGEAEQ PAPELVEVEV GSTALLKCGL SQSQGNLSHV 60
 DWFSVHKEKR TLIFRVRRQG QQSEPGEYEQ RLSLQDRGAT LALTQVTPQD ERIFLCQGR 120
 65 PRSQEYRIQL RVYKAPEEPN IQVNPLGIPV NSKEPEEVAT CVGRNGYPIPI QVIWYKNGRP 180
 LKEEKNRVHI QSSQTVESSE LYTLQSIKLA QLVKEDKDAQ FYCELNYRLP SGNHMKESRE 240
 VTPVPFYFTE KWLVEVEPVG MLKEGDRVEI RCLADGNPPP HFSISKQNP TREAEETTN 300
 DNGVLVLEPA RKEHSGRYEC QAWNLDTMIS LLSEPQELLV NYVSDVRVSP AAPERQEGSS 360
 70 LTLTCEAESS QDLEFQWLER ETDQVLERGP VLQLHDLKRE AGGGYRCVAS VPSIPGLNRT 420
 QLVKLAIFGP PWMAFKERKV WVKENMVLNL SCEASGHPRP TISWNVNGTA SEQDQDPQRV 480
 LSTLNLVLTPELLETGVECT ASNDLGKNTS ILFLELVNLT TLTPDSNTTT GLSTSTASPH 540
 TRANSTSTER KLPEPESRGV VIVAVIVCIL VLAVLGAVLY FLYKKGKLP RRSKGQEIITL 600
 PPSRKTELTV EVKSKDLPEE MGLLQSSGD KRAPGDQGEK YIDLRLH

75

Seq ID NO: 21 Nucleotide sequence:

Nucleic Acid Accession #: NM_002421

Coding sequence: 72..1481 (underlined sequences correspond to start and stop codons)

5

	1	11	21	31	41	51	
	GGGATATTGG	AGTAGCAAGA	GGCTGGGAAG	CCATCACTTA	CCTTGCACTG	AGAAAGAAGA	60
	CAAAGGCCAG	<u>TATGCACAGC</u>	TTTCCTCCAC	TGCTGCTGCT	GCTGTTCTGG	GGTGTGGTGT	120
10	CTCACAGCTT	CCCAGCGACT	CTAGAAACAC	AAGAGCAAGA	TGTGGACTTA	GTCCAGAAAT	180
	ACCTGGAAAA	ATACTACAAC	CTGAAGAATG	ATGGGAGGCA	AGTTGAAAAG	CGGAGAAATA	240
	GTGGCCCACT	GGTTGAAAAA	TTGAAGCAAA	TGCAGGAATT	CTTTGGGCTG	AAAGTGACTG	300
	GGAAACCAGA	TGCTGAAACC	CTGAAGGTGA	TGAAGCAGCC	CAGATGTGGA	GTGCCTGATG	360
	TGGCTCAGTT	TGTCCTCACT	GAGGGGAACC	CTCGCTGGGA	GCAAACACAT	CTGACCTACA	420
15	GGATTGAAAA	TTACACGCCA	GATTTGCCAA	GAGCAGATGT	GGACCATGCC	ATTGAGAAAG	480
	CCTTCCAACT	CTGGAGTAAT	GTCAACCTTC	TGACATTAC	CAAGGTCTCT	GAGGGTCAAG	540
	CAGACATCAT	GATATCTTTT	GTCAAGGGAG	ATCATCGGGA	CAACTCTCCT	TTTGATGGAC	600
	CTGGAGGAAA	TCTTGCTCAT	GCTTTTCAAC	CAGGCCCAGG	TATTGGAGGG	GATGCTCATT	660
	TTGATGAAGA	TGAAAGGTGG	ACCAACAATT	TCAGAGAGTA	CAACTTACAT	CGTGTGCGG	720
20	CTCATGAAGT	CGGCCATTCT	CTTGGACTCT	CCCATTCTAC	TGATATCGGG	GCTTTGATGT	780
	ACCCTAGCTA	CACCTTCACT	GGTGATGTTT	AGCTAGCTCA	GGATGACATT	GATGGCATCC	840
	AAGCCATATA	TGGACGTTCC	CAAAATCCTG	TCCAGCCCAT	CGGCCACAA	ACCCCAAAAG	900
	CGTGTGACAG	TAAGCTAACC	TTTGATGCTA	TAACCTACAT	TCGGGGAGAA	GTGATGTTCT	960
	TTAAAGACAG	ATTCTACATG	CGCACAAATC	CCTTCTACCC	GGAAGTTGAG	CTCAATTTCA	1020
25	TTTCTGTTTT	CTGGCCACAA	CTGCCAAATG	GGCTTGAAGC	TGCTTACGAA	TTTGCCGACA	1080
	GAGATGAAGT	CCGGTTTTTC	AAAGGGAATA	AGTACTGGGC	TGTTCAGGGA	CAGAAATGTC	1140
	TACACGGATA	CCCCAAGGAC	ATCTACAGCT	CCTTTGGCTT	CCCTAGAACT	GTGAAGCATA	1200
	TCGATGCTGC	TCTTCTGAG	GAAAACACTG	GAAAACCTTA	CCTCTTTGTT	GCTAACAAAT	1260
	ACTGGAGGTA	TGATGAATAT	AAACGATCTA	TGGATCCAGG	TTATCCCAA	ATGATAGCAC	1320
30	ATGACTTTCC	TGGAATTGGC	CACAAAGTTG	ATGCAGTTTT	CATGAAAGAT	GGATTTTTCT	1380
	ATTTCTTTCA	TGGAACAAGA	CAATACAAAT	TTGATCCTAA	AACGAAGAGA	ATTTTGATCT	1440
	TCCAGAAAGC	TAATAGCTGG	TTCAACTGCA	GGAAAAATTG	AACATTACTA	ATTTGAATGG	1500
	AAAACACATG	GTGTGAGTCC	AAAGAAGGTG	TTTTCTGTAA	GAACTGTCTA	TTTTCTCAGT	1560
	CATTTTTTAA	CTCTAGAGTC	ACTGATACAC	AGAATATAAT	CTTATTTATA	CCTCAGTTTG	1620
35	CATATTTTTT	TACTATTTAG	AATGTAGCCC	TTTTTGTAAT	GATATAATTT	AGTTCCACAA	1680
	ATGGTGGGTA	CAAAAAGTCA	AGTTTGTGGC	TTATGGATTG	ATATAGGCCA	GAGTTGCAAA	1740
	GATCTTTTCC	AGAGTATGCA	ACTCTGACGT	TGATCCGAGA	GAGCAGCTTC	AGTGACAAAC	1800
	ATATCTTTTC	AAGACAGAAA	GAGACAGGAG	ACATGAGTCT	TTGCCGGAGG	AAAAGCAGCT	1860
40	CAAGAACACA	TGTGCAGTCA	CTGGTGTGAC	CCTGGATAGG	CAAGGGATAA	CTCTTCTAAC	1920
	ACAAAATAAG	TGTTTTATGT	TTGGAATAAA	GTCACCTTGG	TTTCTACTGT	TTT	

Seq ID NO: 22 Protein sequence:

Protein Accession #: NP_002412

45

	1	11	21	31	41	51	
	MHSFPPLLLL	LFWGVVSHSF	PATLETQEQD	VDLVQKYLEK	YYNLKNDGRQ	VEKRRNSGPV	60
	VEKLKQMQUEF	FGLKVTGKPD	AETLKVMKQP	RCGVDPDVAQF	VLTEGNPRWE	QTHLTYRIEN	120
50	YTPDLPRADV	DHAIEKAFQL	WSNVPLTFTT	KVSEGGADIM	ISFVRGDHRD	NSPFDGPGGN	180
	LAHAFQPGPG	IGGDAGPGFG	ERWTNNFREY	NLHRVAAHEL	GHSGLGLSHST	DIGALMYPST	240
	TFSGDVQLAQ	DDIDIGIAIY	GRSQNPVQPI	GPQTPKACDS	KLTFDAITTI	RGEVMFFKDR	300
	FYMRTNPFYP	EVELNFISVP	WPQLPNGLEA	AYEFADRDEV	RFFKGNKYWA	VQQQNVLHGY	360
55	PKDIYSSFGF	PRTVKHIDAA	LSEENTGKTY	FFVANKYWRY	DEYKRSMDPG	YFKMIAHDFP	420
	GIGHKVDVAV	MKGDFFFYFFH	GTRQYKFDPK	TKRILTLQKA	NSWFNCRKN		

Seq ID NO: 23 Nucleotide sequence:

Nucleic Acid Accession #: FGENESH predicted ORF

Coding sequence: 141-1580 (underlined sequences correspond to start and stop codons)

60

	1	11	21	31	41	51	
	TCTGCGTGTG	CCGGGGCTAG	GGGCTGGAAG	TCCTGGCTCT	AGTTGCACCT	CGGAAGGAAA	60
	AGGCAAACAG	AGGAGGGAAG	GCGTCTTAGG	ACTGCCTGGA	TCCAGAGCAC	TTTCCTCGGC	120
	CTCTACAGGC	CTGTGTCGCT	<u>ATGGGTTC</u>	CCGCCGCCCC	GGAGGGAGCG	CTGGGCTACG	180
	TCCGCGAGTT	CAGTCGCCAC	TCCTCCGACG	TGCTGGGCAA	CCTCAACGAG	CTGCGCCTGC	240
70	GCGGGATCCT	CACTGACGTC	ACGCTGCTGG	TTGGCGGGCA	ACCCCTCAGA	GCACACAAGG	300
	CAGTTCTCAT	CGCCTGCAGT	GGCTTCTTCT	ATTCAATTTT	CCGGGGCCGT	GCGGGAGTCG	360
	GGGTGGACGT	GCTCTCTCTG	CCCGGGGGTC	CCGAAGCGAG	AGGCTTCGCC	CCTCTATTGG	420
	ACTTCATGTA	CAGTCGCGCG	CTCGCCTCT	CTCCAGCCAC	TGCACCAGCA	GTCCTAGCGG	480
	CCGCCACCTA	TTTGAGATG	GAGCAGCTGG	TCCAGGCATG	CCACCGCTTC	ATCCAGGCCA	540
75	GCTATGAACC	TCTGGGCATG	TCCCTGCGCT	CCCTGGAAGC	AGAACCCCCA	ACACCCCA	600
	CGGCCCTTCC	ACCAAGTAGT	CCCAGGCGCT	CCGAAGGACA	CCCAGACCCA	CCTACTGAAT	660

CTCGAAGCTG CAGTCAAGGC CCCCCAGTC CAGCCAGCCC TGACCCCAAG GCCTGCAACT 720
 GGAAAAAGTA CAAGTACATC GTGCTAAACT CTCAGGCCTC CCAAGCAGGG AGCCTGGTCG 780
 GGGAGAGAAG TTCTGGTCAA CCTTGCCCCC AAGCCAGGCT CCCCAGTGGA GACGAGGCCT 840
 CCAGCAGCAG CAGCAGCAGC AGCAGCAGCA GTGAAGAAGG ACCCATTTCCT GGTCCCCAGA 900
 5 GCAGGCTCTC TCCAACGTCT GCCACTGTGC AGTTCAAATG TGGGGCTCCA GCCAGTACCC 960
 CCTACCTCCT CACATCCCAG GCTCAAGACA CCTCTGGATC ACCCTCTGAA CGGGCTCGTC 1020
 CACTACCGGG AAGTGAATTT TTCAGCTGCC AGAACTGTGA GGCTGTGGCA GGGTGTCTAT 1080
 CGGGGCTGGA CTCCTTGGTT CTGGGGGACG AAGACAAACC CTATAAGTGT CAGCTGTGCC 1140
 10 GGTCTTCGTT CCGCTACAAG GGCAACCTTG CCAGTCATCG TACAGTGCAC ACAGGGGAAA 1200
 AGCCTTACCA CTGCTCAATC TGCGGAGCCC GTTTTAACCG GCCAGCAAAC CTGAAAACGC 1260
 ACAGCCGCAT CCATTGCGGA GAGAAGCCGT ATAAGTGTGA GACGTGCGGC TCGCGTTTGT 1320
 TACAGGTGGC ACATCTGCGG GCGCACGTGC TGATCCACAC CGGGGAGAAG CCCTACCCCT 1380
 GCCCTACCTG CGGAACCCGC TTCCGCGCAC TGACAGCCCT CAAGAGCCAC GTTCGCATCC 1440
 15 ACACCGGAGA GAAGCCTTAC CACTGCGACC CCTGTGGCCT GCATTTCCGG CACAAGAGTC 1500
 AACTGCGGCT GCATCTGCGC CAGAAACAGC GAGCTGTGAC CAACACCAA GTGCACTACC 1560
 ACATTCTCGG GGGGCCCTAG CTGAGCGCAG GCCCAGGCC CACTTGCTTC CTGCGGGTGG 1620
 GAAAGCTGCA GGCCCAGGCC TTGCTTCCCT ATCAGGCTTG GGCATAGGGG TGTGCCAGGC 1680
 CACTTTGGTA TCAGAAATTG CCACCCTCTT AATTTCTCAC TGGGAGAGC AGGGGTGGCA 1740
 20 GATCCTGGCT AGATCTGCCT CTGTTTTGCT GGTCAAAACC TCTTCCCCAC AAGCCAGATT 1800
 GTTTCTGAGG AGAGAGCTAG CTAGGGGCTG GGAAAGGGGA GAGATTGGAG TCCTGGTCTC 1860
 CCTAAGGGAA TAGCCCTCCA CCTGTGGCCC CCATTGCATT CAGTTTATCT GTAAATATAA 1920
 TTTATTGAGG CCTTTGGGTG GCACCGGGGC CTTCAATCGA TTGCATTTCC CACTCCCCCTC 1980
 TTCCACAAGT GTGATTAAAA GTGACCAGAA ACACAGAAGG TGAGATCACA GCTCTGCTGG 2040
 25 CAGAGATTAC TAGCCCTTGG CTCTCTCGTT TGGCTTGGGT ATTTTATATT ATTTCTGTCA 2100
 TAACTTTAT CTTTAGAATT GTTCTTTCTC CTGTTTGTTC GCTGTGTTAGT TTGTTAAAA 2160
 TGGAAAAAGG GGTTCCTCTG GTTCTGCCCC TGTAATTCTA GGTCTGGAAC CTTTATTTGT 2220
 TCTAGGGCAG CTTCTGGGAAC ATGCGGGATT GTGGAATTGG GTCAGGAACC CTCTCTGGTA 2280
 TTCTGGATGT TGTAGTTTCT CTAGCAGTCT AGAAATGGAT ACAGACATTT CTCTGTTCTT 2340
 30 CAAGGGTGTAT AGGAACCATT ATGTTGAGCC CAAAATGGAA GTAATAATAA ATGCCTCCTG 2400
 GAGGCTGTGG GTGTGGGGGA TTCTGTATCT GGATTCCGTA TCACTCCAAC TGGAGGCTGT 2460
 GGGTGTGGGG GATTCTGTAT CTGGATTCCG TATCACTCCA AGTGGAGGCT GGCAGGTTT 2520
 TCTGCAAGAT GGTCCAGAAT CTAAATGTCT CCATTAATCT GGTCACTTGG GTTTGGCTCT 2580
 GCTGTATCCA TCTATAGTGG TAGAGACCCA CCAGGGCTCA AGTGGAGTCC ATCATCCTCC 2640
 35 CACGGGGGCC TGTTCTTAGC ACTGAGTTGA TCGCTCCATG GGGGAGAGAT CAGACATTCC 2700
 TTATCAGAGA TGATGTGACC TTTTCTGACT CTGCCCAGTC TCTATGAATG TTATGGCCTA 2760
 GGGGAAGATC ATGAAACTCT TTAGCTTGAT TAGATGGTAA ACAGTGTAA CCCATCCTT 2820
 ACTACAGAGG CATATGGGTT TGAATGTTAC CTGGGGTTCT CTCTATTGAG TTGAGCCCTT 2880
 TCTTCTTTTA GTGGGTTTTC GACATCTTCT GGCAAGTGTC CAGATGCCAG AACCTTCTT 2940
 40 TCCTCTAGAA GGGATGGTGC TTGGTAACCT TACCTTTTAA AAGCTGGGTC TGTGACCTGG 3000
 TCTTCCATC CCTGCATTCC TGTCTGGAAC CAGTGAATGC ATTAGAACCT TCCATAGGAA 3060
 AAGAAAAGGG GCTGAGTTCC ATTCTGGGTT TGCTGTAGTT TGGTTGGGAT TATTGTTGGC 3120
 ATTACAGATG TAAAAGATTG ACTAGCCCAT AGGCCAAAGG CCTGTTCTAG TTGACCAAGT 3180
 45 TTCAAGTAGG ATTAAGAGGT TGGTTGAGGG GTGCAGTTTC TGGTGTAGGC CAGGTAGGTA 3240
 GAAAGTAGG AACAGGGTTG CCTCTTGGCT GGGTGGAGTC TCTGAAATGT TAGAAGAAGC 3300
 GCTGAAGCCT TGATTGATAG TTCTGCCCTT GTTTGCCCTG GGGCTTATCT GATTATGGGA 3360
 CGAGGGTAGA AAGTAAGAAG CACTTTTGAA TTTGTGGGGT AGAACTTCAA CAATAAGTCA 3420
 GTTCTAGTGG CTGTCGCTG GGGACTAGTG AGAAAGCTAC TCTTCTCCCT CTTCCCTCTT 3480
 TCTCCCCATG GCCCCACTGC AGAATTAAAG AAGGAAGAAG GGAAGCGGGA GGAGTCTATA 3540
 50 AGAAGGAATC ATGATTTCTA TTTAGCAGAT TGGATGGGCA GGTGGAGAAT GCCTGGGGGT 3600
 AGAAATGTTA GATCTTGCAA CATCAGATCC TTGGAATAAA GAAGCCTCTC TGYGCWRAAA 3660
 AAAAAA AAAAAA

Seq ID NO: 24 Protein sequence:

Protein Accession #: FGENSEH predicted

1 11 21 31 41 51
 60 | | | | |
 MGSPAPEGA LGVREFTRH SSDVLGNLNE LRLRGILTDV TLLVGGQPLR AHKAVLIACS 60
 GFFYSIFRGR AGVGVDVLSL PGGPEARIFA PLLDFMYTSR LRLSPATAPA VLAAATYLOM 120
 EHVVOACHRF IQASYEPLGI SLRPLEAEP TPPTAPPPGS PRRSEGHDPD PTESRSCSQG 180
 PPSPASPPDK ACNWKYKYI VLNSQASQAG SLVGERSSGQ PCPOARLPSG DEASSSSSSS 240
 SSSSEEGPI GPQSRLSPTA ATVQFKCGAP ASTPYLLTSQ AQDTSGPSPE RARPLPGSEF 300
 65 FSCQNCEAVA GCSGLDSL PVDEDKPYK QLCRSSFRYK GNLAHRTVH TGEKPYHCSI 360
 CGARFNRPAN LKTHSRIHSG EKPYKCETCG SRFVQVAHLR AHVLIHTGEK PYPCTCGTR 420
 FRHLQTLKSH VRIHTGEKPY HCDPCGLHFR HKSQRLHLR QKHGAATNTK VHYHILGGP

Seq ID NO: 25 Nucleotide sequence:

Nucleic Acid Accession #: U21551

Coding sequence: 1..1155 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 75 | | | | |
 ATGGATTGCA GTAACGGATC GGCAGAGTGT ACCGGAGAAG GAGGATCAAA AGAGGTGGTG 60

	GGGACTTTTA	AGGCTAAAGA	CCTAATAGTC	ACACCAGCTA	CCATTTTAAA	GGAAAAACCA	120
	GACCCCAATA	ATCTGGTTTT	TGGAACGTGT	TTCACGGATC	ATATGCTGAC	GGTGGAGTGG	180
	TCCTCAGAGT	TTGGATGGGA	GAAACCTCAT	ATCAAGCCTC	TTCAGAACCT	GTCATTGCAC	240
5	CCTGGCTCAT	CAGCTTTGCA	CTATGCAGTG	GAATTATTTG	AAGGATTGAA	GGCATTTCGA	300
	GGAGTAGATA	ATAAAATTCG	ACTGTTTCAG	CCAAACCTCA	ACATGGATAG	AATGTATCGC	360
	TCTGCTGTGA	GGGCAACTCT	GCCGGTATTT	GACAAAGAAG	AGCTCTTAGA	GTGTATTCAA	420
	CAGCTTGTGA	AATTGGATCA	AGAATGGGTC	CCATATTCAA	CATCTGCTAG	TCTGTATATT	480
	CGTCTGTCAT	TCATTGGAAC	TGAGCCTTCT	CTTGGAGTCA	AGAAGCCTAC	CAAAGCCCTG	540
10	CTCTTTGTAC	TCTTGAGCCC	AGTGGGACCT	TATTTTTCAA	GTGGAACCTT	TAATCCAGTG	600
	TCCCTGTGGG	CCAATCCCAA	GTATGTAAGA	GCCTGGAAAG	GTGGAACCTG	GGACTGCAAG	660
	ATGGGAGGGA	ATTACGGCTC	ATCTCTTTTT	GCCCAATGTG	AAGACGTAGA	TAATGGGTGT	720
	CAGCAGGTCC	TGTGGCTCTA	TGGCAGAGAC	CATCAGATCA	CTGAAGTGGG	AACTATGAAT	780
	CTTTTTCTTT	ACTGGATAAA	TGAAGATGGA	GAAGAAGAAC	TGGCAACTCC	TCCACTAGAT	840
	GGCATCATTC	TTCCAGGAGT	GACAAGGCGG	TGCATTCTGG	ACCTGGCACA	TCAGTGGGGT	900
15	GAATTTAAGG	TGTCAGAGAG	ATACCTCACC	ATGGATGACT	TGACAACAGC	CCTGGAGGGG	960
	AACAGAGTGA	GAGAGATGTT	TAGCTCTGGT	ACAGCCTGTG	TTGTTTGCCC	AGTTTCTGAT	1020
	ATACTGTACA	AAGGCGAGAC	AATACACATT	CCAACATATG	AGAATGGTCC	TAAGCTGGCA	1080
	AGCCGCATCT	TGAGCAAATT	AACCTGATAT	CAGTATGGAA	GAGAAGAGAG	CGACTGGACA	1140
20	ATTGTGCTAT	<u>CCTGA</u>					

Seq ID NO: 26 Protein sequence:

Protein Accession #: AAB08528

25	1	11	21	31	41	51	
	MDCSNGSAEC	TGEGGSKEVU	GTFKAKDLIV	TPATILKEKP	DPNNLVFGTV	FTDHMLTVEW	60
	SSEFGWEKPH	IKPLQNLSLH	PGSSALHYAV	ELFEGKLKAFR	GVDNKIRLFQ	PNLNMDRMYR	120
	SAVRATLPVF	DKEELLECIQ	QLVKLDQEWV	PYSTSASLYI	RPAFIGTEPS	LGVKKPTKAL	180
30	LFVLLSPVGP	YFSSGTFNPV	SLWANPKYVR	AWKGGTGDCK	MGGNYGSSLF	AQCEDVDNGC	240
	QQVLWLYGRD	HQITEVGTMN	LFLYWINEDG	EEELATPPLD	GIILPGVTTR	CILDLAHQWG	300
	EFKVSERYLT	MDDLTTALEG	NRVREMFSSG	TACVVCVPSD	ILYKGETIHI	PTMENGPKLA	360
	SRILSKLTDI	QYGREESDWT	IVLS				

Seq ID NO: 27 Nucleotide sequence:

Nucleic Acid Accession #: XM_039209

Coding sequence: 656..2758 (underlined sequences correspond to start and stop codons)

40	1	11	21	31	41	51	
	TCGCGCGGGG	GCCGCCCCCT	CCCCTTCCCT	CCACCCTGGG	CGGGGCGCGG	CGAGAAGCGG	60
	TGACGTCAAG	GGGCGCGCTG	TGGCAGCAC	TCCCGCGCGG	CTAGTTAAAA	AGAAGAAGAA	120
45	AAGAGGGAAC	GAAACATGAG	AGGCTGTGTG	AGAAGCTGCA	GCCGCGGGCA	GAGGAGACCT	180
	CAGCATCATC	TAGAGCCAG	CGCTGGCCCT	GCCTCCGCGT	GCCCCGCGCG	CGCCGTCGCC	240
	GTTTCTGTTC	CTGCTACTGT	CCCACCTAAA	CAACTCCCGT	TACACGGACA	AGTGAACATC	300
	TGTGGCTGTC	CTCTCCTTTT	CTTCTCTCTC	TTCCAACTCC	TTCTCTCTCT	CCCACTTCCC	360
	AGCCGCAGCA	GAAAGCCCCC	AACCCAACTG	AACTGGCAC	AACTGCAAAC	GGTGTCTATC	420
50	GCACAACTTT	ATCTCGCTCC	TCGGGCTCCC	CTAAGGCATT	GGACCCATCG	CCGCGTCTTT	480
	TATTTTGTGC	AAAGTTGCAT	CGCTGTACAT	ATTTTGTGCC	CCGCCACCTC	CCTCTGTCTC	540
	TGGAGTGCCC	TACAGCCCCG	CAAACCTCTC	CTGGAGCTGC	GCCCTAGTGC	CCCTGCTGGG	600
	CAGTGGCGTT	CCCCCCCATC	CTCCCGCGCC	CAGCCCCTGC	TGCTCTGGGC	<u>AGACGATGCT</u>	660
	GAAGATGCTC	TCCTTTAAGC	TGCTGTCTGT	GGCCGTGGCT	CTGGGCTTCT	TTGAAGGAGA	720
55	TGCTAAGTTT	GGGGAAGAAA	ACGAAGGGAG	CGGAGCAAGG	AGGAGAAGGT	GCCTGAATGG	780
	GAACCCCCCG	AAGCGCCTGA	AAAGGAGAGA	CAGGAGGATG	ATGTCCCAGC	TGGAGCTGCT	840
	GAGTGGGGGA	GAGATGCTGT	GCGGTGGCTT	CTACCCTCGG	CTGTCTGTCT	GCCTGCGGAG	900
	TGACAGCCCG	GGGCTAGGGC	GCCTGGAGAA	TAAGATATTT	TCTGTTACCA	ACAACACAGA	960
	ATGTGGGAAG	TTACTGGAGG	AAATCAAATG	TGCACTTTGC	TCTCCACATT	CTCAAAGCCT	1020
60	GTTCCACTCA	CCTGAGAGAG	AAGTCTTGGA	AAGAGACCTA	GTACTTCCTC	TGCTCTGCAA	1080
	AGACTATTGC	AAAGAATTCT	TTTACACTTG	CCGAGGCCAT	ATTCCAGGTT	TCCTTCAAAC	1140
	AACTGCGGAT	GAGTTTGTCT	TTTACTATGC	AAGAAAAGAT	GGTGGGTTGT	GCTTTCCAGA	1200
	TTTTCCAAGA	AAACAAGTCA	GAGGACCAGC	ATCTAACTAC	TTGGACCAGA	TGGAAGAATA	1260
	TGACAAAGTG	GAGAGATACA	GCAGAAAGCA	CAAACACAAC	TGCTTCTGTA	TTCAGGAGGT	1320
65	TGTGAGTGGG	CTGCGGCAGC	CCGTTGGTGC	CCTGCATAGT	GGGGATGGCT	CGCAACGTCT	1380
	CTTCATTCTG	GAAAAAGAAG	GTTATGTGAA	GATACTTACC	CCTGAAGGAG	AAATTTTCAA	1440
	GGAGCCTTAT	TTGGACATTC	ACAAACTTGT	TCAAAGTGGG	ATAAAGGGAG	GAGATGAAAG	1500
	AGGACTGCTA	AGCCTCGCAT	TCCATCCCAA	TTACAAGAAA	AATGGAAAGT	TGTATGTGTC	1560
	CTATACCACC	AACCAAGAAC	GGTGGGCTAT	CGGGCCTCAT	GACCACATTC	TTAGGGTTGT	1620
70	GGAATACACA	GTATCCAGAA	AAAATCCACA	CCAAGTTGAT	TTGAGAACAG	CCAGAGTCTT	1680
	TCTTGAAGTT	GCAGAACTCC	ACAGAAAGCA	TCTGGGAGGA	CAACTGCTCT	TTGGCCCTGA	1740
	CGGCTTTTGT	TACATCATTC	TTGGTGATGG	GATGATTACA	CTGGATGATA	TGGAAGAAAT	1800
	GGATGGGTTA	AGTGATTTCA	CAGGCTCAGT	GCTACGGCTG	GATGTGGACA	CAGACATGTG	1860
	CAACGTGCTT	TATTCCATAC	CAAGGAGCAA	CCCACACTTC	AACAGCACCA	ACCAGCCCCC	1920
75	CGAAGTGTTT	GATCTATGGC	TCCACGATCC	AGGCAGATGT	GCTGTGGATA	GACATCCAC	1980
	TGATATAAAC	ATCAATTATA	CGATACTGTG	TTCAGACTCC	AATGGAAAAA	ACAGATCATC	2040

	AGCCAGAATT	CTACAGATAA	TAAAGGGGAA	AGATTATGAA	AGTGAGCCAT	CACTTTTAGA	2100
	ATTCAAGCCA	TTCAGTAATG	GTCCTTTGGT	TGGTGGATTT	GTATACCGGG	GCTGCCAGTC	2160
	AGAAAGATTG	TATGGAAGCT	ACGTGTTTGG	AGATCCGTAAT	GGGAATTTCC	TAACTCTCCA	2220
5	GCAAAGTCCT	GTGACAAAGC	AGTGGCAAGA	AAAACCACTC	TGTCTCGGCA	CTAGTGGGTC	2280
	CTGTAGAGGC	TACTTTTCCG	GTCACATCTT	GGGATTTGGA	GAAGATGAAC	TAGGTGAAGT	2340
	TTACATTTTA	TCAAGCAGTA	AAAGTATGAC	CCAGACTCAC	AATGGAAAAC	TCTACAAAAT	2400
	TGTAGATCCC	AAAAGACCTT	TAATGCCTGA	GGAATGCAGA	GCCACGGTAC	AACCTGCACA	2460
	GACACTGACT	TCAGAGTGCT	CCAGGCTCTG	TCGAAACGGC	TACTGCACCC	CCACGGGAAA	2520
10	GTGCTGCTGC	AGTCCAGGCT	GGGAGGGGGA	CTTCTGCAGA	ACTGCAAAAT	GTGAGCCAGC	2580
	ATGTCGTCAT	GGAGGTGTCT	GTGTTAGACC	GAACAAGTGC	CTCTGTAAAA	AAGGATATCT	2640
	TGGTCCTCAA	TGTGAACAAG	TGGACAGAAA	CATCCGCAGA	GTGACCAGGG	CAGGTATTCT	2700
	TGATCAGATC	ATTGACATGA	CATCTTACTT	GCTGGATCTA	ACAAGTTACA	TGTATAGTT	2760
	TCTGGGACTG	TTTGAATATT	CTATTCGAAT	GGGCATTTAT	TTTTTATCCT	GTCATTAAAA	2820
15	AAAAAAGACT	GTTATCCTGC	TACACACTCC	TGTGATTTCA	TTCTCTTTTA	TTAATTAAAA	2880
	AATAATTTCC	AGAAATGTGC	AGATCCTCTG	TGTGTATGTC	AGCATGTTTG	TTCACATATG	2940
	CACATACACA	TACTCATAAC	CCCTATATGC	GTTGTTGCAT	AACAGATGAT	TTTTTAAAAAT	3000
	ATATACTTCC	TTATGCAAAAG	TAATTTACAC	AGAAATTCCA	TTGTAAATTG	ATAATGGATT	3060
	TTTTATGTTA	CTAGAAGAGA	TTATTTGACT	TCCCAGGAAT	TTTCTGTCTG	TAATCACTAA	3120
20	AGTCAACTTT	AATAGAGTTT	TGAAACAGTA	CTGTGCAATC	CGATGGATCT	AATTAATAAAA	3180
	AAGGCAATAT	TTTTTATATTA	AAGTACTATA	CTAGGAGAGA	ATGTTTCAGA	ACTCCCTGAT	3240
	GAATTTCTAA	GTGAGCAACT	TGATATAAAA	TTGTAATCTT	CATTTTGTGC	AGTGTATCCA	3300
	GTTACAGAAAT	GCTACACACT	TACCTTTTTA	TTGGCTGAGA	AATCTGGTTA	TTTCATCTTA	3360
	ATCTCAAGAT	TGTTTTCAAG	TGTTTTATAA	TTAAATCATA	ATAGCATATT	TTAAATCAA	3420
25	TCTTCCTAAA	AGGCTGCTT	TTATTTGATA	TTTTTATTTA	CAATAGGCAC	TGGGTTTGTG	3480
	TTACATATTT	ATATATTTTA	TTTTATTTT	ATAATATAGA	CATCACCTAG		

Seq ID NO: 28 Protein sequence:
Protein Accession #: XP_039209

30	1	11	21	31	41	51	
	MLKMLSFKLL	LLAVALGFFE	GDAKFGERNE	GSGARRRRCL	NGNPPKRLKR	RDRRMSQLE	60
	LLSGGEMLCG	GFYPRLSCLL	RSDSPGLGRL	ENKIFSVTNN	TECGKLLLEI	KCALCSPHSQ	120
35	SLFHSPEREV	LERDLVLPPL	CKDYCKEFFY	TCRGHIPGFL	QTTADEFCFY	YARKDGLCF	180
	PDFPRKQVRG	PASNYLDQME	EYDKVEEISR	KHKHNCFCIQ	EVVSGLRQPV	GALHSGDGSQ	240
	RLFILEKEGY	VKILTPEGEI	FKEPYLDIHK	LVQSGIKGGD	ERGLLSLAFH	PNYKNGKLY	300
	VSYTTNQERW	AIGPHDHILR	VVEYTVSRKN	PHQVDLRTAR	VFLEVAELHR	KHLGGQLLFG	360
40	PDGFLYIILG	DGMITLDDME	EMDGLSDFTG	SVLRDLVDVD	MCNVFYSIPR	SNPHFNSTNQ	420
	PPEVFAHGLH	DPGRCAVDRH	PTDININLTI	LCSDSNGKNR	SSARILQIIK	GKDYSESEPSL	480
	LEFKPFSNGP	LVGGFVYRGC	QSERLYGSYV	FGDRNGNFLT	LQSPVTKQW	QEKPLCLGTS	540
	GSCRGYPSGH	ILGFGEDELG	EVYILSSSKS	MTQTHNGKLY	KIVDPKRPLM	PEECRATVQP	600
	AQTLTSECSR	LCRNGYCTPT	GKCCSPGWE	GDFCRTAKCE	PACRHGGVCV	RPNKCLCKKG	660
45	YLGPOCEQVD	RNIRRVTRAG	ILDQIIDMTS	YLLDLTSYIV			

Seq ID NO: 29 Nucleotide sequence:
Nucleic Acid Accession #: NM_024756
Coding sequence: 75..2924 (underlined sequences correspond to start and stop codons)

50	1	11	21	31	41	51	
	AAGACAACGT	CACTAGCAGT	TTCTGGAGCT	ACTTGCCAAG	GCTGAGTGTG	AGCTGAGCCT	60
	GCCCCACCAC	CAAGATGATC	CTGAGCTTGC	TGTTACAGCT	TGGGGGGCCC	CTGGGCTGGG	120
55	GGCTGCTGGG	GGCATGGGCC	CAGGCTTCCA	GTACTAGCCT	CTCTGATCTG	CAGAGCTCCA	180
	GGACACCTGG	GGTCTGGAAG	GCAGAGGCTG	AGGACACCAG	CAAGGACCCC	GTTGGACGTA	240
	ACTGGTGCCC	CTACCCAATG	TCCAAGCTGG	TCACCTTACT	AGCTCTTTGC	AAAACAGAGA	300
	AATTCCCTCAT	CCACTCGCAG	CAGCCGTGTC	CGCAGGGAGC	TCCAGACTGC	CAGAAAGTCA	360
60	AAGTCATGTA	CCGCATGGCC	CACAAGCCAG	TGTACCAGGT	CAAGCAGAAG	GTGCTGACCT	420
	CTTTGGCCTG	GAGGTGCTGC	CCTGGCTACA	CGGGCCCCAA	CTGCGAGCAC	CACGATTCCA	480
	TGGCAATCCC	TGAGCCTGCA	GATCCTGGTG	ACAGCCACCA	GGAACCTCAG	GATGGACCAG	540
	TCAGCTTCAA	ACCTGGCCAC	CTTGCTGCAG	TGATCAATGA	GGTTGAGGTG	CAACAGGAAC	600
	AGCAGGAACA	TCTGCTGGGA	GATCTCCAGA	ATGATGTGCA	CCGGGTGGCA	GACAGCCTGC	660
65	CAGGCCTGTG	GAAAGCCCTG	CCTGGTAACC	TCACAGCTGC	AGTGATGGAA	GCAAAATCAA	720
	CAGGGCACGA	GTTCCCTGAT	AGATCCTTGG	AGCAGGTGCT	GCTACCCAC	GTGGACACCT	780
	TCCTACAAGT	GCATTTTCAGC	CCCATCTGGA	GGAGCTTTAA	CCAAAGCCTG	CACAGCCTTA	840
	CCCAGGCCAT	AAGAAACCTG	TCTCTTGACG	TGGAGGCCAA	CCGCCAGGCC	ATCTCCAGAG	900
	TCCAGGACAG	TGCCGTGGCC	AGGGCTGACT	TCCAGGAGCT	TGGTGCCAAA	TTTGAGGCCA	960
70	AGGTCCAGGA	GAACACTCAG	AGAGTGGGTC	AGCTGCGACA	GGACGTGGAG	GACCGCCTGC	1020
	ACGCCAGCA	CTTTACCCTG	CACCGCTCGA	TCTCAGAGCT	CCAAGCCGAT	GTGGACACCA	1080
	AATTGAAGAG	GCTGCACAAG	GCTCAGGAGG	CCCCAGGGAC	CAATGGCAGT	CTGGTGTGTG	1140
	CAACGCCTGG	GGCTGGGGCA	AGGCCTGAGC	CGGACAGCCT	GCAGGCCAGG	CTGGGCCAGC	1200
	TGCAGAGGAA	CCTCTCAGAG	CTGCACATGA	CCACGGCCCG	CAGGGAGGAG	GAGTTGCAGT	1260
	ACACCCTGGA	GGACATGAGG	GCCACCCTGA	CCCGGCACGT	GGATGAGATC	AAGGAACTGT	1320
75	ACTCCGAATC	GGACGAGACT	TTCGATCAGA	TTAGCAAGGT	GGAGCGGCAG	GTGGAGGAGC	1380
	TGCAGGTGAA	CCACACGGCG	TCCCGTGTAT	TGCGCGTGAT	CCTGATGGAG	AAGTCTCTGA	1440

	TCATGGAGGA	GAACAAGGAG	GAGGTGGAGC	GGCAGCTCCT	GGAGCTCAAC	CTCACGCTGC	1500
	AGCACCTGCA	GGGTGGCCAT	GCCGACCTCA	TCAAGTACGT	GAAGGACTGC	AATTGCCAGA	1560
	AGCTCTATTT	AGACCTGGAC	GTCATCCGGG	AGGGCCAGAG	GGACGCCACG	CGTGCCCTGG	1620
	AGGAGACCCA	GGTGAGCCTG	GACGAGCGGC	GGCAGCTGGA	CGGCTCCTCC	CTGCAGGCCC	1680
5	TGCAGAACGC	CGTGACGCC	GTGTCGCTGG	CCGTGGACGC	GCACAAAGCG	GAGGGCGAGC	1740
	GGGCGCGGGC	GGCCACGTCG	CGGCTCCGGA	GCCAAGTGCA	GGCGCTGGAT	GACGAGGTGG	1800
	GCGCGCTGAA	GGCGGCCGCG	GCCGAGGCC	GCCACGAGGT	GCGCCAGCTG	CACAGCGCCT	1860
	TCGCCGCCCT	GCTGGAGGAC	GCGCTGCGGC	ACGAGGCGGT	GCTGGCCGCG	CTCTTCGGGG	1920
	AGGAGGTGCT	GGAGGAGATG	TCTGAGCAGA	CGCCGGGACC	GCTGCCCCTG	AGCTACGAGC	1980
10	AGATCCGCGT	GGCCTGTCAG	GACGCCGCTA	GCGGGCTGCA	GGAGCAGGCG	CTCGGCTGGG	2040
	ACGAGCTGGC	CGCCCGAGTG	ACGCCCTGG	AGCAGGCCTC	GGAGCCCCCG	CGGCCGCGAG	2100
	AGCACCTGGA	GCCCAGCCAC	GACGCGGGCC	GCGAGGAGGC	CGCCACCACC	GCCCTGGCCG	2160
	GGCTGGCGCG	GGAGCTCCAG	AGCCTGAGCA	ACGACGTCAA	GAATGTCGGG	CGGTGCTGCG	2220
	AGGCCGAGGC	CGGGGCGGG	GCCGCTCCC	TCAACGCCCT	CCTTGACGGC	CTCCACAACG	2280
15	CACCTCTCGC	CACCTAGCGC	AGCTTGGAGC	AGCACCAGCG	GCTCTTCCAC	AGCCTCTTTG	2340
	GGAACCTCCA	AGGGCTCATG	GAAGCCAACG	TCAGCCTGGA	CCTGGGGAAG	CTGCAGACCA	2400
	TGCTGAGCAG	GAAAGGGAAG	AAGCAGCAGA	AAGACCTGGA	AGTCCCCCGG	AAGAGGGACA	2460
	AGAAGGAAGC	GGAGCCTTTG	GTGGACATAC	GGGTACAGG	GCCTGTGCCA	GGTGCCCTTG	2520
	GCGCGGCGCT	CTGGGAGGCA	GGATCCCCTG	TGGCCTTCTA	TGCCAGCTTT	TCAGAAGGGA	2580
20	CGGCTGCCCT	GCAGACAGTG	AAGTTCAACA	CCACATACAT	CAACATTGGC	AGCAGCTACT	2640
	TCCCTGAACA	TGGCTACTTC	CGAGCCCTTG	AGCGTGGTGT	CTACCTGTTT	GCAGTGAGCG	2700
	TTGAATTTGG	CCCAGGGCCA	GGCACCAGGC	AGCTGGTGTT	TGGAGGTCAC	CATCGGACTC	2760
	CAGTCTGTAC	CACCTGGCAG	GGGAGTGGAA	GCACAGCAAC	GGTCTTTGCC	ATGGCTGAGC	2820
	TGCAGAAGGG	TGAGCGAGTA	TGGTTTGAGT	TAACCCAGGG	ATCAATAACA	AAGAGAAGCC	2880
25	TGTCGGGCAC	TGCATTTGGG	GGCTTCTCTA	TGTTTAAGAC	CTGAACCCCA	GCCCCAATCT	2940
	GATCAGACAT	CATGGACTCG	CCCAGCTCTC	CTCGGCCTGG	GGCTCTGGCC	AAGGATGGGC	3000
	TGGAGGTCAT	TCAGTTGGTC	TGTCTCTTCC	CTGGAACCTT	TCTGCAAAGA	TGGTGTGGTG	3060
	TACGTGGCTT	CCCTGTAACC	ACATGGGGCT	TGGCCATTTC	TCCATGATGA	GAAGGACTGG	3120
	AATGCTTCTC	CGGGCAGGAC	ATGGTCTTAG	GAAGCCTGAA	CCTTGGCTTG	GCATGCCTTC	3180
30	TCAGACAGCA	CGGCCCTGGG	TCCAACCTTT	CACCACACCC	TGTATTCTAC	AACTTCTTTG	3240
	GTGTTTGTCT	CCTCCTGTGG	TTGGAACCTT	CTGTACAACA	CTTTAACTT	TTCTCTTGCT	3300
	TCCTCTTCTC	TTCTCCTTTA	TCGTATGATA	GAAAGACATT	CTTCCCCAGG	AGGAATGTTT	3360
	AAAATGGAGG	CAACATTTTG	GCCAACATTG	GAAAGCACTA	GAGGGCAATG	GGATTAAACC	3420
	AACCTGCTTG	GTCTCTATTA	GTCAGTAATG	AAGACGACAG	CCTGGCCAAC	CAAGGGAAAG	3480
35	GAAATTAGTA	TCTTTAGTTT	CAGTCATTCC	TTGTAGGATA	TGGTTTAGCT	GTGCCCCCAC	3540
	CTAAATATATC	ATCTTGAATT	GTAATCCCTA	TAATCCCCAC	ATCAAGGGAG	AGATCAGGTG	3600
	GAGGTAATTG	GATCTTGGGG	GCGGTTCCCC	CATGCTGTTC	TTGTGATAGT	TCTCACGAGA	3660
	TCTGATGATT	TTATAAGTTT	GATAGTTCTC	CCTGTGTTCA	TTCTCCTTCC	TGCCACCTTG	3720
40	TGAAGATGCC	TTGGTTCTCT	TTCACTGTCT	GCCATGATG	TAAGTTTCTC	GAGGCCTCCC	3780
	CAGCCATGTG	GAACAGTGAG	TCAATTAAAC	CTCTTTCCTT	TATAAATT		

Seq ID NO: 30 Protein sequence:
Protein Accession #: NP_079032

45	1	11	21	31	41	51	
	MILSLFLSLG	GPIGWGLLGA	WAQASSTSLS	DLQSSRTPGV	WKAEAEEDTSK	DPVGRNWCPY	60
	PMKSLVTLTA	LCKTEKFLIH	SQQPCPQGAP	DCQKVVMYR	MAHKPVYQVK	QKVLTSIAWR	120
50	CCPGYTGPNL	EHHDSMAIPE	PADPGDSHQE	PQDGPVSFKP	GHLAAVINEV	EVQQEQQEHL	180
	LGLDLQNDVHR	VADSLPGWLK	ALPGLNLTA	MEANQTGHEF	PDRSLEQVLL	PHVDTFLQVH	240
	FSPFIWRSFNQ	SLHSLTQAIR	NLSLDVEANR	QAISRVDQSA	VARADFQELG	AKFEAKVQEN	300
	TQVRVQLRQD	VEDRLHAQHF	TLHRSISELQ	ADVDTKLKR	HKAQEAPGTN	GSLVLATPGA	360
	GARPEPDSLQ	ARLGLQLRNL	SELHMTTARR	EEELQYTLED	MRATLTRHVD	EIKELYSSED	420
55	ETFDQISKVE	RQVEELQVNH	TALRELRLVIL	MEKSLIMEEN	KEEVERQLLE	LNLTLOHLQ	480
	GHADLIKYVK	DCNCQKLYLD	LDVIREGQRD	ATRALEETQV	SLDERRQLDG	SSLQALQNAV	540
	DAVSLAVDAH	KAEGERRARA	TSRLRSQVQA	LDDEVGALK	AAAEARHEVR	QLHSFAFALL	600
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Seq ID NO: 31 Nucleotide sequence:
Nucleic Acid Accession #: AB037715
Coding sequence: 370..3489 (underlined sequences correspond to start and stop codons)

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Seq ID NO: 32 Protein sequence:
 Protein Accession #: BAA92532

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Seq ID NO: 33 Nucleotide sequence:
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65 Seq ID NO: 35 Nucleotide sequence:
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5 GACTCCGACA CTCTGGAGGT GATGCGCAAG CCCAGGTGTG GAGTTCCTGA TGTGGTCAC 360
 TTCAGAACCT TTCCTGGCAT CCGAAGTGG AGGAAAACCC ACCTTACATA CAGGATTGTG 420
 AATTATACAC CAGATTTGCC AAAAGATGCT GTTGATTCTG CTGTTGAGAA AGCTCTGAAA 480
 GTCTGGGAAG AGGTGACTCC ACTCACATTC TCCAGGCTGT ATGAAGGAGA GGCTGATATA 540
 10 ATGATCTCTT TTGCAGTTAG AGAACATGGA GACTTTTACC CTTTGTATGG ACCTGGAAAT 600
 GTTTTGGCCC ATGCCTATGC CCCTGGGCCA GGGATTAATG GAGATGCCCA CTTTGTATGAT 660
 GATGAACAAT GGACAAAGGA TACAACAGGG ACCAATTTAT TTCTCGTTGC TGCTCATGAA 720
 ATTGGCCACT CCCTGGGTCT CTTTCACTCA GCCAACACTG AAGCTTTGAT GTACCCACTC 780
 TATCACTCAC TCACAGACCT GACTCGGTTC CGCCTGTCTC AAGATGATAT AAATGGCATT 840
 15 CAGTCCCTCT ATGGACCTCC CCCTGACTCC CCTGAGACCC CCCTGGTACC CACGGAACCT 900
 GTCCTCCAG AACCTGGGAC GCCAGCCAAC TGTGATCCTG CTTTGTCTCT TGATGCTGTC 960
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 AGGAAGCTTG AACCTGAATT GCATTTGATC TCTTCATTTT GGCCATCTCT TCCTTCAGGC 1080
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 20 TTCTGGGCCA TCAGAGGAAA TGAGGTACGA GCTGGATACC CAAGAGGCAT CCACACCCTA 1200
 GGTTCCTCTC CAACCGTGAG GAAAATCGAT GCAGCCATT CTGATAAGGA AAAGAACAAA 1260
 ACATATTTCT TTGTAGAGGA CAAATACTGG AGATTTGATG AGAAGAGAAA TTCCATGGAG 1320
 CCAGGCTTTC CCAAGCAAAT AGCTGAAGAC TTTCAGGGA TTGACTCAA GATTGATGCT 1380
 GTTTTTGAAG AATTTGGGTT CTTTATTTC TTTACTGGAT CTTACAGTT GGAGTTTGAC 1440
 25 CTTAAATGCAA AGAAAGTGAC ACACACTTTG AAGAGTAACA GCTGGCTTAA TTGTGAAAG 1500
 AGATATGTAG AAGGCACAA ATGGGCACCT TAAATGAAGC TAATAATTCT TCACCTAAGT 1560
 CTCTGTGAAT TGAATGTTC GTTTTCTCCT GCCTGTGCTG TGACTCGAGT CACACTCAAG 1620
 GGAACCTGAG CGTGAATCTG TATCTTGCCG GCATTTTTTA TGTATTACA GGGCATTCAA 1680
 ATGGGCTGCT GCTTAGCTTG CACCTTGTC CATAGAGTGA TCTTTCCAA GAGAAGGGGA 1740
 30 AGCACTCGTG TGCAACAGAC AAGTGACTGT ATCTGTGTAG ACTATTGCT TATTAATAA 1800
 AGACGATTG TCAGTTGTTT T

Seq ID NO: 36 Protein sequence:

Protein Accession #: NP_002413

35 1 11 21 31 41 51
 | | | | |
 MKSLPILLLL CVAVCSAYPL DGAARGEDTS MNLVQKYLEN YYDLKKDVKQ FVRRKDSGPV 60
 VKKIREMQKF LGLEVTKGLD SDTLEVMRKP RCGVPDVGHF RTFPGIPKWR KTHLTYRIVN 120
 YTPDLPKDAV DSAVEKALKV WEEVTPLTFS RLYEGEADIM ISFAVREHGD FYFFDGPENV 180
 LAHAYAPGPG INGDAHFDDE EQWTKDITGT NLFLVAAHEI GHSLGLFHSA NTEALMYPLY 240
 40 HSLTDLTRFR LSQDDINGIQ SLYGPPPDSP ETPLVPTPEP PPEPGTPANC DPALSFDAVS 300
 TLRGEILIFK DRHFWKSLR KLEPELHLIS SFWPSLPSGV DAAYEVTSKD LVFIFKGNQF 360
 WAIRGNEVRA GYPRGIHTLG FPPFVRKIDA AISDKEKNKT YFFVEDKYWR FDEKRNSMEP 420
 GFPKQIAEDF PGIDSKIDAV FEEFGFFYFF TGSSQLEFDP NAKKVTHTLK SNSWLNC

Seq ID NO: 37 Nucleotide sequence:

Nucleic Acid Accession #: NM_003246

Coding sequence: 112..3624 (underlined sequences correspond to start and stop codons)

50 1 11 21 31 41 51
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 CGCCGCGCTC CGGTACACAC AGGATCCCTG CTGGGCACCA ACAGCTCCAC CATGGGGCTG 120
 GCCTGGGGAC TAGGCGTCTT GTTCTGATG CATGTGTGTG GCACCAACCG CATTCCAGAG 180
 55 TCTGGCGGAG ACAACAGCGT GTTTGACATC TTTGAACTCA CCGGGGCCGC CCGCAAGGGG 240
 TCTGGGCGCC GACTGGTGAA GGGCCCCGAC CCTTCCAGCC CAGCTTCCG CATCGAGGAT 300
 GCCAACCTGA TCCCCCTGT GCCTGATGAC AAGTTCCAAG ACCTGGTGGA TGCTGTGCGG 360
 GCAGAAAAGG GTTTCCTCCT TCTGCGATCC CTGAGGCAGA TGAAGAAGAC CCGGGGCACG 420
 CTGTGGCCCC TGGAGCGGAA AGACCACTCT GGCCAGGTCT TCAGCGTGGT GTCCAATGGC 480
 60 AAGGCGGGCA CCCTGGACCT CAGCCTGACC GTCCAAGGAA AGCAGCACGT GGTGTCTGTG 540
 GAAGAAGCTC TCCTGGCAAC CGGCCAGTGG AAGAGCATCA CCTGTTTGT GCAGGAAGAC 600
 AGGGCCAGC TGTACATCGA CTGTGAAAAG ATGGAGAATG CTGAGTTGGA CGTCCCCATC 660
 CAAAGCGTCT TCACCAGAGA CCTGGCCAGC ATCGCCAGAC TCCGCATCGC AAAGGGGGGC 720
 GTCAATGACA ATTTCAGGG GGTGTGAGG AATGTGAGGT TTGTCTTTGG AACCAACCA 780
 65 GAAGACATCC TCAGGAACAA AGGCTGCTCC AGCTCTACCA GTGTCCTCCT CACCCTTGAC 840
 AACAACTGG TGAATGTTT CAGCCCTGCC ATCCGCACTA ACTACATTGG CCACAAGACA 900
 AAGGACTTGC AAGCCATCTG CGGCATCTCC TGTGATGAGC TGTCCAGCAT GGTCTTGAA 960
 CTCAGGGGRC TCGCACCAT TGTGACCAGC CTGAGGACA GCATCCGCAA AGTGACTGAA 1020
 70 GAGAACAAAG AGTTGGCCAA TGAGCTGAGG CGGCCTCCCC TATGCTATCA CAACGGAGTT 1080
 CAGTACAGAA ATAACAGGGA ATGGACTGTT GATAGCTGCA CTGAGTGTCA CTGTGAGAAC 1140
 TCAGTTACCA TCTGCAAAA GGTGTCCTGC CCCATCATGC CTTGCTCAA TGCCACAGTT 1200
 CCTGATGGAG AATGCTGTCC TCGCTGTGG CCCAGCGACT CTGCGGACGA TGGCTGTCT 1260
 CCATGGTCCG AGTGGACCTC CTGTTCTACG AGCTGTGGCA ATGGAATTCA GCAGCGCGGC 1320
 CGCTCTCGCG ATAGCTCAA CAACCGATGT GAGGGCTCCT CGGTCCAGAC ACGGACCTGC 1380
 75 CACATTTCAG AGTGTGACA AAGATTAAAT CAGGATGGTG GCTGGAGCCA CTGGTCCCG 1440
 TGGTCACTTT GTTCTGTGAC ATGTGGTGAT GGTGTGATCA CAAGGATCCG GCTCTGCAAC 1500

	TCTCCCAGCC	CCCAGATGAA	TGGGAAACCC	TGTGAAGGCG	AAGCGCGGGA	GACCAAAGCC	1560
	TGCAAGAAAG	ACGCCTGCCC	CATCAATGGA	GGCTGGGGTC	CTTGGTCACC	ATGGGACATC	1620
	TGTTCTGTCA	CCTGTGGAGG	AGGGGTACAG	AAACGTAGTC	GTCTCTGCAA	CAACCCCGCA	1680
5	CCCCAGTTTG	GAGGCAAGGA	CTGCGTTGGT	GATGTAACAG	AAAACCAGAT	CTGCAACAAG	1740
	CAGGACTGTC	CAATTGATGG	ATGCCCTGTCC	AATCCCTGCT	TGCGCGGCGT	GAAGTGTACT	1800
	AGCTACCCTG	ATGGCAGCTG	GAAATGTGGT	GCTTGTCCCC	CTGGTTACAG	TGGAAATGGC	1860
	ATCCAGTGCA	CAGATGTTGA	TGAGTGCAAA	GAAGTGCCTG	ATGCCTGCTT	CAACCACAAT	1920
	GGAGAGCACC	GGTGTGAGAA	CACGGACCCC	GGCTACAAC	GCCTGCCCTG	CCCCCACGCG	1980
10	TTACCCGGCT	CACAGCCCTT	CGGCCAGGGT	GTCGAACATG	CCACGGCCAA	CAAACAGGTG	2040
	TGCAAGCCCC	GTAACCCCTG	CACGGATGGG	ACCCACGACT	GCAACAAGAA	CGCCAAGTGC	2100
	AACCTACCTG	GCCACTATAG	CGACCCCATG	TACCGCTGCG	AGTGCAAGCC	TGGCTACGCT	2160
	GGCAATGGCA	TCACTGCGG	GGAGGACACA	GACCTGGATG	GCTGGGCCAA	TGAGAACCTG	2220
	GTGTGCGTGG	CCAATGCGAC	TTACCACTGC	AAAAAGGATA	ATTGCCCCAA	CCTTCCCAAC	2280
	TCAGGGCAGG	AAGACTATGA	CAAGGATGGA	ATTGGTGATG	CCTGTGATGA	TGACGATGAC	2340
15	AATGATAAAA	TTCCAGATGA	CAGGGACAAC	TGTCCATTCC	ATTACAACCC	AGCTCAGTAT	2400
	GACTATGACA	GAGATGATGT	GGGAGACCGC	TGTGACAACT	GTCCCTACAA	CCACAACCCA	2460
	GATCAGGCAG	ACACAGACAA	CAATGGGGAA	GGAGACGCCT	GTGCTGCAGA	CATTGATGGA	2520
	GACGGTATCC	TCAATGAACG	GGACAACCTG	CAGTACGTCT	ACAAATGTGA	CCAGAGAGAC	2580
	ACTGATATGG	ATGGGGTTGG	AGATCAGTGT	GACAATTGCC	CCTTGGAACA	CAATCCGGAT	2640
20	CAGCTGGACT	CTGACTCAGA	CCGCATTGGA	GATACCTGTG	ACAACAATCA	GGATATTGAT	2700
	GAAGATGGCC	ACCAGAACAA	TCTGGACAAC	TGTCCTATG	TGCCCAATGC	CAACCAGGCT	2760
	GACCATGACA	AAGATGGCAA	GGGAGATGCC	TGTGACCACG	ATGATGACAA	CGATGGCATT	2820
	CCTGATGACA	AGGACAACCT	CAGACTCGTG	CCCAATCCCG	ACCAGAAGGA	CTCTGACGGG	2880
	GATGGTCGAG	GTGATGCTCG	CAAAGATGAT	TTTGACCATG	ACAGTGTGCC	AGACATCGAT	2940
25	GACATCTGTC	CTGAGAATGT	TGACATCAGT	GAGACCGATT	TCCGCCGATT	CCAGATGATT	3000
	CCTCTGGACC	CCAAAGGGAC	ATCCCAAAAT	GACCCTAACT	GGGTGTACG	CCATCAGGGT	3060
	AAAGAACTCG	TCCAGACTGT	CAACTGTGAT	CCTGGACTCG	CTGTAGGTGA	TGATGAGTTT	3120
	AATGCTGTGG	ACTTCAGTGG	CACCTTCTTC	ATCAACACCG	AAAGGGACGA	TGACTATGCT	3180
30	GGATTTGTCT	TTGGCTACCA	GTCCAGCAGC	CGCTTTTATG	TTGTGATGTG	GAAGCAAGTC	3240
	ACCCAGTCCT	ACTGGGACAC	CAACCCACAG	AGGGCTCAGG	GATACTCGGG	CCTTCTGTG	3300
	AAAGTTGTAA	ACTCCACCAC	AGGGCCTGGC	GAGCACCTGC	GGAACGCCCT	GTGGCACACA	3360
	GGAAACACCC	CTGGCCAGGT	GCGCACCCCT	TGGCATGACC	CTCGTCACAT	AGGCTGGAAA	3420
	GATTTACCCG	CCTACAGATG	GCGTCTCAGC	CACAGGCCAA	AGACGGGTTT	CATTAGAGTG	3480
35	GTGATGTATG	AAGGGAAGAA	AATCATGGCT	GACTCAGGAC	CCATCTATGA	TAAAACCTAT	3540
	GCTGGTGGTA	GACTAGGGTT	GTTTGTCTTC	TCTCAAGAAA	TGGTGTCTCT	CTCTGACCTG	3600
	AAATACGAAT	TAGAGATCC	CTAATCATCA	AATTGTTGAT	TGAAAGACTG	ATCATAAACC	3660
	AATGCTGGTA	TTGACCTTC	TGGAACATATG	GGCTTGAGAA	AACCCCCAGG	ATCACTTCTC	3720
	CTTGGCTTCC	TTCTTTTCTG	TGCTTGATC	AGTGTGGACT	CCTAGAACGT	GCGACCTGCC	3780
40	TCAAGAAAAT	GCAGTTTTCA	AAAACAGACT	CATCAGCAT	CAGCCTCCAA	TGAATAAGAC	3840
	ATCTTCCAAG	CATATAAACA	ATTGCTTTGG	TTTCTTTTGG	AAAAAGCATC	TACTTGCTTC	3900
	AGTTGGGAAG	GTGCCCATTG	CACCTCTGCT	TTGTACACAGA	GCAGGGTGCT	ATTGTGAGGC	3960
	CATCTCTGAG	CAGTGGACTC	AAAAGCATTT	TCAGGCATGT	CAGAGAAGGG	AGGACTCACT	4020
	AGAATTAGCA	AACAAAACCA	CCCTGCATC	CTCCTTCAGG	AACACGGGGA	GCAGAGGCCA	4080
45	AAGCACTAAG	GGGAGGGCGC	ATACCCGAGA	CGATTGTATG	AAGAAAATAT	GGAGGAACTG	4140
	TTACATGTTC	GGTACTAAGT	CATTTTCAGG	GGATTGAAAG	ACTATTGCTG	GATTTTCATGA	4200
	TGCTGACTGG	CGTTAGCTGA	TTAACCCTATG	TAAATAGGCA	CTTAAATAGA	AGCAGGAAAG	4260
	GGAGACAAAG	ACTGGCTTCT	GGACTTCTCT	CCTGATCCCC	ACCCTTACTC	ATCACCTTGC	4320
	AGTGGCCAGA	ATTAGGGAAT	CAGAATCAAA	CCAGTGTAAAG	GCAGTGTCTG	CTGCCATTGC	4380
50	CTGGTCACAT	TGAAATTTGGT	GGCTTCAATC	TAGATGTAGC	TTGTGCAGAT	GTAGCAGGAA	4440
	AATAGGAAAA	CCTACCCTCT	CAGTGAGCAC	CAGCTGCCTC	CCAAAGGAGG	GGCAGCCGTG	4500
	CTTATATTTT	TATGGTTACA	ATGGCACAAA	ATTATTATCA	ACCTAACTAA	AACATTCTCT	4560
	TTCTCTTTTT	TCCGTAATTA	CTAGGTAGTT	TTCTAATCT	CTCTTTTGGA	AGTATGATTT	4620
	TTTTAAAGTC	TTTACGATGT	AAAATATTTA	TTTTTTACTT	ATTCTGGAAG	ATCTGGCTGA	4680
55	AGGATTATTC	ATGGAACAGG	AAGAAGCGTA	AAGACTATCC	ATGTCATCTT	TGTTGAGAGT	4740
	CTTCGTGACT	GTAAGATTGT	AAATACAGAT	TATTTATTAA	CTCTGTTCTG	CCTGGAAATT	4800
	TAGGCTTCAT	ACGGAAAGTG	TTTGAGAGCA	AGTAGTTGAC	ATTTATCAGC	AAATCTCTTG	4860
	CAAGAACAGC	ACAAGGAAAA	TCAGTCTAAT	AAGCTGCTCT	GCCCCCTGTG	CTCAGAGTGG	4920
	ATGTTATGGG	ATTCTTTTTT	TCTCTGTTTT	ATCTTTTCAA	GTGGAATTAG	TGGTTATCC	4980
60	ATTTGCAAA	GTTTTAAATT	GCAAAGAAAG	CCATGAGGTC	TTCAATACTG	TTTTACCCCA	5040
	TCCCTTGTGC	ATATTTCCAG	GGAGAAGGAA	AGCATATACA	CTTTTTTCTT	TCATTTTTC	5100
	AAAAGAGAAA	AAAATGACAA	AAGGTGAAAC	TTACATACAA	ATATTACCTC	ATTTGTTGTG	5160
	TGACTGAGTA	AAGAATTTTT	GGATCAAGCG	GAAAGAGTTT	AAGTGTCTAA	CAAACCTAAA	5220
	GCTACTGTAG	TACCTAAAAA	GTCAGTGTGG	TACATAGCAT	AAAAACTCTG	CAGAGAAGTA	5280
65	TTCCCAATAA	GGAAATAGCA	TTGAAATGTT	AAATACAATT	TCTGAAAGTT	ATGTTTTTTT	5340
	TCTATCATCT	GGTATACCAT	TGCTTTATTT	TTATAAATTA	TTTTTCTATT	GCCATTGGAA	5400
	TAGAATATTC	AGATTGTGTA	GATATGCTAT	TTAAATAATT	TATCAGGAAA	TACTGCCTGT	5460
	AGAGTTAGTA	TTTCTATTTT	TATATAATGT	TTGCACACTG	AATTGAAGAA	TTGTTGGTTT	5520
	TTTCTTTTTT	TTGTTTTTTT	TTTTTTTTTT	TTTTTTTTTG	CTTTTGACCT	CCCATTTTAA	5580
70	CTATTTGCCA	ATACCTTTTT	CTAGGAATGT	GCTTTTTTTT	GTACACATTT	TTATCCATTT	5640
	TACATTCTAA	AGCAGTGTAA	GTTGTATATT	ACTGTTTCTT	ATGTACAAGG	AACRAACAATA	5700
	AATCATATGG	AAATTTATAT	TT				

Seq ID NO: 38 Protein sequence:

Protein Accession #: NP_003237

75

	1	11	21	31	41	51	
	MGLAWGLGVL	FLMHVCGTNR	IPESGGDNSV	FDIFELTGAA	RKSGRRRLVK	GPDPSPPAFR	60
	IEDANLIPPV	PDDKFQDLVD	AVRAEKGFL	LASLRQMKKT	RGTLLALERK	DHSGQVFSV	120
5	SNKGAGTLDL	SLTVQGGQHV	VSVEEALLAT	GQWKSITLFV	QEDRAQLYID	CEKMENAEID	180
	VPIQSVFTRD	LASIARLRIA	KGGVNDNFQ	VLQNVRFVFG	TPEDILRNK	GCSSTSVLL	240
	TLDNNVNGS	SPAIRTNYIG	HKTDLQAIC	GISCDELSSM	VLELRGLRTI	VTTLQDSIRK	300
	VTENKELAN	ELRRPPLCYH	NGVQYRNEE	WTVDSCTECH	CQNSVTICKK	VSCPIMPSCN	360
	ATVPDGECCP	RCWPSDSADD	GWSPWSEWTS	CSTSCGNGIQ	QRGRSCDSL	NRCEGSSVQT	420
10	RTCHIQECDK	RFKQDGGWSH	WSPWSSCSVT	CGDGVITRIR	LCNSPSPQMN	GKPCGEARE	480
	TKACKKDACP	INGGWGPWSP	WDICSVTCGG	GVQKRSLCN	NPAPQFGGKD	CVGDVTENQI	540
	CNKQDCPIDG	CLSNPCFAGV	KCTSYPDGSW	KCGACPPGYS	GNGIQCTDVD	ECKEVPDACF	600
	NHNGEHCEN	TDPGYNCLPC	PPRFTGSQPF	GQGVHATAN	KQVCKPRNPC	TDGTHDCNKN	660
	AKCNYLGHSY	DPMYRCECKP	GYAGNGIICG	EDTDLGWPN	ENLVCVANAT	YHCKKDNCN	720
15	LPNSGQEDYD	KDGTGDACDD	DDDNDKIPDD	RDNCPHYN	AQYDYDRDDV	GDRCDNCPYN	780
	HNPDAQADTN	NGEGDACAAD	IDGDGILNER	DNCQYVNVN	QRDTMDGVG	DQCDNCPLEH	840
	NPDQLSDSD	RIGDTCDNNQ	DIDEDGHQNN	LDNCPYVNA	NQADHDKDGK	GDACDHDDDN	900
	DGIPDDKDNC	RLVNPDPQKD	SDGDGRGDAC	KDDFDHDSVP	DIDDICPEN	DISETDFRRF	960
	QMIPLDPKGT	SQNDPNWVVR	HQGKELVQTV	NCDPGLAVGY	DEFNAVDFSG	TFFINTERDD	1020
20	DYAGVFVGYQ	SSSRFYVVMH	KQVTQSYWDT	NPTRAQYSG	LSVKVNVN	GPGEHLRNAL	1080
	WHTGNTPGQV	RTLWHDPRMI	GWKDFATYRW	RLSHRPKTGF	IRVVMYEGKK	IMADSGPIYD	1140
	KTYAGGRLGL	FVFSQEMVFF	SDLKYECRDP				

25

Seq ID NO: 39 Nucleotide sequence:

Nucleic Acid Accession #: BC004299

Coding sequence: 69..1235 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
	CCCGACCCGT	GCGAGGGCCA	GGTCCGCGCC	TGCCCCGCCA	GGCGAAGCGA	GGCGACCCGC	60
	GTGCGGCCAT	GGCTTCGCTG	CTGGGAGCCT	ACCCTTGGCC	CGAGGGTCTC	GAGTGCCCGG	120
35	CCCTGGACGC	CGAGCTGTCG	GATGGACAAT	CGCCGCCGGC	CGTCCCCCGG	CCCCCGGGGG	180
	ACAAGGGCTC	CGAGAGCCGT	ATCCGGCGGC	CCATGAACGC	CTTCATGGTT	TGGGCCAAGG	240
	ACGAGAGGAA	ACGGCTGGCA	GTGCAGAACC	CGGACCTGCA	CAACGCCGAG	CTCAGCAAGA	300
	TGCTGGGAAA	GTCGTGGAAG	GCGCTGACGC	TGTCCAGAA	GAGGCCGTAC	GTGGACGAGG	360
	CGGAGCGGCT	GCGCCTGCAG	CACATGCAGG	ACTACCCCAA	CTACAAGTAC	CGGCCCGGCA	420
40	GGAAGAGCA	GGCCAAGCGC	CTGTGCAAGC	GCGTGGACCC	GGGCTTCCTT	CTGAGCTCCC	480
	TCTCCCGGGA	CCAGAACGCC	CTGCCGAGGA	AGAGAAGCGG	CAGCCGGGGG	GCGCTGGGGG	540
	AGAAGGAGGA	CAGGGGTGAG	TACTCCCCCG	GCACTGCCCT	GCCCAGCCTC	CGGGGTGCT	600
	ACCACGAGGG	GCCGGCTGGT	GGTGGCGGGC	GCGGCACCCC	GAGCAGTGTG	GACACGTACC	660
	CGTACGGGCT	GCCCACACCT	CCTGAAATGT	CTCCCCTGGA	CGTGTCTGGG	CCGGAGCAGA	720
45	CCTTCTTCTC	CTCCCCCTGC	CAGGAGGAGC	ATGGCCATCC	CCGCCGCATC	CCCCACCTGC	780
	CAGGGCACCC	GTACTCACCG	GAGTACGCCC	CAAGCCCTCT	CCACTGTAGC	CACCCCTTGG	840
	GCTCCCTGGC	CCTTGGCCAG	TCCCCCGGCG	TCTCCATGAT	GTCCCCTGTA	CCCGGCTGTC	900
	CCCATCTCC	TGCTATTAC	TCCCCGGCCA	CCTACCACCC	ACTCCACTCC	AACCTCCAAG	960
50	CCCACTGGG	CCAGCTTTCC	CCGCCTCCTG	AGCACCTGG	CTTCGACGCC	CTGGATCAAC	1020
	TGAGCCAGGT	GGAACCTCTG	GGGGACATGG	ATCGCAATGA	ATTCCGACCAG	TATTTGAACA	1080
	CTCCTGGCCA	CCCAGACTCC	GCCACAGGGG	CCATGGCCCT	CAGTGGGCAT	GTTCCGGTCT	1140
	CCCAGGTGAC	ACCAACGGGT	CCCACAGAGA	CCAGCCTCAT	CTCCGCTCTG	GCTGATGCCA	1200
	CGGCCACGTA	CTACAACAGC	TACAGTGTGT	CATAGAGCTG	GAGGCGCCCC	GTCCGGTCTAG	1260
	CCCTCGCGCC	CTCTCCTTCT	TGTGCTTGA	GTGGCAGAGG	AGCCGTCAG	CCACACCAGC	1320
55	TTTCTCCCA	CCGCTCAGGG	CAGGGAGGTC	TGAAGTCCGG	CCCCAGAGCC	TTTGGCCTAA	1380
	GCTGGACTCT	CCTTATCCGA	GTGCCGCCCT	TATCCCCTTC	CCCACGTTC	AGCCCCCTGA	1440
	GCCCCACATT	TAAGTATATT	CCTTCAAGTG	AGTTTTCCTC	CAGCCCCCTGA	GAGTTGCTGT	1500
	CTCCAGTGG	AATGTTCACT	GACGCTCTTT	CTTGCTAGCC	ATCATCGAAA	CTAATGGGGG	1560
60	GACAGACTTG	ATAGCCAAGG	TCCCTTCTGG	TCCAGTTTTC	TGATTTAGGG	TTCTCTCAAG	1620
	ATTAATAAAG	GAAGATGGGG	AAATTTGACT	CATTAATGAG	CTCGCTAACC	TACGATCTGG	1680
	TGATAATTTT	GTGTGCACAG	CCCAAGGACC	ACGAGGCTTT	CTGCACTTTC	TGCACCCCTT	1740
	TCCAAAGTGA	CCACAAAATT	TCAAAGGGAC	TCATACAATT	TGAGAAAAAA	CAGTCAACCT	1800
	GATTTGAGAA	ATTAACCACT	ATGGCTAACT	ATATCACAGA	AAATGGGATT	GAGTTAAAAC	1860
	TATTTTATTT	TAAATATACA	TTTAAAGCA	GTCTTTTTTT	TTTGTTAATT	TGTTTATTAT	1920
65	ACACACACTT	CAAGAGCCAC	CGCGCCGAGC	CTACATTAT	AATTTTCATT	CTCTTTTACC	1980
	TATAAAATTC	AGTGTATTAG	TTTCATTACA	TAGGAGAAAT	TATATTTCTA	AACATTTTAT	2040
	GATGTTTAAA	AACAAAACAG	GCTGTTGTAA	AAAAAAAAAA	AAAAAAAAAA		

Seq ID NO: 40 Protein sequence:

Protein Accession #: AAH04299

	1	11	21	31	41	51	
	MASLLGAYPW	PEGLECPALD	AELSDGQSPP	AVPRPPGDKG	SESRIIRPMN	AFMVWAKDER	60
75	KRLAVQNPD	HNAELSKMLG	KSWKALTLSQ	KRPVDEAER	LRLQHMODYP	NYKYRPRRKK	120
	QAKRLCKRVD	PGFLLSSLR	DQNALPEKRS	GSRGALGEKE	DRGEYSPGTA	LPSLRGCYHE	180

GPAGGGGGGT PSSVDTPYVG LPTPPEMSPL DVLEPEQTFE SSPCQEEHGH PRRIPHLPGH 240
 PYSPEYAPSP LHCSHPLGSL ALGQSPGVSM MSPVPGCPPS PAYYSPATYH PLHSNLQAH 300
 GQLSPPEHPH GFDALDQLSQ VELLGDMDRN EFDQYLNTGP HPDSATGAMA LSGHVPVSQV 360
 TPTGPTETSL ISVLADATAT YNSYSVS

Seq ID NO: 41 Nucleotide sequence:

Nucleic Acid Accession #: NM_004449

Coding sequence: 1..1389 (underlined sequences correspond to start and stop codons)

1	11	21	31	41	51	
15	ATGATTGAGA	CTGTCCCGGA	CCCAGCAGCT	CATATCAAGG	AAGCCTTATC	AGTTGTGAGT 60
	GAGGACCACT	CGTTGTTTGA	GTGTGCCCTAC	GGAACGCCAC	ACCTGGCTAA	GACAGAGATG 120
	ACCGCGTCTT	CCTCCAGCGA	CTATGGACAG	ACTTCCAAGA	TGAGCCCACG	CGTCCCTCAG 180
	CAGGATTGGC	TGTCTCAACC	CCCAGCCAGG	GTCAACCATCA	AAATGGAATG	TAACCTTAGC 240
	CAGGTGAATG	GCTCAAGGAA	CTCTCTGTAT	GAATGCAGTG	TGGCCAAAGG	CGGGAAGATG 300
20	GTGGGCAGCC	CAGACACCGT	TGGGATGAAC	TACGGCAGCT	ACATGGAGGA	GAAGCACATG 360
	CCACCCCAA	ACATGACCAC	GAACGAGCGC	AGAGTTATCG	TGCCAGCAGA	TCCTACGCTA 420
	TGGAGTACAG	ACCATGTGCG	GCAGTGGCTG	GAGTGGGCGG	TGAAAGAATA	TGGCCTTCCA 480
	GACGTCAACA	TCTTGTATT	CCAGAACATC	GATGGGAAGG	AACCTGTGCA	GATGACCAAG 540
	GACGACTTCC	AGAGGCTCAC	CCCCAGCTAC	AACGCCGACA	TCCTTCTCTC	ACATCTCCAC 600
25	TACCTCAGAG	AGACTCCTCT	TCCACATTTG	ACTTCAGATG	ATGTTGATAA	AGCCTTACAA 660
	AACCTCTCCAC	GGTTAATGCA	TGCTAGAAAC	ACAGATTTAC	CATATGAGCC	CCCCAGGAGA 720
	TCAGCCTGGA	CCGGTCACGG	CCACCCACAG	CCCCAGTCGA	AAGCTGCTCA	ACCATCTCCT 780
	TCCACAGTGC	CCAAACTGA	AGACCAGCGT	CCTCAGTTAG	ATCCTTATCA	GATTCTTGGA 840
	CCAACAAGTA	GCCGCTTTCG	AAATCCAGGC	AGTGGCCAGA	TCCAGCTTTG	GCAGTTCCCT 900
30	CTGGAGCTCC	TGTCGGACAG	CTCCAACTCC	AGCTGCATCA	CCTGGGAAGG	CACCAACGGG 960
	GAGTTCAAGA	TGACGGATCC	CGACGAGGTG	GCCCGGCGCT	GGGGAGAGCG	GAAGAGCAAA 1020
	CCCAACATGA	ACTACGATAA	GCTCAGCCGC	GCCCTCCGTT	ACTACTATGA	CAAGAACATC 1080
	ATGACCAAGG	TCCATGGGAA	GCGCTACGCC	TACAAGTTCG	ACTTCCACGG	GATCGCCACG 1140
	GCCCTCCAGC	CCCAACCCCC	GGAGTCATCT	CTGTACAAGT	ACCCCTCAGA	CCTCCCGTAC 1200
35	ATGGGCTCCT	ATCACGCCCA	CCCACAGAAG	ATGAACCTTG	TGGCGCCCCA	CCCTCCAGCC 1260
	CTCCCCGTGA	CATCTTCCAG	TTTTTTTGCT	GCCCCAAACC	CATACTGGAA	TTCACCAACT 1320
	GGGGGTATAT	ACCCCAACAC	TAGGCTCCCC	ACCAGCCATA	TGCCTTCTCA	TCTGGGCACT 1380
	<u>TACTACTAA</u>					

Seq ID NO: 42 Protein sequence:

Protein Accession #: NP_004440

1	11	21	31	41	51	
45	MIQTVPDPAA	HIKEALSVVS	EDQSLFECAY	GTPHLAKTEM	TASSSSDYGQ	TSKMSPRVPQ 60
	QDWLSQPPAR	VTIKMECNPS	QVNGSRNSPD	ECSVAKGGKM	VGSPDVTGMN	YGSYMEEKHM 120
	PPPNMTTNER	RVIVPADPTL	WSTDHVRQWL	EWAVKEYGLP	DVNILLFQNI	DGKELCKMTK 180
50	DDFQRLTPSY	NADILLSHLH	YLRETPPLPH	TSDDVDKALQ	NSPRLMHARN	TDLPYEPPRR 240
	SAWTGHGHPT	PQSKAAQPS	STVPKTEDQR	PQLDPYQILG	PTSSRLANPG	SGQIQLWQFL 300
	LELLSDSSNS	SCITWEGTNG	EFKMTDPDEV	ARRWGERKSK	PNMNYDKLSR	ALRYYYDKNI 360
	MTKVHGKRYA	YKFDFHGIAQ	ALQPHPPESS	LYKYPSDLPY	MGSYHAHPQK	MNFVAPHPPA 420
55	LPVTSSSFFA	APNPYWNST	GGIYPNTRLP	TSHMPSHLGT	YY	

Seq ID NO: 43 Nucleotide sequence:

Nucleic Acid Accession #: NM_005100

Coding sequence: 192..5537 (underlined sequences correspond to start and stop codons)

1	11	21	31	41	51	
65	CCTTCTTTTA	AGGAGTTTGC	CGCGAGCGCG	TCTCCTTCAT	TCGCAGGCTG	GGCGCGTTTCG 60
	CAGTCGGCTG	GCGGCGAAGG	AAGGCGCTCT	CGGGACCTCA	CGGGCGCGCG	TCTTTTGGCT 120
	CTTGCCCTTG	TCCCTGCGGC	TGCGGGAAAG	CGTAACCCGG	CGGCTAGGCG	CGGGAGAAGT 180
	GCGGAGGAGC	<u>CATGGGCGCC</u>	GGGAGCTCCA	CCGAGCAGCG	CAGCCCGGAG	CAGCCGCCCC 240
	AGGGGAGCTC	CAGCCCGGCT	GAGCCCGGCG	CCAGCGGCGG	CGGCCCTTCG	GCCGAGGCGG 300
	CGCCAGACAC	CACCGCGGAC	CCCGCCATCG	CTGCCTCGGA	CCCGGCCACC	AAGCTCCTAC 360
70	AGAAGAATGG	TCAGCTGTCC	ACCATCAATG	GCGTAGCTGA	GCAAGATGAG	CTCAGCCTCC 420
	AGGAGGGTGA	CCTAAATGGC	CAGAAAGGAG	CCCTGAACGG	TCAAGGAGCC	CTAAACAGCC 480
	AGGAGGAAGA	AGAAGTCATT	GTCACGGAGG	TTGGACAGAG	AGACTCTGAA	GATGTGAGCG 540
	AAAGAGACTC	CGATAAAGAG	ATGGCTACTA	AGTCAGCGGT	TGTTACACGAC	ATCACAGATG 600
75	ATGGGCAGGA	GGAGAACCGA	AATATCGAAC	AGATTCTTTC	TTCAAGAAAG	AATTTAGAAG 660
	AGCTAACACA	ACCCACTGAG	TCCAGGCTA	ATGATATTGG	ATTAAAGAAG	GTGTTTAAGT 720
	TTGTTGGCTT	TAAATTCAC	GTGAAAAAGG	ATAAGACAGA	GAAGCCTGAC	ACTGTCCAGC 780

	TACTCACTGT	GAAGAAAGAT	GAAGGGGAGG	GAGCAGCAGG	GGCTGGCGAC	CACCAGGACC	840
	CCAGCCTTGG	GGCTGGAGAA	GCAGCATCCA	AAGAAAGCGA	ACCCAACAA	TCTACAGAGA	900
	AACCCGAAGA	GACCTTGAAG	CGTGAGCAAA	GCCACGCAGA	AATTTCTCCC	CCAGCCGAAT	960
5	CTGGCCAAGC	AGTGGAGGAA	TGCAAGAGG	AAGGAGAAGA	GAAACAAGAA	AAAGAACCTA	1020
	GCAAGTCTGC	AGAATCTCCG	ACTAGTCCCG	TGACCAGTGA	AACAGGATCA	ACCTTCAAAA	1080
	AATTCTTCAC	TCAAGGTTGG	GCCGGCTGGC	GCAAAAAGAC	CAGTTTCAGG	AAGCCGAAGG	1140
	AGGATGAAGT	GGAGCTTCA	GAGAAGAAAA	AGGAACAAGA	GCCAGAAAAA	GTAGACACAG	1200
	AAGAAGACGG	AAAGGCAGAG	GTTGCTCCCG	AGAAACTGAC	CGCCTCCGAG	CAAGCCCACC	1260
	CACAGGAGCC	GGCAGAAAGT	GCCCACGAGC	CCCGGTTATC	AGCTGAATAT	GAGAAAGTTG	1320
10	AGTGCCCTC	AGAGGAGCAA	GTCACTGGCT	CGCAGGGACC	TTCTGAAGAG	AAACCTGCTC	1380
	CGTTGGCGAC	AGAAGTGTTC	GATGAGAAAA	TAGAAGTCCA	CCAAGAAGAG	GTGTGTGGCCG	1440
	AAGTCCACGT	CAGCACCCTG	GAGGAGAGAA	CCGAAGAGCA	GAAAAACGGAG	GTGGAAGAAA	1500
	CAGCAGGGTC	TGTGCCAGCT	GAAGAATTGG	TTGGAATGGA	TGCAGAACCT	CAGGAAGCCG	1560
	AACCTGCCAA	GGAGCTGGTG	AAGCTCAAAAG	AAACGTGTGT	TTCCGGAGAG	GACCCTACAC	1620
15	AGGGAGCTGA	CCTCAGTCCT	GATGAGAAGG	TGCTGTCCAA	ACCCCCCGAA	GGCGTTGTGA	1680
	GTGAGGTGGA	AATGCTGTCA	TCACAGGAGA	GAATGAAGGT	GCAGGGAAGT	CCACTAAAGA	1740
	AGCTTTTTTAC	CAGCACTGCG	TTTAAAAAGC	TTTCTGGAAA	GAAACAGAAA	GGGAAAAGAG	1800
	GAGGAGGAGA	CGAGGAATCA	GGGGAGCACA	CTCAGGTTCC	AGCCGATTCT	CCGGACAGCC	1860
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20	GTCTGGAAAA	GGGCTTAGCC	GAGGTGCAGC	AGGATGGGGA	AGCTGAAGAA	GGAGCTACTT	1980
	CCGATGGAGA	GAAAAAAGA	GAAGGTGTCA	CTCCCTGGGC	ATCATTCAAA	AAGATGGTGA	2040
	CGCCCAAGAA	GCGTGTTAGA	CGGCCTTCGG	AAAGTGATAA	AGAAGATGAG	CTGGACAAGG	2100
	TCAAGAGCGC	TACCTTGTCT	TCCACCAGAG	GCACAGCCTC	TGAAATGCAA	GAAGAAATGA	2160
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25	CTTGGGAAGC	TTTAATTTGT	GTGGGATCAT	CCAAGAAAAG	AGCAAGGAGA	AGGTCTCTCT	2280
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	CCTGGGAGTC	ATTTAAAGG	TTAGTCACGC	CAAGAAAAAA	ATCAAAGTCC	AAGCTGGAAG	2520
30	AGAAAAGCGA	AGACTCCATA	GCTGGGTCTG	GTGTAGAACA	TTCCACTCCA	GACTGAAC	2580
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	GGCCAGATGG	GAAACAAGAA	CAAGCCCTTG	TTGAAGACGC	AGGGCCAACA	GGGGCCAACG	2700
	AAGATGACTC	TGATGTCCCG	GCCGTGGTCC	CTCTGTCTGA	GTATGATGCT	GTAGAAAGGG	2760
	AGAAAATGGA	GGCAGAGCAA	GCCCAAAAAG	GCGCAGAGCA	GCCCGAGCAG	AAGGCAGCCA	2820
35	CTGAGGTGTC	CAAGGAGCTC	AGCGAGAGTC	AGGTTTATAT	GATGGCAGCA	GCTGTGCTG	2880
	ACGGGACGAG	GGCAGCTACC	ATTATTGAAG	AAAGGTCTCC	TTCTTGGATA	TCTGCTTCAG	2940
	TGACAGAACC	TCTTGAACAA	GTAGAAGCTG	AAGCCGCACT	GTTAACTGAG	GAGGTATTGG	3000
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40	GAGAGGCCCG	GGGCGACACG	GTGTTAGTGG	AGGCGGAATT	GACCCCGGAA	GCTGTGACAG	3120
	CTGCAGAAAC	TGCAGGGCCA	TTGGGTTCCG	AAGAAGGAAC	CGAAGCATCT	GCTGCTGAAG	3180
	AGACACAGAA	AATGGTGTCA	GAGTCTCCCT	AGTTAACCAG	CTCCCCAGAC	ACCACAGAGG	3240
	AGGCCACTCC	GGTGCAGGAG	GTGGAAGGTG	GCGTACCTGA	CATAGAAGAG	CAAGAGAGGC	3300
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45	GCACCCGTGG	GCCAGAAGAT	GTGCTTCAGC	CTGTGCAGAG	AGCAGAGGCA	GAAAGACCAG	3420
	AAGAGCAGGC	TGAAGCGTCG	GGTCTGAAGC	AAGAGACGGA	TGTAGTGTG	AAAGTAGATG	3480
	CTCAGGAGGC	AAAAACTGAG	CCTTTTACAC	AAGGGAAGGT	GGTGGGGCAG	ACCACCCAG	3540
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	CTTGTCAAGC	CGAAACCTTA	GCTGGGGTAA	AATCACAGGA	GATGGTGATG	GAACAGGCTA	3660
50	TCCCCCTGTA	CTCGGTGGAA	ACCCCTACAG	ACAGTGAGAC	TGATGGAAGC	ACCCCGTAG	3720
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	ATGAGGTGCG	ATCTGCTACC	CAGTCAGGGG	GCACAGAAGC	AGAGGCAGTT	CCTGCACAGA	3840
	AAGAGAGGCC	TCCAGCACCT	TCCAGTTTTG	TGTTCCAGGA	AGAAACTAAA	GAACAATCAA	3900
	AGATGGAAGA	CACCTCTAGAG	CATACAGATA	AAGAGGTGTC	AGTGGAAACT	GTATCCATTG	3960
	TGTCAAAGAC	TGAGGGGACT	CAAGAGGCTG	ACCAGTATGC	TGATGAGAAA	ACCAAAGACG	4020
55	TAGCATTTT	CGAAGGACTT	GAGGGGTCTA	TAGACACAGG	CATAACAGTC	AGTCGGGAAA	4080
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	ATGCTCTTGA	ACTGCAGAGT	CACGCTAAGT	CTCCTCCATC	CCCCGTGGAG	AGAGAGATGG	4200
	TAGTTCAAGT	CGAAAGGGAG	AAAACAGAAG	CAGAGCCAAC	CCATGTGAAT	GAAGAGAAGC	4260
60	TTGAGCACGA	AACAGCTGTT	ACCGTATCTG	AAGAGGTCAG	TAAGCAGCTC	CTCCAGACAG	4320
	TGAATGTGCC	CATCATAGAT	GGGGCAAAGG	AAGTCAGCAG	TTTGGAAGGA	AGCCCTCCTC	4380
	CCTGCCTAGG	TCAAGAGGAG	GCAGTATGCA	CCAAAATTCA	AGTTTCAAGC	TCTGAGGCAT	4440
	CATTCACTCT	AACAGCGGCT	GCAGAGGAGG	AAAAGGTCTT	AGGAGAAACT	GCCAACATTT	4500
	TAGAAACAGG	TGAAACGTTG	GAGCCTGCAG	GTGCACATTT	AGTTCTGGAA	GAGAAATCCT	4560
	CTGAAAAAAA	TGAAGACTTT	GCCGCTCATC	CAGGGGAAGA	TGCTGTGCCC	ACAGGGCCCC	4620
65	ACTGTCAAGC	AAAATCGACA	CCAGTGTATG	TATCTGCTAC	TACCAAGAAA	GGCTTAAGTT	4680
	CCGACCTGGA	AGGAGAGAAA	ACCACATCAC	TGAAGTGGAA	GTCAGATGAA	GTCGATGAGC	4740
	AGGTTGCTTG	CCAGGAGGTC	AAAGTGAGTG	TAGCAATTGA	GGATTTAGAG	CCTGAAAATG	4800
	GGATTTTGGG	ACTTGAGACC	AAAAGCAGTA	AACTTGTTCA	AAACATCATC	CAGACAGCCG	4860
	TTGACCAAGT	TGTACGTACA	GAAGAAACAG	CCACCAGAA	GTTGACGTCT	GAGTTACAGA	4920
70	CACAAGCTCA	CGTGATAAAA	GCTGACAGCC	AGGACGCTGG	ACAGGAAACG	GAGAAAGAAG	4980
	GAGAGGAACC	TCAGGCCTCT	GCACAGGATG	AAACACCAAT	TACTTCAGCC	AAAGAGGAGT	5040
	CAGAGTCAAC	CGCAGTGGGA	CAAGCACATT	CTGATATTTT	CAAGACATG	AGTGAAGCCT	5100
	CAGAAAAGAC	CATGACTGTT	GAGGTAGAAG	GTTCCACTGT	AAATGATCAG	CAGCTGGAAG	5160
	AGGTGCTCCT	CCCCTCTGAG	GAAGAGGGAG	GTGGAGCTGG	AACAAAGTCT	GTGCCAGAAG	5220
75	ATGATGGTCA	TGCCTTGTGA	GCAGAAAGAA	TAGAGAAGTC	ACTAGTTGAA	CCGAAAGAAG	5280
	ATGAAAAAGG	TGATGATGTT	GATGACCTCG	AAAACCAGAA	CTCAGCCCTG	GCTGATACTG	5340

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 10 GAACTGGAGT TGGCAATACC TAGTTCTGCT TCTGAACTG GAGTATCATT CTTTACATAT 5880
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 20 GACTGCATTC ACACATGGCA TGAATAAAGT CAGGTCTTTT ACAAATGGTA TTTTGATAGA 6480
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Seq ID NO: 44 Protein sequence;
 Protein Accession #: NP_005091

1 11 21 31 41 51
 30 MGAGSSTEQR SPEQPPEGSS TPAEPEPSGG GPSAEAPDPT TADPAIAASD PATKLLQKNG 60
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 DKEMATKSAV VHDITDDQGE ENRNIEQIPS SESNLEELTQ PTESQANDIG FKKVFKFVGF 180
 KFTVKKDKTE KPDTVQLLTV KKDEGEAAG AGDHQDPSLG AGEAASKESK PKQSTFKPPEE 240
 35 TLKREQSHAE ISPPAESGQA VEECKEEGEE KQEKPSKSA ESPTSPVTSE TGSTFKKFPT 300
 QGWAGWRKKT SPRKPKEDV EASEKKKEQE PEKVDTEEDG KAEVASEKLT ASEQAHPQEP 360
 AESAHEPRLS ABEYKVELPS EEQVSGSQGP SEEKPAPLAT EVFDEKIEVH QEEVVAEVHV 420
 STVEERTBEQ KTEVEETAGS VPABELVGM D AEPQEAEPK ELVKLKETCV SGEDPTQGD 480
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 40 EESGEHTQVP ADSPDSQEEQ KGESSASSPE EPEEITCLEK GLAEVQQDGE AEEGATSDGE 600
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 50 ETLAGVKSQE MVMEQAIPPD SVETPTDSET DGSTPVADFD APGTTQKDEI VEIHEENEVA 1200
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 60 ALLAEERIEKS LVEPKEDKDG DDVDDPENQN SALADTDASG GLTKESPDNT GPKQKEKEDA 1740
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Seq ID NO: 45 Nucleotide sequence;
 Nucleic Acid Accession #: NM_001290
 Coding sequence: 110..1231 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
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 70 ACCACATGAC CCCTTCTATT CTTCTCCTTT CGGCCCATTT TATAGGAGGC ATACACCATA 180
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 75 CAAACTCTG AAAGAGTCAT ACCACAATC ATCCATCACG GTGGACTGCG ACCAGTGATC 480
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 15 CTTTCTTTTT TTCTAATTGA GAGGATTATT CCCAGTAAGC TTCCATGACC CTTTCTTGGA 1440
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Seq ID NO: 46 Protein sequence:
 Protein Accession #: NP_001281

35

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 45 VVGEPTLMGG EFGDEDERLI TRLENTQYDA ANGMDDEEDF NNSPALGNNS PWNSKPPATQ 360
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Seq ID NO: 47 Nucleotide sequence:
 Nucleic Acid Accession #: NM_004126
 Coding sequence: 108..329 (underlined sequences correspond to start and stop codons)

50

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 60 TGAAATTTAA AGGAGACTTT CTTAAGCACC ATATAGATAG GGTTATGTAT AAAAGCATAT 480
 GTGCTACTCA TCTTTGCTCA CTATGCAGTG TTTTAAAGA GAGCAGAGAG TATCAGATGT 540
 ACAATTATGG AATAAGAAC ATTACTGAG CATGACACTT CTTTCAGTAT ATTGCTTGAT 600
 GCTTCAATAA AAGTTTGTCT TT

65

Seq ID NO: 48 Protein sequence:
 Protein Accession #: NP_004117

1 11 21 31 41 51
 | | | | |
 70 MPALHIEDLP EKEKLKMEVE QLRKEVKLQR QQVSKCSEEI KNYIEERSGE DPLVKGIPED 60
 KNPFKEKGSC VIS

75

Seq ID NO: 49 Nucleotide sequence:
 Nucleic Acid Accession #: XM_051896
 Coding sequence: 139..2388 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
5	GTTTTAAAGA	CGCTAGAGTG	CCAAAGAAGA	CTTTGAAGTG	TGAAAACATT	TCCTGTAATT	60
	GAAACCAAAA	TGTCATTTAT	AGATCCTTAC	CAGCACATTA	TAGTGGAGCA	CCAGTATTCC	120
	CACAAGTTTA	CGGTAGTGGT	GTTACGTGCC	ACCAAAGTGA	CAAAGGGGGC	CTTTGGTGAC	180
	ATGCTTGATA	CTCCAGATCC	CTATGTGGAA	CTTTTATCT	CTACAACCCC	TGACAGCAGG	240
	AAGAGAACAA	GACATTTTCA	TAATGACATA	AACCTGTGT	GGAATGAGAC	CTTTGAATTT	300
10	ATTTTGGATC	CTAATCAGGA	AAATGTTTTG	GAGATTACGT	TAATGGATGC	CAATTATGTC	360
	ATGGATGAAA	CTCTAGGGAC	AGCAACATTT	ACTGTATCTT	CTATGAAGGT	GGGAGAAAAG	420
	AAAGAAGTTC	CTTTTATTTT	CAACCAAGTC	ACTGAAATGG	TTCTAGAAAT	GTCTCTTGAA	480
	GTTTGCTCAT	GCCCAGACCT	ACGATTTAGT	ATGGCTCTGT	GTGATCAGGA	GAAGACTTTC	540
	AGACAACAGA	GAAAAGAACA	CATAAGGGAG	AGCATGAAGA	AACTCTTGGG	TCCAAAGAAT	600
15	AGTGAAGGAT	TGCATTCTGC	ACGTGATGTG	CCTGTGGTAG	CCATATTGGG	TTCAGGTGGG	660
	GGTTTCCGAG	CCATGGTGGG	ATTCTCTGGT	GTGATGAAGG	CATTATACGA	ATCAGGAATT	720
	CTGGATTGTG	CTACCTACGT	TGCTGGTCTT	TCTGGCTCCA	CCTGGTATAT	GTCAACCTTG	780
	TATTCTCACC	CTGATTTTCC	AGAGAAAGGG	CCAGAGGAGA	TTAATGAAGA	ACTAATGAAA	840
	AATGTTAGCC	ACAATCCCCT	TTTACTTCTC	ACACCACAGA	AAGTTAAAAG	ATATGTTGAG	900
20	TCTTTATGGA	AGAAGAAAAG	CTCTGGACAA	CCTGTCACCT	TTACTGATAT	CTTTGGGATG	960
	TTAATAGGAG	AAACACTAAT	TCATAATAGA	ATGAATACTA	CTCTGAGCAG	TTTGAAGGAA	1020
	AAAGTTAATA	CTGCACAATG	CCCTTTACCT	CTTTTCACCT	GTCTTCATGT	CAAACCTGAC	1080
	GTTTCAGAGC	TGATGTTTGC	AGATTGGGTT	GAATTTAGTC	CATACGAAAT	TGGCATGGCT	1140
25	AAATATGGTA	CTTTTATGGC	TCCCAGACTTA	TTTGGAAAGCA	AATTTTATAT	GGGAACAGTC	1200
	GTTAAGAAGT	ATGAAGAAAA	CCCTTGCAT	TTCTTAATGG	GTGCTGGGG	CAGTGCCTTT	1260
	TCCATATTGT	TCAACAGAGT	TTTGGGCGTT	TCTGGTTCAC	AAAGCAGAGG	CTCCACAATG	1320
	GAGGAAGAAT	TAGAAAAATAT	TACCACAAAG	CATATTGTGA	GTAATGATAG	CTCGGACAGT	1380
	GATGATGAAT	CACACGAACC	CAAAGGCAC	GAAAATGAAG	ATGCTGGAAG	TGACTATCAA	1440
	AGTGATAATC	AAGCAAGTTG	GATTTCATCGT	ATGATAATGG	CCTTGGTGAG	TGATTCAAGT	1500
30	TTATTCAATA	CCAGAGAAGG	ACGTGCTGGG	AAGGTACACA	ACTTCATGCT	GGGCTTGAAT	1560
	CTCAATACAT	CTTATCCACT	GTCTCCTTTG	AGTGACTTTG	CCACACAGGA	CTCCTTTGAT	1620
	GATGATGAAC	TGGATGCAGC	TGTAGCAGAT	CCTGATGAAT	TTGAGCGAAT	ATATGAGCCT	1680
	CTGGATGTCA	AAAGTAAAAA	GATTTCATGTA	GTGGACAGTG	GGCTCACATT	TAACCTGCCG	1740
	TATCCCTTGA	TACTGAGACC	TCAGAGAGGG	GTTGATCTCA	TAATCTCCTT	TGACTTTTCT	1800
35	GCAAGGCCAA	GTGACTCTAG	TCCTCCGTTT	AAGGAACTTC	TACTTGCAGA	AAAGTGGGCT	1860
	AAAATGAACA	AGCTCCCTTT	TCCAAAGATT	GATCCTTATG	TGTTTGATCG	GGGAAGGGCTG	1920
	AAGGAGTGGT	ATGTCTTTAA	ACCAAGAAT	CCTGATATGG	AGAAAGATTG	CCCAACCATC	1980
	ATCCACTTTG	TTCTGGCCAA	CATCAACTTC	AGAAAGTACA	GGGCTCCAGG	TGTTCCAAGG	2040
	GAAACTGAGG	AAGAGAAGAA	AATCGCTGAC	TTTGATATTT	TTGATGACCC	AGAATCACCA	2100
40	TTTTCAACCT	TCAATTTTCA	ATATCCAAAT	CAAGCATTCA	AAAGACTACA	TGATCTTATG	2160
	CACCTCAATA	CTCTGAACAA	CATTGATGTG	ATAAAAGAAG	CCATGGTTGA	AAGCATTGAA	2220
	TATAGAAGAC	AGAATCCATC	TCGTTGCTCT	GTTTCCCTTA	GTAATGTTGA	GGCAAGAAGA	2280
	TTTTTCAACA	AGGAGTTTCT	AAGTAAACCC	AAAGCATAGT	TCATGTACTG	GAAATGGCAG	2340
	CAGTTTCTGA	TGCTGAGGCA	GTTTGCAATC	CCATGACAAC	TGGATTTTAA	AGTACAGTAG	2400
45	AGATAGTCGT	ACTGATCATG	AGAGACTGGC	TGATACTCAA	AGTTGCAGTT	ACTTAGCTGC	2460
	ATGAGAATAA	TACTATTATA	AGTTAGGTTG	ACAAATGATG	TTGATTATGT	AAGGATATAC	2520
	TTAGCTACAT	TTTCACTCAG	TATGAACCTC	CTGATACAAA	TGTAGGGATA	TATACTGTAT	2580
	TTTTAAACAT	TTCTCACCAA	CTTCTTATG	TGTGTTCTTT	TTAAAAATTT	TTTTTCTTTT	2640
	AAAATATTTA	ACAGTTCAAT	CTCAATAAGA	CCTCGCATT	TGTATGAATG	TTATTCAGT	2700
50	ACTAGATTTA	TTCATACCAT	GAGACAACAC	TATTTTATT	TATATATGCA	TATATATACA	2760
	TACATGAAAT	AAATACATCA	ATATAAAAA				

Seq ID NO: 50 Protein sequence:
Protein Accession #: XP_051896

	1	11	21	31	41	51	
55	MSFIDPYQHI	IVEHQYSHKF	TVVVLRAKTV	TKGAFGMDLD	TPDPYVELFI	STTPDSRKRT	60
	RHFNNNDINPV	WNETFEFILD	PNQENVLEIT	LMDANYVMDE	TLGTATFTVS	SMKVGEKKEV	120
60	PFIFNQVTEM	VLEMSLEVCS	CPDLRFSMAL	CDQEKTFRQQ	RKEHIRESMK	KLLGPKNSEG	180
	LHSARDVPV	AILGSGGGFR	AMVGFSGVMM	ALYESGILD	ATYVAGLSGS	TWYMSTLYSH	240
	PDFPEKGPEE	INEELMKNV	HNPLLLLTPO	KVKRYVESLW	KKKSSGQPV	FTDIFGMLIG	300
	ETLIHNRMT	TLSSLKEKVN	TAQCPLPLFT	CLHVKPDVSE	LMFADWVEFS	PYEIGMAKYG	360
	TFMAPDLFGS	KFFMGTVVKK	YEENPLHFLM	GVWGSAPFSL	FNRVLGVSGS	QSRGSTMEE	420
65	LENITTKHIV	SNDSSDSDE	SHEPKGTENE	DAGSDYQSDN	QASWIHRMIM	ALVSDSALFN	480
	TREGRAGKVH	NFMLGLNLNT	SYPLSPLSDF	ATQDSFDDE	LDAVADPDE	FERIYEPLDV	540
	KSKKIHVVDS	GLTFNLPYPL	ILRPQRGVLD	IISFDFSA	SDSSPPFKEL	LLAEKWAKMN	600
	KLPPFKIDPY	VFDREGLKEC	YVFKPKNPDM	EKDCPTIIHF	VLANINFRLKY	KAPGVPRETE	660
70	EEKBIADFDI	FDDPESPFST	FNFOYPNQAF	KRLHDLMHFN	TLNNIDVIKE	AMVESIEYRR	720
	QNPSRCSVSL	SNVEARRFFN	KEFLSKPKA				

Seq ID NO: 51 Nucleotide sequence:
Nucleic Acid Accession #: NM_006528

Coding sequence: 57..764 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
	GCCGCCACGCG	GCTTTCTCGG	ACGCCTTGCC	CAGCGGGCCG	CCCGACCCCG	TGCACCATGG	60
	ACCCCGCTCG	CCCCCTGGGG	CTGTCTGATT	TGCTGCTTTT	CCTGACGGAG	GCTGCACTGG	120
5	GCGATGCTGC	TCAGGAGCCA	ACAGGAAATA	ACGCGGAGAT	CTGTCTCCTG	CCCCTAGACT	180
	ACGGACCCCTG	CCGGGCCCTA	CTTCTCCGTT	ACTACTACGA	CAGGTACACG	CAGAGCTGCC	240
	GCCAGTTCCT	GTACGGGGGC	TGCGAGGGCA	ACGCCAACAA	TTTCTACACC	TGGGAGGCTT	300
	GCGACGATGC	TTGCTGGAGG	ATAGAAAAAG	TTCCCAAAAGT	TTGCCGGCTG	CAAGTGAGTG	360
	TGGACGACCA	GTGTGAGGGG	TCCACAGAAA	AGTATTTCTT	TAATCTAAGT	TCCATGACAT	420
10	GTGAAAAATT	CTTTTCCGGT	GGGTGTCACC	GGAACCGGAT	TGAGAACAGG	TTTCCAGATG	480
	AAGCTACTTG	TATGGGCTTC	TGCGCACCAA	AGAAAAATCC	ATCATTTTGC	TACAGTCCAA	540
	AAGATGAGGG	ACTGTGCTCT	GCCAATGTGA	CTCGCTATTA	TTTTAATCCA	AGATACAGAA	600
	CCTGTGATGC	TTTCACCTAT	ACTGGCTGTG	GAGGGAATGA	CAATAACTTT	GTTAGCAGGG	660
	AGGATTGCAA	ACGTGCATGT	GCAAAAAGCTT	TGAAAAAGAA	AAAGAAGATG	CCAAAGCTTC	720
15	GCTTTGCCAG	TAGAATCCGG	AAAATTCGGA	AGAAGCAATT	TTAAACATTC	TTAATATGTC	780
	ATCTTGTTTG	TCTTTATGGC	TTATTTGCCT	TTATGGTTGT	ATCTGAAGAA	TAATATGACA	840
	GCATGAGGAA	ACAAATCATT	GGTGATTTAT	TCACCAAGTT	TTATTAATAC	AAGTCACTTT	900
	TTCAAAAAATT	TGGATTTT	TATATATAAC	TAGCTGCTAT	TCAAATGTGA	GTCTACCATT	960
	TTTAAATTTAT	GGTTCAACTG	TTGTGAGAC	GAATTCCTGC	AATGCATAAG	ATATAAAAGC	1020
20	AAATATGACT	CACTCATTTT	TTGGGGTCGT	ATTCCTGATT	TCAGAAGAGG	ATCATAACTG	1080
	AAACAACATA	AGACAATATA	ATCATGTGCT	TTTAACATAT	TTGAGAATAA	AAAGGACTAG	1140
	CC						

Seq ID NO: 52 Protein sequence:
Protein Accession #: NP_006519

	1	11	21	31	41	51	
	MDPARPLGLS	ILLFLTEAA	LGDAAEPTG	NNAEICLLPL	DYGPCRALLL	RYYYDRYTQS	60
	CRQFLYGGCE	GNANNFYWE	ACDDACWRIE	KVPKVCRLQV	SVDDQCEGST	EKYFFNLSSM	120
30	TCEKFFSGGC	HRNRIENRFP	DEATCMGFCA	PKKIPSFYCS	PKDEGLCSAN	VTRYFNPRI	180
	RTCDAFTYTG	CGGNDNNFVS	REDCKRACAK	ALKKKKKMPK	LRFASRIRKI	RKKQF	

Seq ID NO: 53 Nucleotide sequence:
Nucleic Acid Accession #: AA478778
Coding sequence: no ORF found

	1	11	21	31	41	51	
	TATTTTTGTA	CGTAAATGA	TTCTATTATG	ACTGCCTTTG	CATGTAGTAA	TATGACAAAG	60
	TGATCCTTCA	TTATCACGGT	ACACTATTGT	TTACTTTTCA	TCTGTAAATG	TTTTATTGTT	120
	ACTTTTTTAA	AATGAATTTT	TTTAAACAA	TCTAGCCATC	ATCAAGGTGC	TATAAGAGTT	180
45	GTATAAAAGA	TATTTTGGC	ATTTCTAGGC	AAGTATCAGC	CAATAAGTAT	GTTAGTGATA	240
	TCACAGATTG	TACCAACTAT	TAACATAGTT	AAATAAGTAT	TCAGTTTCAT	GTGATCTCTG	300
	GGAAAAAAT	ATGCTGCCTT	GGTGCTAATA	TTGTATGTAT	TTAAATGATC	ATCTGACTCA	360
	GAAATATAAA	CACTTTAAAT	GAAAGGGAGG	AACGGAAGGA	CAATTTCCAG	TGCACAGAAT	420
	CACCTGGATG	AAATAAGACC	AGCTCTTTAC	CCTTATTTT	GGATATGCCT	TTTTTGGAAG	480
50	AGACTTAGAC	TTTATCCTTA	TTGTTGTTAG	TGTTGTAAAT	ATTCGTTGCT	TCAGCCCACG	540
	GTGCCTTGGT	CTCTCCACAA	TCAAATGGAG	GATCCCCCAA	GCAGCTTCAT	TACAGAGTGA	600
	TATTGGGAAA	GTGAGATCCT	CTCACCATT	TGCCAAGATA	CTCTAAATG	ACATCCAAGT	660
	TTACCAAGTAG	AAAGACACAG	GATGCACAGA	ATGGGCATGA	CCTTCAGTCC	ACGAGCACAC	720
	CTGGAGAAAT	TCAGAACCAG	GTTCTGAATC	ATCACGATTG	CCTTTTGCAT	GAAAACATCG	780
55	GCTGGTGATG	TGACTTCTCT	TCAGGCCATG	AGCCTAACAY	CCTGCCGTT	TTCATGCCCG	840
	CTGCAGTAAT	GGACGTTTGT	GTGAAGAAAT	GAAGTGTGGA	GTACAAAATG	CCTTGAGTCT	900
	TTCCGATTGC	TCATTAATTC	ACTTTTGTGT	TACTTCTTTC	CAAAATGGAA	GTGCTGAAGC	960
	CATGGTCTTT	CTGCCCTCC	AAGCTGATGA	AGGGAAGCCT	TTGCCAATGG	CCCATGGAAG	1020
	ACACTTGGTT	TGAGAAACCC	TGCCCACTTC	CAAAGACCAA	AGAGATTAGG	AAAAGCCTGG	1080
60	CAGTATTCTC	CAACTCCAAA	CAAGCTCTAG	AGTGCTCCAG	GAAAAGTTAT	ATTCAGTATA	1140
	TGAATAAGTG	TTATTCTCCA	TTATTAATGT	GTTCTGAAAA	TATATTATGA	ATAAATACAT	1200
	CACCACACCC	AAAAAAAAAA	AAAAAAAAAA	AAAA			

Seq ID NO: 54 Nucleotide sequence:
Nucleic Acid Accession #: NM_020663
Coding sequence: 1..645 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
	<u>ATG</u> AACTGCA	AAGAGGGAAC	TGACAGCAGC	TGCGGCTGCA	GGGGCAACGA	CGAGAAGAAG	60
	ATGTTGAAGT	GTGTGGTGGT	GGGGGACGGT	GCCGTGGGGA	AAACCTGCCT	GCTGATGAGC	120
	TACGCCAACG	ACGCCTTCCC	AGAGGAATAC	GTGCCCACTG	TGTTTGACCA	CTATGCAGTT	180
75	ACTGTGACTG	TGGGAGGCAA	GCAACACTTG	CTCGGACTGT	ATGACACCGC	GGGACAGGAG	240
	GACTACAACC	AGCTGAGGCC	ACTCTCCTAC	CCCAACACGG	ATGTGTTTTT	GATCTGCTTC	300

TCTGTCGTAA ACCCTGCCTC TTACCACAAT GTCCAGGAGG AATGGGTCCC CGAGCTCAAG 360
 GACTGCATGC CTCACGTGCC TTATGTCTC ATAGGGACCC AGATTGATCT CCGTGATGAC 420
 CCAAAAACCT TGGCCCGTTT GCTGTATATG AAAGAGAAAC CTCTCACTTA CGAGCATGGT 480
 GTGAAGCTCG CAAAAGCGAT CGGAGCACAG TGCTACTTGG AATGTTTCAGC TCTGACTCAG 540
 AAAGGTCTCA AAGCGGTTTT TGATGAAGCA ATCCTCACCA TTTTCCACCC CAAGAAAAAG 600
 AAGAAACGCT GTTCTGAGGG TCACAGCTGC TGTCAATTA TCTGA

Seq ID NO: 55 Protein sequence:
 Protein Accession #: NP_065714

1 11 21 31 41 51
 | | | | |
 MNCKEGTDSS CGCRGNDEKK MLKCVVVGDG AVGKTCLLMS YANDAFPEEY VPTVPDHYAV 60
 TVTVGGKQHL LGLYDTAGQE DYNQLRPLSY PNTDVFLICF SVVNPASYHN VQEEWVPELK 120
 DCMHPVPYVL IGTQIDLRDD PKTLARLLYM KEKPLTYEHG VKLAKAIGAQ CYLECSALTQ 180
 KGLKAVFDEA ILTIFHPKKK KKRCSEGHSC CSII

Seq ID NO: 56 Nucleotide sequence:
 Nucleic Acid Accession #: fgenesh prediction
 Coding sequence: 1-546 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 ATGGCCTTGG GCAGCTCCGC CCCTGTGGCT TTGCAGGGTA ATGCCCACTT CCCTGCTGCT 60
 TTCATGGCTG GCATTAAGTG TCTGTGGCTT TTCCAGGTAG TCCCCCTGGG GCTCCCCGAG 120
 TTGGTGCAAA GGCTCCTGGG TGGAGCTCGA ACTGAAATC GCTTTGTGCC CGCAGCCCTG 180
 CAGCTCGCCG GTGCCCTCGA CCTGCCCGCT GGGTCCTGTG CCTTTGAAGA GAGCACTTGC 240
 GGCTTTGACT CCGTGTGTGG CTCTCTGCCG TGGATTTTAA ATGAGGAAGG CCAGCAACCT 300
 TTCTGGTCTT CAGGAGACAT GTCTGACTGG GACTACTGGG TTGGCTGGCG GAAGTTAATT 360
 CATTCTCCTC TGAGCACTCC AGGGTGGAGC AGGCAGGTTA GGCTCCAGTT GTTCCAGCTT 420
 CAGTTTGTCA AAGGCCAGAA CTTGGACGTA ACAGTGTA CTGAGGCTCCA GGGCAGTGAG 480
 AAACCTTTG AAAGTGGTTC CATGGTTCCA TTCACCTTCA TGTACTGGAT CCACCATGGA 540
 AAGTAG

Seq ID NO: 57 Protein sequence:
 Protein Accession #: fgenesh prediction

1 11 21 31 41 51
 | | | | |
 MALGSSAPVA LQGNHFPAA FMAGIKLWL FQVPLGLPE LVQRLLGGAR TETRFVPAAL 60
 QLAGALDLPV GSCAPEESTC GFDSVLASLP WILNEEQQP FWSSGDMSDW DYWVGWRKLI 120
 HSPLSTPGWS RQVRLQLFQL QFVKQGNLDV TVYCRLQGSB KPFETGSMVP FTFMYWIHHG 180
 K

Seq ID NO: 58 Nucleotide sequence:
 Nucleic Acid Accession #: XM_050478
 Coding sequence: 27..4508 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 CCGGCGGCGC CTGAGCCAG CCGAGGATGG AGAACCAGCC TGGGTCCTTC CAGTACGTCC 60
 CTGTGCAGCT GCAAGGGGGG GCACCCTGGG GCTTCACCCT TAAGGGGGGT CTGGAACACT 120
 GTGAGCCGCT CACAGTGTCT AAGATTGAAG ATGGAGGCAA GGCAGCTTGT TCCAGAAAGA 180
 TGAGGACTGG TGATGAGCTG GTGAATATCA ATGGCACTCC ATTATATGGC TCCCGCCAAG 240
 AGGCCCTCAT TCTCATCAA GGCTCCTTCC GGATTCTCAA GCTGATTGTC AGGAGGAGGA 300
 ACGCCCTGT CAGTAGGCCG CACTCATGGC ATGTGGCCAA GCTGCTGGAG GGATGCCCTG 360
 AAGCAGCCAC CACCATGCAT TTCCCTTCTG AAGCCTTCAG CTGTCTCTGG CATTTCTGGCT 420
 GCAACACAAG TGACGTGTGT GTGCAGTGGT GTCCACTCTC CCGGCATTGC AGCACCAGGA 480
 AAAGCAGCTC CATTGGCAGC ATGGAGAGCC TGGAGCAACC AGGCCAAGCC ACCTATGAGA 540
 GCCATCTGTT GCCTATTGAC CAGAACATGT ACCCTAACCA GCGTGACTCA GCCTACAGCT 600
 CCTTCTCGGC CAGTCAAAAT GCTTCTGACT GTGCCCTTTC CCTCAGGCCA GAGGAGCCAG 660
 CCTCTACAGA CTGCATCATG CAAGGCCAGT GGCCAACTAA GGCCCCAGT GGCCGGCCTA 720
 ATGTGGCTGA GACCTCAGGA GGTAGTCGGC GCACCAATGG GGGCCACCTG ACCCCAGCT 780
 CTCAGATGTC ATCCCGTCCA CAGGAGGGAT ACCAGTCAGG GCCCGCCAAA GCAGTCAGGG 840
 GCCCACCACA ACCTCCAGTG AGGCGGGACA GCCTTCAGGC CTCAGAGCC CAACTCCTCA 900
 ATGGAGAGCA GCGCAGGGCA TCTGAGCCTG TGGTCCCCTT GCCACAGAAG GAGAACTGA 960
 GCTTAGAGCC TGTGCTACCC GCAAGGAACC CTAATAGGTT CTGTTGCCTC AGTGGGCATG 1020
 ACCAAGTGAC AAGTGAGGCG CATCAGAACT GTGAGTTTCA TCAGCCTCCT GAATCCAGCC 1080
 AACAGGGCTC TAGCATCTTA CTGATGCAGG CCTCAACCAA AGCTGTGGA TCCCCAAAAG 1140
 CCTGTGACAG AGCTTCCAGC GTGGATTCCA ACCCACTCAA TGAGGCTTCT GCAGAGCTAG 1200
 CTAAGGCTTC TTTTGGCAGA CCTCCACATC TCATAGGACC CACAGGGCAT CGCCATAGTG 1260
 CCCTGAAACA GCTGTGGCA TCCACCTGTG AGCATGTGCA CCTTGATACC AGGGGCAGCA 1320
 AAGGGATGGA GCTCCACCC GTACAGGATG GGCACCAGTG GACTCTGTCC CCTTTGCACA 1380

	GCAGCCACAA	AGGGAAGAAA	AGTCCATGCC	CCCCTACAGG	AGGAACCCAT	GACCAGTCCA	1440
	GCAAAGAAAG	AAAGACCAGA	CAAGTGGATG	ACAGGTCTTT	AGTTTTGGGA	CACCAGAGCC	1500
	AAAGCAGTCC	CCCACATGGA	GAGGCTGATG	GACACCCCTC	AGAAAAAGGT	TTCTCTGGACC	1560
5	CAAACAGAAC	AAGCAGAGCA	GCCAGTGAAT	TGGCCAACCA	GCAACCCTCT	GCCTCTGGCT	1620
	CCCTTGTTCA	ACAAGCCACG	GACTGTTCTT	CAACCACTAA	AGCAGCTAGT	GGCACAGAGG	1680
	CAGGTGAAGA	AGGGGACAGC	GAGCCCAAGG	AGTGCAGCCG	GATGGGTGGT	AGGCGAAGTG	1740
	GAGGGACCCG	GGGCCGCTCG	ATCCAAAACC	GGCGGAAGAG	TGAGCGTTTT	GCTACCAATC	1800
	TGCGTAATGA	AATTTCAGAG	AGGAAGGCC	AGCTCCAGAA	AAGCAAGGGT	CCCTTGTCAC	1860
	AGCTGTGTGA	CACTAAGGAG	CCAGTGGAG	AGACCCAGGA	GCCCCAGAA	AGTCTCCAC	1920
10	TCACTGCCTC	TAACACATCT	CTTCTATCTT	CATGTAAAAA	ACCTCCCAGC	CCCAGAGACA	1980
	AGCTCTTCAA	CAAAAGCATG	ATGCTCAGAG	CTAGGTCTTC	CGAGTGCCTC	AGCCAAGCCC	2040
	CTGAGAGCCA	TGAATCTAGG	ACAGGCTTAG	AGGGACGAAT	AAGCCCTGGC	CAGAGGCCTG	2100
	GCCAGTCTCT	TTTGGGCTGT	AACACCTGGT	GGAAAGCACC	TGACCCATCC	TCCTCAGACC	2160
	CTGGAAGAAG	ACATGCTCAC	TGTGGAGTTC	TGTGAGGTCA	TTGGAGATGG	TCTCCAGAGC	2220
15	ATAATTCA	GCCACTTGTG	GCAGCAGCCA	TGGAAGGCC	TTCCAACCCA	GGTGACAACA	2280
	AGGAATTGAA	GGTCTTCTACT	GCTCAAGCTG	GGGAGGATGC	CATCCTCTTG	CCTTTTGCAG	2340
	ACAGAAGAAA	TTTCTTTGAA	GAGAGTAGCA	AATCCTTATC	TACATCTCAT	TTGCCAGGTT	2400
	TAACCACTCA	TAGCAACAAG	ACTTTTACCC	AGAGACCAAA	ACCTATAGAC	CAAAACTTCC	2460
	AGCCAATGAG	CTCCAGCTGT	AGGGAATTGA	GGCGCCATCC	CATGGACCAA	TCATATCATT	2520
20	CCGCAGACCA	ACCATATCAT	GCCACAGACC	AATCATATCA	TTCCATGTCA	CCCCTTCAGT	2580
	CAGAAACTCC	CACCTTACTCA	GAATGTTTTG	CAAGCAAAGG	TCTAGAAAAT	TCCATGTGTT	2640
	GTAAGCCACT	ACACTGTGTT	GATTTTGATT	ACCACAGGAC	CTGCTCTTAC	TCCTGCAGTG	2700
	TTCAAGGAGC	TCTAGTCCAT	GATCCTTGCA	TTTATTGTTT	TGGGGAATC	TGCCCTGCCT	2760
25	TGCTAAAGAG	AAATATGATG	CCAAATTGCT	ACAACTGCCG	GTGCCACCCAC	ACCAATGCA	2820
	TTGCGTGTTC	AGTTTGCTAT	CATAATCCTC	AGCACAGTGC	CCTCGAGGAC	AGCAGCTTGG	2880
	CACCTGGCAA	CACCTGGAAA	CCCAGGAAGC	TGACAGTGCA	GGAAATTCCT	GGGGACAAAT	2940
	GGAATCCAAT	AACAGGAAAC	AGGAAGACCA	GCCAGTCAGG	GAGGGAAATG	GCTCATTTCA	3000
	AGACTAGCTT	TTTATGGGCA	ACCCCTTTCC	ATCCTTGCTT	TGAGAACCCTA	GCACTGGACT	3060
	TGTCAGCTA	CCGAGCAATT	TCTTCTCTTG	ACCTCCTTGG	AGACTTCAAA	CATGCTTTGA	3120
30	AAAAATCAGA	GGAAACTTCA	GTTTATGAGG	AGGGGAGCTC	CCTTGCCCTCC	ATGCCCCACC	3180
	CACCTGCGCAG	CCGTGCCCTTC	TCAGAGAGTC	ACATCAGCTT	GGCGCCCCAA	AGCACCCGGG	3240
	CCTGGGGGCA	GCATAGGAGG	GAGCTCTTTA	GCAAAGGTGA	TGAGACCCAG	TCGGATCTTC	3300
	TCGAGGCCAG	GAAGAAGGCC	TTTCTCTCTC	CTCGCCCTCC	TCCTCCCAAC	TGGGAGAAGT	3360
35	ACAGGCTCTT	TCGTGCAGCC	CAGCAGCAGA	AGCAGCAACA	GCAGCAGCAG	AAGCAACAGG	3420
	AGGAGGAGGA	GGAGGAGGAA	GAAGAAGAAG	AAGAGGAAGA	GGAAGAGGAG	GAGGAGGAGG	3480
	CAGAGGAGGA	GGAGAGGAGG	CTGCCACCCC	AGTATTTCAG	TTCAAGAAACC	TCTGGTTTCT	3540
	GTGCTCTCAA	TCCTGAGGAG	GTCTTAGAGC	AGCCACAACC	CCTCAGCTTT	GGCCACCTGG	3600
	AGGGCTCGAG	ACAGGGTTCA	CAAAGTGCTC	CAGCAGAGCA	AGAATCCTTT	GCACTCCATT	3660
40	CCAGTGATTT	CTTGCCCTCCA	ATAAGGGGTC	ACTTGGGATC	TCAACCTGAG	CAGGCTCAGC	3720
	CCCCCTGTCTA	CTATGGCATT	GGTGGGCTTT	GGAGGACATC	GGGACAGGAA	GCCACTGAAT	3780
	CCGCCAAACA	AGAGTTTTCAG	CACCTTTCGC	CTCCTTCAGG	GGCCCCAGGA	ATCCCTACCT	3840
	CTTACTCAGC	TTATTACAAT	ATTTCTGTGG	CCAAGGCAGA	GCTGCTGAAC	AAACTGAAAG	3900
	ACCAACCTGA	GATGGCAGAG	ATTGGCCTAG	GAGAGGAGGA	AGTTGACCAT	GAAGTGGCTC	3960
45	AAAAAAGAT	ACAGCTTATC	GAAAGCATCA	GCAGAAAAC	TTCTGTCTTG	CGGGAGGCC	4020
	AGCGAGGGCT	GCTAGAGGAC	ATCAATGCCA	ATTCTGCCCT	TGGGGAGGAG	GTGGAGGCCA	4080
	ACTTAAAGC	CGTCTGCAAA	TCCAATGAAT	TTGAAAAGTA	CCACTTGTTT	GTTGGGGACC	4140
	TGGACAAAGT	GGTCAACCTG	TTGCTGTCAC	TCTCTGGACG	ACTGGCCCGG	GTGGAGAATG	4200
	CTCTGAACAG	CATCGATTCA	GAGGCCAAC	AGGAGAAGTT	GGTACTGATA	GAGAAGAAGC	4260
50	AGCAGCTGAC	GGGGCAGTTG	GCAGATGCCA	AGGAGCTGAA	GGAGCACGTG	GACCGCCGGG	4320
	AGAAGTTGGT	GTTTGGCATG	GTCTCCCGCT	ACCTGCCTCA	GGACCAGCTC	CAAGATTACC	4380
	AGCACTTTGT	CAAGATGAAA	TCTGCTCTCA	TCATTGAACA	GCGAGAGCTG	GAGGAGAAGA	4440
	TCAAAGCTCGG	GGAGAGGACAA	CTCAAATGTC	TCAGGGAGAG	TCTACTCTTG	GGGCCAGCA	4500
	ATTTCTTAAT	CTACCAGCAC	TCTGCCACAG	CATCCCTGCC	CAGCCATGTG	GGAAGTGCTT	4560
55	TCAATCTTCT	TTGTTAGCAG	TTTCTCAGCA	AGTAGATAGC	AATTAGCAGT	TTGTTCCAGC	4620
	CCTCTACCTT	GGATGCTCTC	CACCTACCCCT	TCCCTAGCAG	TGGTCCCTAAC	CAGCTAGGAG	4680
	ACCCTGGGGA	AGCCACAAGC	TTCTACCCAA	GGGAGCTGCA	GCAAGGTGTG	ATCTTAGAAC	4740
	CACACTCTCC	TTCCACACAGT	TGCCAAGGGC	AAGTACTTGC	TGCACAGAGA	ACCAAGGAAG	4800
	TGCTCTTCAAT	CTGCTTTGTA	CTAGGACACC	AAAGACATCA	AGTACTCATC	ACCCACCCAT	4860
60	ATCATCAACA	GCCTCTAAAG	GCTCAGAGGG	AATCTGCCTT	GCAGCTCTAC	TCTGCCCCAG	4920
	GGCTTGTGGC	CAGCCATTTT	TCACAGAGAG	CTGGCTGCCT	TGAGGGCATT	CACCTGGCAC	4980
	CAGTTTCAGG	GCCTCACCCA	AGCTTTTGAC	GGGAAAGCAC	AGAGGGAGGA	ATTACTACTGA	5040
	AAAAAATGCA	AGCAAAGGTT	GAGTACCCCT	AGGTGCCCTT	TAGGAAGGAA	CCAGGTTTAA	5100
	ATAGGCTCTA	CCCTTACCTT	TCCCAGCAGC	AAGTTTCAGG	GAAGAGGCCT	ACTCTTAGCC	5160
65	CTGGCTAGTG	TGACCTCTTT	CCTGTCTTAA	GACTTTGGTC	CTACCACCTC	TTGTTTCATC	5220
	TTTCTTTTAC	ATTGCTGGGG	GTTACCCGAG	GTGCTTACCC	CAGGGCTTCA	CCATATGGGC	5280
	CATTAATAGC	TCTACTAAAA	CTGACTTCTA	GATGTAGGTT	TCATTATTGG	GGGAGGGGGT	5340
	TCTTATGTGT	ATATTTTAAA	TGGCCTTTTG	ATTTTATTTA	TTTTTATGTT	TTGATTATT	5400
	TTTTCTTTTT	TAATCTAATA	GGCGAGAAGA	GGGAAGTTGG	AGAGGGAAAA	GTTAGCCCA	5460
70	AAGGAAGCA	TTTTCTGAG	ATCAGCCTGA	ATCCACCGTG	GCTAGGCATA	TTCTTGCTCT	5520
	TCTCGTGTG	CTCACAACCTA	CCTGCCTGGA	TGAATTTAGG	AAAGTTGCAG	GATACAAGGT	5580
	TAAACACAA	GATCAATATGA	ACAATCCGAA	AATGTTATTA	AGAAAACAGT	TCCGGCCGGG	5640
	CATGGTGGCT	CACGCCCTGAA	ATCCAGCAC	TTTGGGAGGC	CGAGGCAGGT	GGATCACGAG	5700
	GTCAGGAGAT	CAAGACCATC	CTGGCTAACA	CGGTGAAACC	CTATCTCTAC	TAAAAATACA	5760
	AAAAATTAGC	CAGGTGTGGT	GGCACGCACC	AGTAGTCCCA	GCTACTCGGG	AGGCTGAGGC	5820
75	AGGAGAATTG	CTTGAACCTG	GAAGGCAGAG	ATTGCAGTGA	GCTGAGACCA	CACCACTGCA	5880
	CTCCATCTCTG	GGCAACAGAG	TGAGACTTTG	TCTCAAAAAG	AAAGAAAGAA	AGAAAGAAAG	5940

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ATC

Seq ID NO: 59 Protein sequence:
Protein Accession #: XP_050478

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	SEAFSLSWHS	GCNTSDVCVQ	WCPLSRHCST	EKSSSIGSME	SLEQPGQATY	ESHLLPIDQN	180
	MYPNQRDSAY	SSFSASSNAS	DCALSLRPEE	PASTDCIMQG	PGPTKAPSGR	PNVAETSGGS	240
	RRTNGGHLTP	SSQMSRRPQE	GYQSGPAKAV	RGPPQPPVRR	DSLQASRAQL	LNGEQRRASE	300
	PVVPLPQKEK	LSLEPVLPAR	NPNRFCCLSG	HDQVTSEGHQ	NCEFSQPPES	SQQGSEHLIM	360
15	QASTKAVGSP	KACDRASSVD	SNPLNEASAE	LAKASFGRRP	HLIGPTGHRH	SAPEQLLASH	420
	LQHVHLDTRG	SKGMELPPVQ	DGHQWTLSP	HSSHKGKSP	CPPTGGTHDQ	SSKERKTRQV	480
	DDRSVLVLGHQ	SQSSPPHGEA	DGHPSEKGF	DPNRTSRAAS	ELANQQPSAS	GSLVQQATDC	540
	SSTTKAASGT	EAGEEGDSEP	KECSRMGGR	SGGTRGRSIQ	NRKRSEFAT	NLRNEIQRRK	600
	AQLQKSKGPL	SQLCDTKPEV	EETQEPPESP	PLTASNTSL	SSCKKPPSPR	DKLFNKSMML	660
20	RARSSECLSQ	APESHESRTG	LEGRISPGQR	PGQSSLGLNT	WWKAPDPSS	DPEKAHAHCG	720
	VRGGHWRWSP	EHNSQLPLVAA	AMEGPSNPGD	NKELKASTAQ	AGEDAILLPF	ADRRKPFEEES	780
	SKSLSTSHLP	GLTTHSNKTF	TQRPKPIDQN	FQPMSSSCRE	LRHPMDQSY	HSADQPYHAT	840
	DQSYHMSPL	QSETPTYSEC	FASKGLENSM	CKPLHCGDF	DYHRTCSYSC	SVQGLVHDP	900
	CIYCSGEICP	ALLKRNMPN	CYNCRCHHHQ	CIRCSVCYHN	PQHSALDSS	LAPGNTWKPR	960
25	KLTVQEFPGD	KWNPITGNRK	TSQSGREMAH	SKTSFWSWATP	FHPCLNPAL	DLSSYRAISS	1020
	LDLLGDFKHA	LKKSEETSVY	EEGSSLASMP	HPLRSRAFSE	SHISLAPQST	RAWGQHRREL	1080
	FSKGDDETQSD	LLGARKKAPP	PPRPPPPNWE	KYRLFRAAQQ	QKQQQQQKQ	QEEEEEEEE	1140
	EEEEEEEEEE	EAEEEEEELP	PQYFSSETSG	SCALNPPEVL	EQPQLPSFGH	LEGSRQGSQS	1200
	VPAEQESFAL	HSSDFLPPIR	GHLGSQPEQA	QPPCYGIGG	LWRTSGQEAT	ESAKQEFQHF	1260
30	SPPSGAPGTP	TSYSAYYNIS	VAKAELLNKL	KDQPEMAEIG	LGEEVDHEL	AQKKIQLIES	1320
	ISRKLSVLRE	AQRGLLEDIN	ANSALGEEVE	ANLKAVCKSN	EFEKYHLFVG	DLDKVVNLLL	1380
	SLSGRLARVE	NALNSIDSEA	NQEKLVLEK	KQQLTGQLAD	AKELKEHVDR	REKLVFGMVS	1440
	RYLPQDQLQD	YQHFVKMKA	LIIEQRELEE	KIKLGEEQLK	CLRESLLGSP	SNF	

Seq ID NO: 60 Nucleotide sequence:
Nucleic Acid Accession #: NM_014705
Coding sequence: 192..2489 (underlined sequences correspond to start and stop codons)

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45	AATGCTTCCT	GGATTAGAAT	TCCACTATTT	GGTCCCTATC	CTAGTCTACT	AAAGAAAATT	180
	GAGCGGGAAA	CATGGCGGAA	AAGTGGCGTT	TCATTAATTG	CTACTGTAAC	TCGTCTAATG	240
	GAGAGGTTGT	TAGATTACAG	AACCTCTATA	AGACTGAACT	GAACAAGGAG	GAGATGTATA	300
	TACGCTACAT	TCACAACTC	TATGATCTGC	ATCTCAAAGC	ACAGAACTTT	ACAGAAGCTG	360
	CATATAACCT	CCTCTTATAT	GACGAGCTAC	TGGAATGGTC	TGATCGGCCC	CTCAGGGAGT	420
50	TCCTGACCTA	CCCCATGCAA	ACAGAAATGC	AGCGCAAAGA	GCACCTGCAC	CTCACCATCA	480
	TCCAGAACTT	TGACAGAGGC	AAATGTTGGG	AGAATGGCAT	TATCTTGTC	CGGAAGATTG	540
	CAGAGCAGTA	TGAGAGTTAT	TATGACTACA	GAAACCTGAG	CAAGATGCGG	ATGATGGAAG	600
	CCTCTTTGTA	TGACAAAAAT	ATGGACCAGC	AACGCTCTGA	ACCAGAGTTC	TTCAGAGTTG	660
	GATTTTATGG	AAAAAAATTT	CCATTTTCT	TAAGAAATAA	GGAGTTTGTG	TGTCGAGGGC	720
55	ATGACTACGA	GAGGCTGGAA	GCCTTCCAAC	AGAGAATGCT	GAACGAGTTC	CCCCATGCCA	780
	TCGCCATGCA	GCACGCCAAC	CAGCCCGATG	AGACCATCTT	CCAGGCAGAA	GCTCAGTATT	840
	TGCAGATATA	TGCTGTGACT	CCCATCCAG	AGAGCCAGGA	GGTCCTGCAG	AGAGAGGGTG	900
	TTCCGGACAA	CATCAAAAGC	TTCTATAAAG	TGAATCACAT	CTGGAATTC	CGCTATGACC	960
	GACCATTTCA	CAAAGGCACA	AAAGATAAAG	AGAATGAATT	CAAGAGTCTC	TGGGTGGAGA	1020
60	GAACGTCATT	ATACCTGGTG	CAGAGTTTGC	CTGGCATCTC	TCGCTGGTTT	GAAAGTGGAAA	1080
	AGCGTGAAGT	GGTAGAAATG	AGTCCTCTGG	AAAATGCAAT	TGAAGTGCTA	GAAAAATAAGA	1140
	ATCAGCAGCT	GAAGACTCTG	ATTAGTCAGT	GTCAGACAAG	ACAGATGCAG	AATATTAATC	1200
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65	TTGCACGATT	AAGAGAGCTG	ATGCTTGAGC	AGGCACAGAT	TCTGGAATTT	GGTTTGCCCG	1380
	TGCATGAGAA	GTTTGATACCT	CAAGATATGA	GACCCCTTCA	CAAAAAGCTG	GTTGACCAAT	1440
	TCTTTGTGAT	GAAGTCGAGC	TTAGGGATAC	AGGAGTTCTC	TGCTTGATG	CAAGCCAGTC	1500
	CTGTCCATTT	TCCTAATGGA	AGCCCTCGTG	TGTGTAGAAA	CTCAGCACCT	GCTTCTGTGA	1560
	GCCCAGATGG	TACCAGGGTA	ATTCTTAGAC	GCAGCCCGTT	AAGTTACCCA	GCTGTCAACC	1620
70	GATATTCTTC	CTCCTCACTG	TCCTCACAAG	CTTCTGCTGA	AGTAAGCAAT	ATTACAGGGC	1680
	AATCAGAAAAG	CTCTGATGAA	GTCTTTAACA	TGCAGCCAAG	TCCATCTACC	TCAAGCTTGA	1740
	GTTCTACTCA	CTCGGCTTCA	CCTAATGTGA	CAAGTTCTGC	TCCATCGAGT	GCCAGAGCTT	1800
	CTCCTTTGTT	GTCTGACAAA	CACAAACATT	CCCCAGAAAA	CTCTTGCCCTG	TCACCAAGAG	1860
	AGAGACCATG	CAGTGCCATT	TATCCAACAC	CTGTGGAGCC	TTCCGAGAGG	ATGCTGTTTA	1920
75	ATCATATTGG	AGACGGGGCC	TGCGACCGCA	GTGACCCAAA	TCTCTCTGCA	CCTGAAAAAG	1980
	CTTCACCAGC	AAGACACACG	ACATCAGTAT	CCCCCTCGCC	TGCCGGGCGA	TCTCCATTGA	2040

	AGGGCTCTGT	GCAGTCTTTC	ACCCCTCTCT	CAGTGGAGTA	CCACTCGCCA	GGACTCATCT	2100
	CCAACCTCCCC	TGCTTGTGCG	GGCAGCTACA	GCAGTGGGAT	TTCTTCTCTC	AGCCGGTGCA	2160
	GCACGTCCGA	AACCTCAGGC	TTTGAATAATC	AGGTGAATGA	ACAGTCGGCC	CCCTGCGCGG	2220
	TGCCAGTGCC	GGTGCCCGTG	CCGAGCTACG	GCGGGGAGGA	GCCAGTGCGC	AAGGAGAGCA	2280
5	AGACTCCGCG	CCCGTACAGC	GTCTACGAGC	GGACTCTGCG	GCGCCCCGTC	CCGCTACCTC	2340
	ACAGCTCTCT	CATCCCGCTC	ACGTCCGAGC	CGCCCGCGCT	GCCCCCAAG	CCTCTGGCAG	2400
	CGCGATCCAG	CCACCTGGAG	AATGGGGCCC	GGAGGACTGA	CCCCGGCCCC	CGGCCCAGGC	2460
	CCCTGCCCGG	CAAGGTCTCT	CAGTTATAAG	TCACTTTTCT	ATGTACCTGC	GATGCATTCT	2520
	TTGCCCGTTT	ACAAAATAAG	AAGTATGATG	AGAAGACATT	TAGTGTAGGC	ACTTTAATAA	2580
10	CTTACTCAGC	TCCTTCGATG	AATGGAATTA	AAACTTGCTT	ATTAAATATC	ATGTTGCACA	2640
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	AAACCGTTTC	TCATTGGGAA	GTGGTAAATA	GTGATAAAGA	CTCCTTTTGT	ACCTTTTAT	2760
	GTTCACTTTT	TTTTATATAG	TTTAATCTTA	AAACCAATAC	GATATTGTCA	AACGATACAA	2820
	TGTGTGACAA	TGTTGTATCG	TTTTTACTGA	ATACTTGATA	CTTGAGAGAA	GCTTATTAAG	2880
15	TCAGTGCACA	TCCTAACACA	GTGGTCCTTA	TTTLAGAAGA	CTTCTGTAAA	TAAGGCAAGG	2940
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	GGGGTTGCAA	AGCTTGGGAC	TGGAAATTGT	TTTGTCTTGT	AAACAAAATA	CTTCTTTAAG	3060
	GTTGCTTTTG	CTGTTTGA	GCTGTCTACA	TTCGTAAAT	TCTATTTTGT	GAATTGGTAG	3120
	CTAAATCCCT	TACTACCTCG	ACACCGTGGT	ATCTACTGTA	TTTCTTTTCA	AGGTGCAATT	3180
20	TGCTTCAGAG	TTCCAATCAG	CTAGATTAA	CAAGAGGCTC	CAGAAGAAAT	GTTTACTTGA	3240
	ATTTTGCCT	TCCTTTCTTG	ATAGTTTCCT	ATATAAAAT	TGTCATTGAA	CAAGAGCAAA	3300
	TGCTGAAGTA	TTAATGAGGC	ACAAATGACT	GTGCCCCATT	AGCAAGAAAT	CAGGAATCAA	3360
	TACAGACAGT	ATTAATTA	TAGCTTAAGT	GAAGAAAAA	AAAAACTTAG	TGAAATGTGA	3420
	TTAGCACGAT	TAAATGGCAA	AAGGACTTAT	AAAAGGCAAG	GGCATTAACT	TTCAGTCTTG	3480
25	CACAAATAA	AAAATTCCTC	ACGACTCTCC	ACTTTTACCA	GTGGAGTTTG	TCTTAGCTGA	3540
	CCTGTGCTCT	TTCTCTTGAA	GGAGGATTGC	TGTAGACTTC	TCTAGCTTGA	ATATTGCAAC	3600
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	TCAATGACA	ATAGATATGA	ACTGTATTTT	AAATCATACT	GTAAATATT	TTCCCTCTTT	3780
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	AGTGACCACT	TTTTATATAT	CTCTTAATGA	AACCATTCAG	CAGGTATATG	CTGTTGAGGC	3900
	TGGTTATAGA	GGTTTTCTAT	AATAAATGTT	CAAGTATTTT	TGTATATAAC	TGGTTAATTT	3960
	TAATAAGAGA	TACCATTATG	TGTAAAAAAA	AGTAAAAATA	AACGCAACA	GTTGTTGATG	4020
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	ATATGTTAAA	TATTTATGTT	TAGTGAAAGT	GTTTCAATTT	GAGAAAAGGA	ACATATGCAT	4200
	TTTAGCTTTG	TATCTTGCAA	GTTTTCAGT	CAGAAATTTT	TTGAACTAGC	TTTTGCTTTT	4260
	GATAACACTT	CGTGTGTTGA	ACCACATTCA	TATATATATA	CATATATATG	TGAAGCTCCA	4320
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40	AACAAAGCTT	CCTTGATTTC	CTTTTCCTGT	GTAATTTAAT	AGATTGTTTG	ACTAGTGCTT	4440
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	AGTGAGCAGT	TGAATTTATC	TTGAATTTAT	CATGTGTGTG	TATTTCTGAA	GCAGTACAT	4560
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Seq ID NO: 61 Protein sequence:
Protein Accession #: NP_055520

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	ESYYDYRNLS	KMRMEASLY	DKIMDQQRLE	PEFFRVGFYQ	KKFPFFLRNK	EFVCRGHDIY	180
	RLEAFQQRML	NEFPHALAMQ	HANQPDETIF	QAEAQYLQIY	AVTPIESQE	VLQREGVPDN	240
55							
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	VEMSPLENAI	EVLENKNQQL	KTLISQCQTR	QMQNINPLTM	CLNGVIDAAV	NGGVSRVQEA	360
	FFVKEYILSH	PEDGEKIARL	RELMLQAQI	LEFGLAVHEK	FVPQDMRPLH	KKLVDQFFVM	420
	KSLGIQEFSS	ACMQASPVHF	PNGSPRVCRN	SAPASVSPDG	TRVIPRRSPL	SYPAVNRYSS	480
	SSLSSQASAE	VSNITQSES	SDEVFNMQPS	PSTSSLSTSH	SASPNVTSSA	PSSARASPLL	540
60							
	SDKHKHSREN	SCSPRERPC	SAIYPTPVEP	SQRMFLFNHIG	DGALPRSDPN	LSAPEKASPA	600
	RHTTSVSPSP	AGRSPLKGSV	QSFTSPVEY	HSPGLISNSP	VLSGSYSSGI	SSLSRCSTSE	660
	TSGFENQVNE	QSAPLPVPVP	VPVPSYGEE	PVRKESKTPP	PYSVYERTLR	RPVPLPHSLS	720
	IPVTSEPPAL	PPKPLAARSS	HLENGARRTD	PGPRPRPLPR	KVSQ		

65 Seq ID NO: 62 Nucleotide sequence:
Nucleic Acid Accession #: fgenesh prediction
Coding sequence: 1..2561 (underlined sequences correspond to start and stop codons)

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	CGGGGGCTGA	GGAACGCTCG	GAGGGGACTG	GGAGACGCGG	CGCTTATGCA	AAGGTGCCTT	180
75							
	CGGCTGCCCG	GACAACCCCG	CAGCAACCAG	GTACAGCTCT	CAGAGGTTCC	ACAGAGGAAG	240
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 CTTCTCAACC CCAACTACT TGACATTTTG GACCAGTAA

Seq ID NO: 63 Protein sequence:
 Protein Accession #: fgenesh prediction

45 1 11 21 31 41 51
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 50 YLSDTTLEKK MAVASILQSL QPLPAKEVSY LYVNTADLHS GPSFVESLFE EFDCLSDLR 180
 DMPEDDGEPS KGASPELAKS PRLRNAADLP PPLPNKPPPE DYEEALPLG PGKSPEYISS 240
 HNGCSPSHSI VDGYYEDADS SYPATRVNGE LKSSYNDSDA MSSSYESYDE EEEGKSPQP 300
 RHQWPSEAS MHLVRECRIC AFLLRKKRFG QWAKQLTVIR EDQLLCYKSS KDRQPHLRLA 360
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 55 EVPRSPVLLC KLDDLKRLSQ EKQTSDDSV GVDNCSLTG RRETCDHKGK KKSLSAELKG 480
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 LYFHKDHMDL RTHVNAIALQ GCEVAPGFGP RHPFAFRILR NRQEVAILA SCSEDMGRWL 600
 GLLLVEMGSR VTPEALHYDY VDVETLTSIV SAGRNSFLYA RSCQNQWPEP RVYDDVPYK 660
 MQDEEPERPT GAQVKRHASS CSEKSHRVDP QVKVKRHASS ANQYKYGNR AEEDARRYLV 720
 60 EKEKLEKEKE TIRTELIALR QEKRELKEAI RSSPGAKLKA LEEAVATLEA QCRAKEERRI 780
 DLEKLVAVK ERLQQSLAGG PALGLSVSSK PKSGQLSEED TLTSNGALSE RTSITSSTPG 840
 LLNPNTDIL DQ

Seq ID NO: 64 Nucleotide sequence:
 Nucleic Acid Accession #: NM_004126.1
 Coding sequence: 108-129 (underlined sequences correspond to start and stop codons)

70 1 11 21 31 41 51
 | | | | | |
 GGCACGAGCT CGTGCCGGCC TTCAGTTGTT TCGGGACGCG CCGAGCTTCG CCGCTCTTCC 60
 AGCGGCTCCG CTGCCAGAGC TAGCCGAGC CCGTTCTGG GCGGAAAATG CCTGCCCTTC 120
 ACATCGAAGA TTTGCCAGAG AAGGAAAAAC TGAAAATGGA AGTTGAGCAG CTTGCGAAAG 180
 AAGTGAAGTT GCAGAGACAA CAAGTGTCTA AATGTTCTGA AGAAATAAAG AACTATATTG 240
 75 AAGAACGTTT TGGAGAGGAT CCTCTAGTAA AGGGAATTCC AGAAGACAAG AACCCTTTA 300
 AAGAAAAAGG CAGCTGTGTT ATTTCA~~TAA~~ TAACTTGGGA GAAACTGCAT CTAAGTGGGA 360
 AGAACTAGTT TGTTTATGTT TTCCAGATA AAACCAACAT GCTTTTAAAG GAAGGAAGAA 420

TGAAATTAAG AGGAGACTTT CTTAAGCACC ATATAGATAG GGTATGTAT AAAAGCATAT 480
 GTGCTACTCA TCTTTGCTCA CTATGCAGTC TTTTTTAAGA GAGCAGAGAG TATCAGATGT 540
 ACAATTATGG AAATAAGAAC ATTACTTGAG CATGACACTT CTTTCAGTAT ATTGCTTGAT 600
 GCTTCAAATA AAGTTTTGTC TT

Seq ID NO: 65 Protein sequence:
 Protein Accession #: NP_004117

1 11 21 31 41 51
 | | | | |
 MPALHIEDLP EKEKLKMEVE QLRKEVKLQR QVSKCSEEI KNYIERSGE DPLVKGIPED 60
 KNPFKEKGSC VIS

Seq ID NO: 66 Nucleotide sequence:
 Nucleic Acid Accession #: NM_003842.1
 Coding sequence: 1-1236 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 ATGGAACAAC GGGGACAGAA CGCCCCGGCC GCTTCGGGGG CCCGAAAAG GCACGGCCCA 60
 GGACCCAGGG AGGCGCGGGG AGCCAGGCCT GGGCCCCGGG TCCCAAGAC CCTTGTGCTC 120
 GTTGTGCGCG CGTTCCTGCT GTTGGTCTCA GCTGAGTCTG CTCTGATCAC CCAACAAGAC 180
 CTAGCTCCCC AGCAGAGAGC GGCCCCACAA CAAAGAGGT CCAGCCCCTC AGAGGGATTG 240
 TGTCCACCTG GACACCATAT CTCAGAAGAC GGTAGAGATT GCATCTCCTG CAAATATGGA 300
 CAGGACTATA GCACTCACTG GAATGACCTC CTTTCTGCT TCGCTGCAC CAGGTGTGAT 360
 TCAGGTGAAG TGGAGCTAAG TCCCTGCACC ACGACCAGAA ACACAGTGTG TCAGTGCAGAA 420
 GAAGGCACCT TCCGGGAAGA AGATTCTCCT GAGATGTGCC GGAAGTGCCG CACAGGGTGT 480
 CCCAGAGGGA TGGTCAAGGT CGGTGATTGT ACACCCTGGA GTGACATCGA ATGTGTCCAC 540
 AAAGAATCAG GCATCATCAT AGGAGTCACA GTTGCAGCCG TAGTCTTGAT TGTGGCTGTG 600
 TTTGTTTGCA AGTCTTTACT GTGGAAGAAA GTCCTTCCTT ACCTGAAAGG CATCTGCTCA 660
 GGTGGTGGTG GGGACCTTGA GCGTGTGGAC AGAAGCTCAC AACGACCTGG GGCTGAGGAC 720
 AATGTCCTCA ATGAGATCGT GAGTATCTTG CAGCCACCC AGGTCCCTGA GCAGGAAATG 780
 GAAGTCCAGG AGCCAGCAGA GCCAACAGGT GTCAACATGT TGTCCCCCGG GGAGTCAGAG 840
 CATCTGCTGG AACCGGCAGA AGCTGAAAGG TCTCAGAGGA GGAGGCTGCT GGTTCAGCA 900
 AATGAAGGTG ATCCCACTGA GACTCTGAGA CAGTGCTTCG ATGACTTTGC AGACTTGGTG 960
 CCTTTGACT CCTGGGAGCC GCTCATGAGG AAGTTGGGCC TCATGGACAA TGAGATAAAG 1020
 GTGGCTAAAG CTGAGGCAGC GGGCCACAGG GACACCTTGT ACACGATGCT GATAAAGTGG 1080
 GTCAACAAAA CCGGGCGAGA TGCCTCTGTC CACACCCTGC TGGATGCCCT GGAGACGCTG 1140
 GGAGAGAGAC TTGCCAAGCA GAAGATTGAG GACCATTGTG TGAGCTCTGG AAAGTTCATG 1200
 TATCTAGAAG GTAATGCAGA CTCTGCCATG TCCTAA

Seq ID NO: 67 Protein sequence:
 Protein Accession #: NP_003833.1

1 11 21 31 41 51
 | | | | |
 MEQRGQNAPA ASGARKRHP GPREARGAR GPRVPKTLVL VVAAVLLLVV AESALITQDD 60
 LAPQQAAPQ QKRSSPSEGL CPPGHHISED GRDCISCKYG QDYSTHWN DL LFCLRCTRCD 120
 SGEVELSPCT TTRNTVCQCE EGTFREEDSP EMCRCRTGC PRGMVKVGD C TPWSDIECVH 180
 KESGLIIGVT VAAVLIVAV FVCKSLWK K VLPYLKIGS GGGGDPERVD RSSQRPGEAD 240
 NVLNEIVSIL QPTQVPEQEM EVQEPAEPTG VNMLSPGESE HLEPAEAE R SQRRRLVPA 300
 NEGDPETLR QCFDDFADLV PFDSWEPLMR KLGLMDNEIK VAKAEAAHR DTLYTMLIKW 360
 VNKTGRDASV HTLLDALETL GERLAKQKIE DHLLSSGKFM YLEGNADSAM S

Seq ID NO: 68 Nucleotide sequence:
 Nucleic Acid Accession #: FGENESH predicted ORF
 Coding sequence: 361- 2220 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 GGCACCATCT GCTCCCTGCC CTGCCAGAG GGCTTTCACG GACCCAATG CTCCAGGAA 60
 TGTCGCTGCC ACAACGGCGG CCTCTGTGAC CGATTCACTG GGCAGTGCCG CTGCGCTCCG 120
 GGTTACTACT GGGATCGGTG CCGGGAGGAG TGCCCGGTGG GCCGCTTTGG GCAGGACTGT 180
 GCTGAGACGT GCGACTGCGC CCCGGACGCC CGTTGCTTCC CGGCCAACGG CGCATGTCTG 240
 TGCGAACACG GCTTCACTGG GGACCGCTGC ACGGATCGCC TCTGCCCGCA CGGCTTCTAC 300
 GGTCTCAGCT GCCAGGCCCC CTGCACCTGC GACCGGGAGC ACAGCCTCAG CTGCCACCCG 360
 ATGAACGGGG AGTGCTCTG CCTGCCGGGC TGGGCGGGCC TCCACTGCAA CGAGAGCTGC 420
 CCGCAGGACA CGCATGGGCC AGGGTGCCAG GAGCACTGTC TCTGCCTGCA CGGTGGCGTC 480
 TGGCAGGCTA CCAGCGGCTT CTGTCACTGC GCGCCGGGTT ACACGGGCCC TCACTGTGCT 540
 AGTCTTTGTC CTCCTGACAC CTACGGTGTC AACTGTTCTG CACGCTGCTC ATGTGAAAAT 600
 GCCATCGCTT GCTCACCCTA CGACGGCGAG TGCGTCTGCA AGGAAGGTTG GCAGCGTGGT 660
 AACTGCTCTG TGCCCTGCCC ACCCGGAACC TGGGGCTTCA GTTGCAATGC CAGCTGCCAG 720
 TGTGCCCATG AGGCAGTCTG CAGCCCCCAA ACTGGAGCCT GTACCTGCAC CCCTGGGTGG 780

	CATGGGGCCC	ACTGCCAGCT	GCCCTGTCCG	AAGGGGCAGT	TTGGAGAAGG	TTGTGCCAGT	840
	CGCTGTGACT	GTGACCACTC	TGATGGCTGT	GACCCCTGTT	ATGGACGCTG	TCAGTGCCAG	900
	GCTGGCTGGA	TGGGTGCCCC	CTGCCACCTG	TCCTGCCCTG	AGGGCTTATG	GGGAGTCAAC	960
5	TGTAGCAACA	CCTGCACCTG	CAAGAATGGG	GGCACCTGTC	TCCCTGAGAA	TGGCAACTGC	1020
	GTGTGTGCAC	CCGATTCCG	GGGCCCTCT	TCCAGAGAT	CCTGTCAGCC	TGGCCGCTAT	1080
	GGCAAACGCT	GTGTGCCCTG	CAAGTGCCT	TAACCACTCT	TCTGCCACCC	CTCGAACGGG	1140
	ACCTGTACT	GCCTGGCTGG	CTGGACAGGC	CCCGACTGCT	CCCAGCGCTG	CCCTCTGGGG	1200
	ACATTTGGTG	CTAACTGCTC	CCAGCCATGC	CAGTGTGGTC	CTGGAGAAAA	GTGCCACCCA	1260
10	GAGACTGGGG	CCTGTGTATG	TCCCCCAGGG	CACAGTGGTG	CACCTTGCAG	GATTGGAATC	1320
	CAGGAGCCCT	TTACTGTGAT	GCCGACCACT	CCAGTAGCGT	ATAACTCGCT	GGGTGCAGTG	1380
	ATTGGCATTG	CAGTGTGGG	GTCCCTTGTG	GTAGCCCTGG	TGGCACTGTT	CATTGGCTAT	1440
	CGGCACTGGC	AAAAAGGCAA	GGAGCACCAC	CACCTGGCTG	TGGCTTACAG	CAGCGGGCGC	1500
	CTGGACGGCT	CCGAGTATGT	CATGCCAGAT	GTCCCTCCGA	GCTACAGTCA	CTACTACTCC	1560
	AACCCCAGCT	ACCACACCCT	GTCGCAGTGC	TCCCCAAACC	CCCCACCCCC	TAACAAGGTT	1620
15	CCAGGCCCGC	TCTTTGCCAG	CCTGCAGAAC	CCTGAGCGGC	CAGGTGGGGC	CCAAGGGCAT	1680
	GATAACCACA	CCACCCTGCC	TGCTGACTGG	AAGCACCGCC	GGGAGCCCCC	TCCAGGGCCT	1740
	CTGGACAGGG	GGAGCAGCCG	CCTGGACCGA	AGCTACAGCT	ATAGCTACAG	CAATGGCCCA	1800
	GGCCCATTTCT	ACAATAAAGG	GCTCATCTCT	GAAGAGGAGC	TCGGGGCCAG	TGTGGCTTCC	1860
	CTGAGCAGTG	AGAACCATA	TGCCACCATC	CGGGACCTGC	CCAGCTTGCC	AGGGGGCCCC	1920
20	CGGGAGAGCA	GCTACATGGA	GATGAAAGGC	CCTCCCTCAG	GATCTCCCCC	CAGGCAGCCT	1980
	CCTCAGTTCT	GGGACAGCCA	GAGGCGGCGG	CAACCCAGC	CACAGAGAGA	CAGTGGCACC	2040
	TACGAGCAGC	CCAGCCCCCT	GATCCATGAC	CGAGACTCTG	TGGGCTCCCA	GCCCCCTCTG	2100
	CCTCCGGGCG	TACCCCGCGG	CCACTATGAC	TCACCCAAGA	ACAGCCACAT	CCCTGGACAT	2160
25	TATGACTTGC	CTCCAGTACG	GCATCCCCCA	TCACCTCCAC	TTCGAGCCCA	GGACCGTTGA	

Seq ID NO: 69 Protein sequence:

Protein Accession #: FGENESH prediction

30	1	11	21	31	41	51	
	GTICSLPCPE	GFHGPNCSEQ	CRCHNGGLCD	RFTGQCRCAP	GYTGDRCREE	CPVGRFQGDC	60
	AETCDCAFDA	RCFPANGACL	CEHGFTGDRC	TDRLCPDGFY	GLSCQAPCTC	DREHSLSCHP	120
35	MNGECSCLP	WAGLHCNESC	PQDTHGPGCQ	EHCLCLHGGV	CQATSGLCQC	APGYTGPHCA	180
	SLCPPDITYGV	NCSARCSCE	AIACSPIDGE	CVCKEGWQRG	NCSVPCPPGT	WGFSCNASCQ	240
	CAHEAVCSQ	TGACTCTPGW	HGAHCQLPCP	KQFGECCAS	RCDCDHSDGC	DPVHGRCQCQ	300
	AGWMGARCHL	SCPEGLWGVN	CSNTCTCKNG	GTCLPENGNR	VCAFGFRGFS	CQRSCQPGRY	360
	GKRCVPCCKA	NHSFCHPSNG	TCYCLAGWTG	PDCSQRCLPG	TFGANCSQPC	QCGPGEKCHP	420
40	ETGACVCPGP	HSGAPCRIGI	QEPFTVMPTT	PVAYNSLGAV	IGIAVLGSLV	VALVALFIGY	480
	RHWQKGKEHH	HLAVAYSSGR	LDGSEYVMPD	VPPSYSHYYS	NPSYHTLSQC	SPNPPPPNKV	540
	PGPLFASLQN	PERPGGAQGH	DNHTTLPADW	KHRREPPPGP	LDRGSSRLDR	SYSYSYNGP	600
	GPFFYNKGLIS	EEELGASVAS	LSSENPHYAT	RDLPSPGPGP	RESSYMEMKG	PSPGSPPRQP	660
	PQFWDSSQRR	QFQPPQDSGT	YEQPSPLIHD	RDSVGSQPPL	PPGLPPGHYD	SPKNSHIPGH	720
45	YDLPPVRHPP	SPPLRRQDR					

Seq ID NO: 70 Nucleotide sequence:

Nucleic Acid Accession #: NM_005458

Coding sequence: 1..2826 (underlined sequences correspond to start and stop codons)

50	1	11	21	31	41	51	
	<u>ATGGCTTCCC</u>	CGCGGAGGTC	CGGGCAGCCA	GGGCGGCCGC	CGCCGCCGCC	ACCGCCGCCC	60
	GCGCGCCTGC	TACTGCTACT	GCTGCTGCCG	CTGCTGTGTC	CTCTGGCGCC	CGGGGCCTGG	120
55	GGCTGGGCGC	GGGGCGCCCC	CCGGCCGCCG	CCCAGCAGCC	CGCCGCTCTC	CATCATGGGC	180
	CTCATGCCGC	TCACCAAGGA	GGTGGCCAAG	GGCAGCATCG	GGCGCGGTGT	GCTCCCGGCC	240
	GTGGAACTGG	CCATCGAGCA	GATCCGCAAC	GAGTCACTCC	TGCGCCCTTA	CTTCTCGAC	300
	CTGCGGCTCT	ATGACACGGA	GTGCGACAAC	GCAAAAGGGT	TGAAAGCCTT	CTACGATGCA	360
60	ATAAAATACG	GGCCGAACCA	CTTGATGGTG	TTTGGAGGCG	TCTGTCCATC	CGTCACATCC	420
	ATCATTGCAG	AGTCCCTCCA	AGGCTGGAAT	CTGGTGCAGC	TTTCTTTTGC	TGCAACCACG	480
	CCTGTTCTAG	CCGATAAGAA	AAAATACCCT	TATTTCTTTC	GGACCGTCCC	ATCAGACAAT	540
	GCGGTGAATC	CAGCCATTCT	GAAGTTGCTC	AAGCACTACC	AGTGGGAAGCG	CGTGGGCACG	600
	CTGACGCAAG	ACGTTACAGG	GTCTCTGAG	GTGCGGAATG	ACCTGACTGG	AGTTCTGTAT	660
65	GGCGAGGACA	TTGAGATTTC	AGACACCGAG	AGCTTCTCCA	ACGATCCCTG	TACCAAGTGC	720
	AAAAAGCTGA	AGGGGAATGA	TGTGCGGATC	ATCCTTGGCC	AGTTTGACCA	GAATATGGCA	780
	GCAAAAGTGT	TCTGTTGTGC	ATACGAGGAG	AACATGTATG	GTAGTAAATA	TCAGTGGATC	840
	ATTCCGGGCT	GGTACGAGCC	TTCTTGGTGG	GAGCAGGTGC	ACACGGAAGT	CAACTCATCC	900
70	CGTGCCTTCC	GGAAGAATCT	GCTTGTGCCC	ATGGAGGGCT	ACATTGGCGT	GGATTTCGAG	960
	CCCCTGAGCT	CCAAGCAGAT	CAAGACCATC	TCAGGAAAGA	CTCCACAGCA	GTATGAGAGA	1020
	GAGTACAACA	ACAAGCGGTC	AGGCGTGGGG	CCCAGCAAGT	TCCACGGGTA	CGCCTACGAT	1080
	GGCATCTGGG	TCATCGCCAA	GACACTGCAG	AGGGCCATGG	AGACACTGCA	TGCCAGCAGC	1140
	CGGCACCAGC	GGATCCAGGA	CTTCAACTAC	ACGGACCACA	CGTGGGCAG	GATCATCCTC	1200
	AATGCCATGA	ACGAGACCAA	CTTCTTCGGG	GTCACGGGTC	AAGTTGTATT	CCGGAATGGG	1260
75	GAGAGAATGG	GGACCATTA	ATTTACTCAA	TTTCAAGACA	GCAGGGAGGT	GAAGGTGGGA	1320
	GAGTACAACG	CTGTGGCCGA	CACACTGGAG	ATCATCAATG	ACACCATCAG	GTTCCAAGGA	1380
	TCCGAACCAC	CAAAGACAA	GACCATCATC	CTGGAGCAGC	TGCGGAAGAT	CTCCCTACCT	1440

	CTCTACAGCA	TCCTCTCTGC	CCTCACCATC	CTCGGGATGA	TCATGGCCAG	TGCTTTTCTC	1500
	TTCTTCAACA	TCAAGAACCG	GAATCAGAAG	CTCATAAAGA	TGTCGAGTCC	ATACATGAAC	1560
	AACCTTATCA	TCCTTGGAGG	GATGCTCTCC	TATGCTTCCA	TATTTCTCTT	TGGCCTTGAT	1620
5	GGATCCTTTG	TCTCTGAAAA	GACCTTTGAA	ACACTTTGCA	CCGTCAGGAC	CTGGATTCTC	1680
	ACCGTGGGCT	ACACGACCGC	TTTTGGGGCC	ATGTTTGCAA	AGACCTGGAG	AGTCCACGCC	1740
	ATCTTCAAAA	ATGTGAAAAT	GAAGAAGAAG	ATCATCAAGG	ACCAGAAACT	GCTTGTGATC	1800
	GTGGGGGGCA	TGCTGCTGAT	CGACCTGTGT	ATCCTGATCT	GCTGGCAGGC	TGTGGACCCC	1860
	CTGCGAAGGA	CAGTGGAGAA	GTACAGCATG	GAGCCGGACC	CAGCAGGACG	GGATATCTCC	1920
10	ATCCGCCCTC	TCCTGGAGCA	CTGTGAGAAC	ACCCATATGA	CCATCTGGCT	TGGCATCGTC	1980
	TATGCCCTACA	AGGGACTTCT	CATGTTGTTC	GGTTGTTTCT	TAGCTTGGGA	GACCCGCAAC	2040
	GTCAGCATCC	CCGCACTCAA	CGACAGCAAG	TACATCGGGA	TGAGTGTCTA	CAACGTGGGG	2100
	ATCATGTGCA	TCATCGGGGC	CGCTGTCTCC	TTCCTGACCC	GGGACCAGCC	CAATGTGCAG	2160
	TTCTGTCATG	TGGCTCTGGT	CATCATCTTC	TGCAGCACCA	TCACCCCTCG	CCTGGTATTC	2220
	GTGCCGAAGC	TCATCACCTC	GAGAACAAAC	CCAGATGCAG	CAACGCAGAA	CAGGCGATTG	2280
15	CAGTTCACTC	AGAATCAGAA	GAAAGAAGAT	TCTAAAACGT	CCACCTCGGT	CACCAAGTGTG	2340
	AACCAAGCCA	GCACATCCCG	CCTGGAGGGC	CTACAGTCAG	AAAACCATCG	CCTGCGAATG	2400
	AAGATCACAG	AGCTGGATAA	AGACTTGGAA	GAGGTACCCA	TGCAGCTGCA	GGACACACCA	2460
	GAAAAGACCA	CCTACATTAA	ACAGAACCAC	TACCAAGAGC	TCAATGACAT	CCTCAACCTG	2520
	GGAAACTTCA	CTGAGAGCAC	AGATGGAGGA	AAGGCCATTT	TAAAAAATCA	CCTCGATCAA	2580
20	AATCCCCAGC	TCAGATGGAA	CACAACAGAG	CCCTCTCGAA	CATGCAAGA	TCCTATAGAA	2640
	GATATAAACT	CTCCAGAACA	CATCCAGCGT	CGGCTGTCCC	TCCAGCTCCC	CATCCTCCAC	2700
	CACGCCTACC	TCCCATCCAT	CGGAGGCGTG	GACGCCAGCT	GTGTGAGCCC	CTGCGTCAGC	2760
	CCCACCGCCA	GCCCCCGCCA	CAGACATGTG	CCACCCTCCT	TCCGAGTCAT	GGTCTCGGGC	2820
25	CTGTAA						

Seq ID NO: 71 Protein sequence:
Protein Accession #: NP_005449

30	1	11	21	31	41	51	
	MASPRRSQGP	GRPPPPPPPP	ARLLLLLLLP	LLLPLAPGAW	GWARGAPRPP	PSSPPLSIMG	60
	LMPLTKEVAK	GSIGRGVLP	VELAIEQIRN	ESLLRPYFLD	LRLYDTECDN	AKGLKAFYDA	120
	IKYGNHLMV	FGGVCPSVTS	IIAESLQGW	LVQLSFAATT	PVLADKKKYP	YFFRTVPSDN	180
35	AVNPAILKLL	KHYQWKRVGT	LTQDVQRFS	VRNDLTGVLY	GEDIEISDTE	SFSNDPCTSV	240
	KKLKGNDVRI	ILGQFDQDMA	AKVFCCAYEE	NMYGSKYQWI	IPGWYEPSWW	EQVHTEANSS	300
	RCLRKNLLAA	MEGYIGVDPE	PLSSKQIKTI	SGKTPQQYER	EYNNKRSVG	PSKFHGYAYD	360
	GIWVIAKTLQ	RAMETLHASS	RHQRIQDFNY	TDHTLGRIL	NAMNETNFFG	VTGQVVRNG	420
	ERMGTIKFTQ	FQDSREVKVG	EYNAVADTLE	IINDTIRFQG	SEPPPKDKTII	LEQLRKISLP	480
40	LYSILSALTI	LGMIMASATF	FFNIKNRNQK	LIKMSPPYMN	NLIILGMLS	YASIFLFLGD	540
	GSFVSEKTFE	TLCTVRTWIL	TVGYTTAFGA	MFAKTWRVHA	IFKNVMMKKK	IKDQKLLVI	600
	VGGMLLIDLC	ILICWQAVDP	LRRTVEKYSM	EPDPAGRDIS	IRPLLEHCEN	THMTIWLIV	660
	YAYKGLLMF	CSFLAWETRN	VSI PALNDSK	YIGMSVYNVG	IMCIIGAAVS	FLTRDQPNVQ	720
	FCIVALVIIIF	CSTITLCLVF	VPKLITLRTN	PDAATQNRRF	QFTQNKKEB	SKTSTSVTSV	780
45	NQASTSRLEG	LQSENHRLRM	KITELDKDLE	EVTMQLQDTP	EKTTYIKQNH	YQELNDILNL	840
	GNFTESTDGG	KAILKNHLDQ	NPQLQWNTTE	PSRTCKDPIE	DINSPEHIQR	RLSLQLPILH	900
	HAYLPSIGGV	DASCVSPCVS	PTASPRHRHV	PPSFRVMVSG	L		

Seq ID NO: 72 Nucleotide sequence:
Nucleic Acid Accession #: NM_005795
Coding sequence: 522-1940 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
55	GCACGAGGGA	ACAACCTCTC	TCTCTSCAGC	AGAGAGTGTC	ACCTCCTGCT	TTAGGACCAT	60
	CAAGCTCTGC	TAACCTGAATC	TCATCCTAAT	TGCAGGATCA	CATTGCAAAG	CTTCACTCT	120
	TTCCCACCTT	GCTTGTGGGT	AAATCTCTTC	TGCGGAATCT	CAGAAAGTAA	AGTTCCATCC	180
	TGAGAATATT	TCACAAAGAA	TTTCCTTAAG	AGCTGGACTG	GGTCTTGACC	CCTGGAATTT	240
	AAGAAATTCT	TAAAGACAAT	GTCAAATATG	ATCCAAGAGA	AAATGTGATT	TGAGTCTGGA	300
60	GACAAATGTG	CATATCGTCT	AATAATAAAA	ACCCATACTA	GCCTATAGAA	AACAATATTT	360
	GAATAATAAA	AACCCATACT	AGCCTATAGA	AAACAATATT	TGAAAGATTG	CTACCACTAA	420
	AAAGAAAACT	ACTACAACCT	GACAAGACTG	CTGCAAACTT	CAATTGGTCA	CCACAACCTG	480
	ACAAGGTTGC	TATAAAACAA	GATTGCTACA	ACTTCTAGTT	TATGTTATAC	AGCATATTTT	540
	ATTTGGGCTT	AATGATGGAG	AAAAAGTGTA	CCCTGTATTT	TCTGGTTCTC	TTGCCTTTTT	600
65	TTATGATTCT	TGTTACAGCA	GAATTAGAAG	AGAGTCCCTG	GGACTCAATT	CAGTTGGGAG	660
	TTACTAGAAA	TAAAATCATG	ACAGCTCAAT	ATGAATGTTA	CCAAAAGATT	ATGCAAGACC	720
	CCATTCAACA	AGCAGAAAGC	GTTTACTGCA	ACAGAACCTG	GGATGGATGG	CTCTGCTGGA	780
	ACGATGTTGC	AGCAGGAAC	GAATCAATGC	AGCTCTGCCC	TGATTACTTT	CAGGACTTTG	840
	ATCCATCAGA	AAAAGTTTACA	AAGATCTGTG	ACCAAGATGG	AAACTGGTTT	AGACATCCAG	900
70	CAAGCAACAG	AACATGGACA	AATTATACCC	AGTGTAATGT	TAACACCCAC	GAGAAAGTGA	960
	AGACTGCACT	AAATTGTTTT	TACCTGACCA	TAATTGGACA	CGGATTGTCT	ATTGCATCAC	1020
	TGCTTATCTC	GCTTGGCATA	TTCTTTTATT	TCAAGAGCCT	AAGTTGCCAA	AGGATTACCT	1080
	TACACAAAAA	TCTGTTCTTC	TCATTTGTTT	GTAACCTCTG	TGTAACAATC	ATTACCTCA	1140
	CTGCAGTGGC	CAACAACCAG	GCCTTAGTAG	CCACAAATCC	TGTTAGTTGC	AAAGTGTCCC	1200
75	AGTTCAATTCA	TCTTACCTG	ATGGGCTGTA	ATTACTTTTG	GATGCTCTGT	GAAGGCATTT	1260
	ACCTACACAC	ACTCATTTGTG	GTGGCCGTGT	TTGCAGAGAA	GCAACATTTA	ATGTGGTATT	1320

ATTTTCTTGG CTGGGGATTG CCACTGATTC CTGCTTGTAT ACATGCCATT GCTAGAAGCT 1380
 TATATTACAA TGACAATTGC TGGATCAGTT CTGATACCCA TCTCCTCTAC ATTATCCATG 1440
 GCCCAATTG TGCTGCTTTA CTGGTGAATC TTTTCTTCTT GTTAAATATT GTACGCGTTC 1500
 5 TCATCACCAA GTTAAAAGTT ACACACCAAG CGGAATCCAA TCTGTACATG AAAGCTGTGA 1560
 GAGCTACTCT TATCTTGGTG CCATTGCTTG GCAITGAATT TGTGCTGATT CCATGGCGAC 1620
 CTGAAGGAAA GATTGCAGAG GAGGTATATG ACTACATCAT GCACATCCTT ATGCACTTCC 1680
 AGGGTCTTTT GGTCTCTACC ATTTCTGCT TCTTTAATGG AGAGGTTCAA GCAATTCTGA 1740
 GAAGAACTG GAATCAATAC AAAATCCAAT TTGGAAACAG CTTTCCAAAC TCAGAAAGCTC 1800
 10 TTCGTAGTGC GTCTTACACA GTGTCAACAA TCAGTGATGG TCCAGGTTAT AGTCATGACT 1860
 GTCTAGTGA ACCTTAAAT GGAAAAAGCA TCCATGATAT TGAAAAATGTT CTCTTAAAC 1920
 CAGAAAATTT ATATAATTGA AAATAGAAGG ATGGTTGTCT CACTGTTTGG TGCTTCTCCT 1980
 AACTCAAGGA CTTGGACCCA TGACTCTGTA GCCAGAAGAC TTCAATATTA AATGACTTTG 2040
 GGAATGTCA TAAAGAAGAG CCTTCACATG AAATTAGTAG TGTGTTGATA AGAGTGAAC 2100
 ATCCAGCTCT ATGTGGGAAA AAAGAAATCC TGGTTTGTA TGTTTGTGAG TAAATACTCC 2160
 15 CACTATGCTT GATGTGACGC TACTAACCTG ACATCACCAA GTGTGGAATT GGAGAAAAGC 2220
 ACAATCAACT TTTCTGAGCT GGTGAAGCC AGTCCAGCA CACCATGTAT GAATCAAAC 2280
 AAATGGCTGT AAACTAAAC ATACATGTTG GGCATGATTC TACCCTTATT CSCCCCAAGA 2340
 GACCTAGCTA AGGTCTATAA ACATGAAGGG AAAATTAGCT TTTAGTTTAA AAACCTTTTA 2400
 TCCCATCTTG ATTGGGGCAG TTGACTTTTT TTTTCCCA GAGTGCCGTA GTCCTTTTGG 2460
 20 TAACTACCCT CTCAAATGGA CAATACCGA AGTGAATTAT CCCTGCTGGC TTTCTTTTCT 2520
 CTATGAAAAG CAACTGAGTA CAATTGTTAT GATCTACTCA TTTGCTGACA CATCAGTTAT 2580
 ATCTTGTTGGC ATATCCATTG TGGAACTGG ATGAACAGGA TGTATAATAT GCAATCTTAC 2640
 TTCTATATCA TTAGGAAAAC ATCTTAGTTG ATGCTACAAA ACACCTTGTC AACCTCTTCC 2700
 25 TGTCTTACCA AACAGTGGGA GGAATTTCCT AGCTGTAAAT ATAAATTTTG TCCCTTCCAT 2760
 TTCTACTGTA TAAACAAATT AGCAATCAAT TTATATAAAG AAAATCAATG AAGGATTTCT 2820
 TATTTTCTTG GAATTTTGTG AAAAGAAATT GTGAAAAATG AGCTTGTAAT TACTCCATTA 2880
 TTTTATTTTA TAGTCTCAAA TCAAATACAT ACAACCTATG TAATTTTAA AGCAAATATA 2940
 TAATGCAACA ATGTGTGTAT GTTAATATCT GATACTGTAT CTGGGCTGAT TTTTAAATA 3000
 30 AAATAGAGTC TGAATGCTA TATTTGGTAA ATATTTTAA GACAACCAGA TGCCAGCATC 3060
 AGAAGTCTGT TTGAGAACTA AGAGAACAGA AACATCTATC ATAAGATATA TTTATTTAA 3120
 AAACACAAGG TCACTATTTT ACTGAATATA TTTGTTTTGA TAACCTATAC CTTAATAATA 3180
 GGTGTGTTTG ACATATTTCT TTTTTCATT TGACAATGAA CTCACATTCT AATCCAGAAA 3240
 TTTTAAACAA CTACTGTGAT AAATACCAAT CTGCTACTTT TATAGATTTT ACCCCATTAA 3300
 35 AATATTACTT TACTGACTTT TACTATGTGA AGATATATAG CTTTGGAAT GTCCCAGGCT 3360
 ATTCAAGAAA TATAAAAAC TAGAAGGATA CTATATATAC CATATACAAT GCTTTAATAT 3420
 TTTAATAGAG CTACTGTATA TAATACAAAT TAGGGAATA CTTGAATATA TCATTGAGAA 3480
 AAAATTATTG TCAGATCTTA CTGAATTATT GTCAGACTTT ATTAATAATA GATAGAAGAA 3540
 AACCTTGCTA ATGAATTAAA GTGAAATTTG CATGGGATTC AGTTTCTCTA ATGTTATTTT 3600
 40 CCGTGAAAT CTCTAAAGAA CAAGAATGAC TTCAATTAGT AAAAGTCAAT TTTGGGAAA 3660
 GTCATGGGTA TCTGTTTTT AAGTGTGTC ATCTGATTAA AATGGATGAA ACAAAATTACT 3720
 CATCATAAGT TGTTCCTTAA GCTGTCAATA TGTCAATAGA TGGTGAGTTC AGAAGCTTAT 3780
 TCAAATTGCT AAGACAAAT ATCTAAATTC GTAAGAATTA ACATATAGAA TGGTCTGGTC 3840
 AGTACATTTA TAATTTATCT ATGCATGAAA AAGTATTGTT TTGTTTGAAA CATGAATTTT 3900
 45 ATAGCAAGCT GCCATAGAAA GGA

Seq ID NO: 73 Protein sequence:
 Protein Accession #: NM_005795

50 1 11 21 31 41 51
 | | | | | |
 MLYSIFHLGL MMEKKCTLYF LVLLPFFMIL VTAELEESPE DSIQLGVTRN KIMTAQYECY 60
 QKIMQDPIQQ AEGVYCNRTW DGWLCWNDVA AGTESMQLCP DYFQDFDPSE KVTKICDQDG 120
 NWFRRHPASNR TWTNYTCNV NTHEKVTAL NLFYLTIIHG GLSIASLLIS LGIFFYFKSL 180
 55 SCQRITLHKH LFFSFVCNSV VTIIHLTAVA NNQALVATNP VSCKVSQFIH LYLMGCNVFW 240
 MLCEGIYLLHT LIVVAVFAEK QHLMWYFFLG WGFPLIPACI HAIARSLYYN DNCWISSDTH 300
 LLYIIHGPIC AALLVNLFFL LNIVRVLITK LKVTHQAESN LYMKAVRATL ILVPLLGIEF 360
 VLIPWRPEGK IAEVYDYIM HILMHFQGLL VSTIFCFFNG EVQAILRRNW NQYKIQFGNS 420
 60 FSNSEALRSA SYTVSTISDG PGYSHDCPSE HLNGKSIHDI ENVLLKPENL YN

Seq ID NO: 74 Nucleotide sequence:
 Nucleic Acid Accession #: NM_000450.1
 Coding sequence: 117..1949 (underlined sequences correspond to start and stop codons)

65 1 11 21 31 41 51
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 CCTGAGACAG AGGCAGCAGT GATACCCACC TGAGAGATCC TGTGTTTGAA CAACTGCTTC 60
 CCAAAACGGA AAGTATTTCA AGCCTAAACC TTTGGGTGAA AAGAACTCTT GAAGTCATGA 120
 70 TTGCTTCACA GTTCTCTCA GCTCTCACTT TGGTGCTTCT CATTAAAGAG AGTGGAGCCT 180
 GGTCTTACAA CACCTCCACG GAAGCTATGA CTTATGATGA GGCCAGTGCT TATTGTGAGC 240
 AAAGGTACAC ACACCTGGTT GCAATTCAAA ACAAGAAGA GATTGAGTAC CTAACTCCA 300
 TATTGAGCTA TTCACCAAGT TATTACTGGA TTGGAATCAG AAAAGTCAAC AATGTGTGGG 360
 TCTGGGTAGG AACCAGAAA CCTCTGACAG AAGAAGCCAA GAACTGGGCT CCAGGTGAAC 420
 CCAACAATAG GCAAAAAGAT GAGGACTGCG TGGAGATCTA CATCAAGAGA GAAAAAGATG 480
 75 TGGGCATGTG GAATGATGAG AGGTGCAGCA AGAAGAAGCT TGCCCTATGC TACACAGCTG 540
 CCTGTACCAA TACATCCTGC AGTGGCCACG GTGAATGTGT AGAGACCATC AATAATTACA 600

	CTTGCAAGTG	TGACCTGGC	TTCAGTGGAC	TCAAGTGTGA	GCAAATTGTG	AACTGTACAG	660
	CCCTGGAATC	CCCTGAGCAT	GGGAGCCTGG	TTTGCAAGTCA	CCCACTGGGA	AACTTCAGCT	720
	ACAATTCTTC	CTGCTCTATC	AGCTGTGATA	GGGTTTACCT	GCCAAGCAGC	ATGGAGACCA	780
5	TGCAGTGTAT	GTCCTCTGGA	GAATGGAGTG	CTCCTATTCC	AGCCTGCAAT	GTGGTTGAGT	840
	GTGATGCTGT	GACAAATCCA	GCCAATGGGT	TCGTGGAATG	TTTCCAAAAC	CCTGGAAGCT	900
	TCCCATTGAA	CACAACCTGT	ACATTGACT	GTGAAGAAGG	ATTTGAACCT	ATGGGAGCCC	960
	AGAGCCTTCA	GTGTACCTCA	TCTGGGAATG	GGGACAACGA	GAAGCCAACG	TGTAAAGCTG	1020
	TGACATGCAG	GGCCGTCCGC	CAGCCTCAGA	ATGGCTCTGT	GAGGTGCAGC	CATTCCTCTG	1080
	CTGGAGAGTT	CACCTTCAAA	TCATCCTGCA	ACTTCACCTG	TGAGGAAGGC	TTCATGTTGC	1140
10	AGGGACCAGC	CCAGGTTGAA	TGCACCACTC	AAGGGCAGTG	GACACAGCAA	ATCCCAAGTTT	1200
	GTGAAGCTTT	CCAGTGCACA	GCCTTGTCCA	ACCCCGAGCG	AGGCTACATG	AATTGTCTTC	1260
	CTAGTGCTTC	TGGCAGTTTC	CGTTATGGGT	CCAGCTGTGA	GTTCTCCTGT	GAGCAGGGTT	1320
	TTGTGTTGAA	GGGATCCAAA	AGGCTCCAAT	GTGGCCCCAC	AGGGGAGTGG	GACAACGAGA	1380
	AGCCCACTG	TGAAGCTGTG	AGATGCGATG	CTGTCCACCA	GCCCCGAAG	GGTTTGGTGA	1440
15	GGTGTGCTCA	TCCCCCTATT	GGAGAATTCA	CCTACAAGTC	CTCTGTGACC	TTCAGCTGTG	1500
	AGGAGGGATT	TGAATTATAT	GGATCAACTC	AACITGAGTG	CACATCTCAG	GGACAATGGA	1560
	CAGAAGAGGT	TCCTTCCCTG	CAAGTGGTAA	AATGTTCAAG	CCTGGCAGTT	CCGGGAAAGA	1620
	TCAACATGAG	CTGCAGTGGG	GAGCCCGTGT	TTGGCACTGT	GTGCAAGTTC	GCCTGTCTCTG	1680
	AAGGATGGAC	GCTCAATGGC	TCTGCAGCTC	GGACATGTGG	AGCCACAGGA	CAGTGGTCTG	1740
20	GCCTGCTACC	TACCTGTGAA	GCTCCCCTAG	AGTCCAACAT	TCCCTTGGTA	GCTGGACTTT	1800
	CTGCTGCTGG	ACTCTCCCTC	CTGACATTAG	CACCATTCTT	CCTCTGGCTT	CGGAAATGCT	1860
	TACGGAAGC	AAAGAAATTT	GTTCTCTGCCA	GCAGCTGCCA	AAGCCTTGAA	TCAGACGGAA	1920
	GCTACCAAAA	GCCTTCTTAC	ATCCTTTAAG	TTCAAAAGAA	TCAGAAACAG	GTGCATCTGG	1980
	GGAACTAGAG	GGATACACTG	AAGTTAACAG	AGACAGATAA	CTCTCTCGG	GTCTCTGGCC	2040
25	CTTCTTGCTT	ACTATGCCAG	ATGCCTTTAT	GGCTGAAACC	GCAACACCCA	TCACCACTTC	2100
	AATAGATCAA	AGTCCAGCAG	GCAAGGACGG	CCTTCAACTG	AAAAGACTCA	GTGTTCCCTT	2160
	TCCTACTCTC	AGGATCAAGA	AAGTGTGGC	TAATGAAGGG	AAAGGATATT	TTCTTCCAAG	2220
	CAAAAGTGAA	GAGACCAAGA	CTCTGAAATC	TCAGAATTCC	TTTTCTAACT	CTCCCTTGCT	2280
	CGCTGTAAAA	TCCTGGCACA	GAAACACAAT	ATTTTGTGGC	TTTCTTCTCT	TTGCCCTTCA	2340
30	CAGTGTTTTG	ACAGCTGATT	ACACAGTTGC	TGTCATAAGA	ATGAATAATA	ATTATCCAGA	2400
	GTTTAGAGGA	AAAAAATGAC	TAAAAATATT	ATAACTTAAA	AAAATGACAG	ATGTTGAATG	2460
	CCCACAGGCA	AATGCATGGA	GGGTTGTAA	TGGTGCAAT	CCTACTGAAT	GCTCTGTGCG	2520
	AGGGTTACTA	TGCACAATTT	AATCACTTTT	ATCCCTATGG	GATTCAAGTG	TTCTTAAAGA	2580
	ATCTTAAAG	ATTGTGATAT	TTTTACTTGC	ATTGAATATA	TTATAATCTT	CCATACTTCT	2640
35	TCATTCAATA	CAAGTGTGGT	AGGGACTTAA	AAAACCTGTA	AATGCTGTCA	ACTATGATAT	2700
	GGTAAAAGTT	ACTTATTCTA	GATTACCCCT	TCATTGTTTA	TTAACAAATT	ATGTTACATC	2760
	TGTTTTAAAT	TTATTTCAAA	AAGGGAAACT	ATTGTCCCTT	AGCAAGGCAT	GATGTTAACC	2820
	AGAATAAAGT	TCTGAGTGT	TTTACTACAG	TTGTTTCTTG	AAAACATGGT	AGAATTGGAG	2880
	AGTAAAAACT	GAATGGAAGG	TTTGTATATT	GTCAGATATT	TTTTTCAGAA	TATGTGGTTT	2940
40	CCACGATGAA	AAACTTCCAT	GAGGCCAAAC	GTTTTGAACT	AATAAAAGCA	TAAATGCAAA	3000
	CACACAAAGG	TATAATTTTA	TGAATGTCTT	TGTTGGAAAA	GAATACAGAA	AGATGGATGT	3060
	GCTTTGCATT	CCTACAAAGA	TGTTTGTGAG	ATGTGATATG	TAAACATAAT	TCTTGTATAT	3120
	TATGGAAGAT	TTTAAATTCA	CAATAGAAAC	TCACCATGTA	AAAGAGTCAT	CTGGTAGATT	3180
	TTTAAACGA	GAAGATGTCT	AATAGTTATT	CCCTATTTGT	TTTCTCTGT	ATGTTAGGGT	3240
45	GCTCTGGAAG	AGAGGAATGC	CTGTGTGAGC	AAGCATTTAT	GTTTATTTAT	AAGCAGATTT	3300
	AACAATTCCA	AAGGAATCTC	CAGTTTTCAG	TTGATCACTG	GCAATGAAAA	ATTCTCAGTC	3360
	AGTAATTGCC	AAAGCTGCTC	TAGCCTTGAG	GAGTGTGAGA	ATCAAACTC	TCCTACACTT	3420
	CCATTAACCT	AGCATGTGTT	GAAAAAATAA	GTTTCAGAGA	AGTTCTGGCT	GAACACTGGC	3480
50	AACGACAAAG	CCAACAGTCA	AAACAGAGAT	GTGATAAGGA	TCAGAACAGC	AGAGGTTCTT	3540
	TTAAAGGGGC	AGAAAAACTC	TGGGAAATAA	GAGAGAACAA	CTACTGTGAT	CAGGCTATGT	3600
	ATGGAATACA	GTGTTATTTT	CTTTGAAATT	GTTTAAAGTG	TGTAAATATT	TATGTAAACT	3660
	GCATTAGAAA	TTAGCTGTGT	GAAATACCAG	TGTGGTTTGT	GTTTGAGTTT	TATTGAGAAAT	3720
	TTTAAATTAT	AACCTAAAT	ATTTTATAAT	TTTTAAAGTA	TATATTATT	TAAGCTTATG	3780
55	TCAGACCTAT	TTGACATAAC	ACTATAAAGG	TTGACAATAA	ATGTGCTTAT	GTTT	

Seq ID NO: 75 Protein sequence:

Protein Accession #: NP_000441

60	1	11	21	31	41	51	
	MIASQFLSAL	TLVLLIKESG	AWSYNTSTEA	MTYDEASAYC	QQRVTHLVAI	QNKKEIEYLN	60
	SILSYSPSY	WIGIRKVNNV	WVWVGTKPL	TEEAKNWAPG	EPNNRQKDED	CVEIYIKREK	120
	DVGMWNDERC	SKKKLALCYT	AACTNTSCSG	HGECVETINN	YTCKCDPGFS	GLKCEQIVNC	180
	TALESPEHGS	LVCSHPLGNF	SYNSSCSISC	DRGYLPSSME	TMQCMSSGEW	SAPIPACNVV	240
65	ECDVNTNPAN	GFVECFNPG	SFPWNTTCTF	DCEEGFELMG	AQSLQCTSSG	NWDNEKPTCK	300
	AVTCRAVRQP	QNGSVRCSHS	PAGEFTFKSS	CNFTCEEFGM	LQGPAQVECT	TQQQWTQQIP	360
	VCEAFQCTAL	SNPERGYMNC	LPSASGSFRY	GSSCEFSCEQ	GFVLKGSKRL	QCQPTGEWDN	420
	EKPTCEAVRC	DAVHPQPKGL	VRCAHSPIGE	PTYKSSCAFS	CEEGFELYGS	TQLECTSQGQ	480
70	WTEEVPSQV	VKCSLAVPG	KINMSCSGEP	VFGTVCKFAC	PEGWTLNGSA	ARTCGATGHW	540
	SGLLPTCEAP	TESNIPLVAG	LSAAGLSLLT	LAPFLWLRLK	CLRKAKKFPV	ASSCQSLESD	600
	GSYQKPSYIL						

Seq ID NO: 76 Nucleotide sequence:

Nucleic Acid Accession #: NM_031439

Coding sequence: 69..1235 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
5	CCCCACCCGT	GCGAGGGCCA	GGTCCGCGCC	TGCCCCGCCA	GGCGAAGCGA	GGCGACCCGC	60
	GTGCGGCCAT	GGCTTCGCTG	CTGGGAGCCT	ACCCCTTGCC	CGAGGGTCTC	GAGTGCCCGG	120
	CCCTGGACGC	CGAGCTGTGC	GATGGACAAT	CGCCGCCGGC	CGTCCCCCGG	CCCCCGGGGG	180
	ACAAGGGCTC	CGAGAGCCGT	ATCCGGCGGC	CCATGAACGC	CTTCATGGTT	TGGGCCAAGG	240
10	ACGAGAGGAA	ACGGCTGGCA	GTGCAGAAC	CGGACCTGCA	CAACGCCGAG	CTCAGCAAGA	300
	TGCTGGGAAA	GTCGTGGAAG	GCGCTGACGC	TGTCCAGAA	GAGGCCGTAC	GTGGACGAGG	360
	CGGAGCGGCT	GCGCTGACAG	CACATGCAGG	ACTACCCCAA	CTACAAGTAC	CGGCCGCGCA	420
	GGAAGAAGCA	GGCCAAGCGG	CTGTGCAAGC	GCGTGGACCC	GGGCTTCTT	CTGAGCTCCC	480
	TCTCCCGGGA	CCAGAACGCC	CTGCCGGAGA	AGAGAAGCGG	CAGCCGGGGG	GCGCTGGGGG	540
15	AGAAGGAGGA	CAGGGGTGAG	TACTCCCCCG	GCACTGCCCT	CCCCAGCCTC	CGGGGCTGCT	600
	ACCACGAGGG	GCCGGCTGGT	GGTGGCGGCG	GCGGCACCCC	GAGCAGTGTG	GACACGTACC	660
	CGTACGGGCT	GCCACACCT	CCTGAAATGT	CTCCCCTGGA	CGTGTGGAG	CCGGAGCAGA	720
	CCTTCTTCTC	CTCCCCCTGC	CAGGAGGAGC	ATGGCCATCC	CCGCCGCATC	CCCCACCTGC	780
	CAGGGCACCC	GTACTCACCG	GAGTACGCC	CAAGCCTCT	CCACTGTAGC	CACCCCTGG	840
	GCTCCCTGGC	CCTTGCCAG	TCCCCCGCG	TCTCCATGAT	GTCCCCGTGA	CCCGGCTGTC	900
20	CCCCATCTCC	TGCTATTAC	TCCCCGGCCA	CCTACCACCC	ACTCCACTCC	AACCTCCAAG	960
	CCACCTGGG	CCAGCTTCC	CCGCTCCTG	AGCACCTGG	CTTCGACGCC	CTGGATCAAC	1020
	TGAGCCAGGT	GGAACCTCTG	GGGACATGG	ATCGCAATGA	ATTCGACCAG	TATTTGAACA	1080
	CTCCTGGCCA	CCAGACTCC	GCCACAGGG	CCATGGCCCT	CAGTGGGCAT	GTTCCGGTCT	1140
25	CCCAGGTGAC	ACCAACGGGT	CCACAGAGA	CCAGCCTCAT	CTCCGTCTTG	GCTGATGCCA	1200
	CGGCCACGTA	CTACAACAGC	TACAGTGTGT	CATAGAGCTG	GAGGCGCCCC	GTCCGGTCAG	1260
	CCCTCGCGCC	CTCTCTTCT	TGTGCCTTGA	GTGGCAGAGG	AGCCGTCCAG	CCACACCAGC	1320
	TTTCTCTCCA	CCGCTCAGGT	CAGGGAGGTC	TGAACTGCGG	CCCCAGAGCC	TTTGGCCTAA	1380
	GCTGGACTCT	CCTTATCCGA	GTGCCGCCCT	TATCCCTTTC	CCCACGTTCC	AGCCCCTGCA	1440
30	GCCCCATT	TAAGTATATT	CCTTCAAGTG	AGTTTTCCTC	CAGCCCTTGA	GAGTTGCTGT	1500
	CTCCAGTGG	AATGTTCACT	GACGTCTTTT	CTTGTTAGCC	ATCATCGAAA	CTAATGGGGG	1560
	GACAGACTTG	ATAGCCAAGG	TCCCTTCTGG	TCCAGTTTTT	TGATTTAGGG	TTCTCTCAAG	1620
	ATTAATAAAG	GAAGATGGG	AAATTTGACT	CATTAATGAG	CTCGCTAACC	TACGATCTGG	1680
	TGATAATTTT	GTGTGCACAG	CCCAAGGACC	ACGAGGCTTT	CTGCACTTTC	TGCACCCCTT	1740
35	TCCAAAGTGA	CCACAAAT	TCAAAGGGAC	TCATACAATT	TGAGAAAAAA	CAGTCAACCT	1800
	GATTTGAGAA	ATTAACCACT	ATGGCTAACT	ATATCACAGA	AAATGGGATT	GAGTTAAAC	1860
	TATTTTATTT	TAAATATACA	TTTTAAAGCA	GTTCTTTTTT	TTTGTTAATT	TGTTTATTAT	1920
	ACACACACTT	CAAGAGCCAC	CGCGCCACG	CTACATTTAT	AATTTTCATT	CTCTTTTACC	1980
	TATAAAATTC	AGTGATTAG	TTTCATTACA	TAGGAGAAAT	TATATTTCTA	AACATTTTAT	2040
40	GATGTTTAAA	AACAAAACAG	GCTGTTGTAA	AAAAAAAAAA	AAAAAAAAAA		

Seq ID NO: 77 Protein sequence:

Protein Accession #: NP_113627

	1	11	21	31	41	51	
45	MASLLGAYPW	PEGLECPALD	AELSDGQSP	AVPRPPGDKG	SESRIRPMN	AFMVWAKDER	60
	KRLAVQNPD	HNAELSKMLG	KSWKALTL	KRPYVDEAER	LRLQHMQDYP	NYKYRPRRK	120
50	QAKRLCKRVD	PGFLLSSLSR	DQNALPEKRS	GSRGALGEKE	DRGEYSPGTA	LPSLRGCYHE	180
	GPAGGGGGT	PSSVDTPYFG	LPTPPMSP	DVLEPEQTF	SSPCQEEHGH	PRRIPHLPGH	240
	PYSPEYAPSP	LHCSHPLGSL	ALGQSPGVSM	MSPVPGCPPS	PAYYSPATYH	PLHSNLQAH	300
	GQLSPPEHP	GFDALDQLSQ	VELLGDMDRN	EPDQYLNTPG	HPDSATGAMA	LSGHVPVSQV	360
55	TPTGTETSL	ISVLADATAT	YNSYSVS				

Seq ID NO: 78 Nucleotide sequence:

Nucleic Acid Accession #: XM_035787

Coding sequence: 329..949 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
60	TGCCCCGCCC	CGCTCCCCAG	CGCCCCGGAA	GTGATCTGTG	GCGGCTGCTG	CAGAGCCGCC	60
	AGGAGGAGGG	TGGATCTCCC	CAGAGCAAAG	CGTCGGAGTC	CTCCTCTCTC	TTCTCTCTCT	120
65	CCTCCTCCTC	CTCCTCCAGC	CGCCAGGCT	CCCCCGCCAC	CCGTCCAGACT	CCTCCTTCGA	180
	CCGCTCCCGG	CGCGGGGCT	TCCAGGCGAC	AAGGACCGAG	TACCCTCCGG	CCGGAGCCAC	240
	GCAAGCCGCG	CTTCCGGAGC	CCTCGGGGCG	GCGGACTGGC	TCGCGGTGCA	GATTCTTCTT	300
	AATCCTTTGG	TGAAAACCTGA	GACACAAAT	GGCTGCAAA	AAGCCCAAGG	GTCAGAATTC	360
70	TTTGGCTTTA	CACAAAGTCA	TCATGGTGGG	CAGTGGTGGC	GTGGGCAAGT	CAGCTCTGAC	420
	TCTACAGTTC	ATGTACGATG	AGTTTGTGGA	GGACTATGAG	CCTACCAAAG	CAGACAGCTA	480
	TCGGAAGAAG	GTAGTGCTAG	ATGGGGAGGA	AGTCCAGATC	GATATCTTAG	ATACAGCTGG	540
	GCAGGAGGAC	TACGCTGCAA	TTAGAGACAA	CTACTTCCGA	AGTGGGGAGG	GGTTCTCTCT	600
	TGTTTTCTCT	ATTACAGAAA	TGGAATCCTT	TGCAGTACA	GCTGACTTCA	GGGAGCAGAT	660
75	TTTAAGAGTA	AAAGAAGATG	AGAATGTTCC	ATTTCTACTG	GTTGGTAACA	AATCAGATT	720
	AGAAGATAAA	AGACAGGTTT	CTGTAGAAGA	GGCAAAAAAC	AGAGCTGAGC	AGTGAATGT	780
	TAACTACGTG	GAAACATCTG	CTAAAACACG	AGCTAATGTT	GACAAGGTAT	TTTTTGATT	840

5 AATGAGAGAA ATTCGAGCGA GAAAGATGGA AGACAGCAAA GAAAAGAATG GAAAAAGAA 900
 GAGGAAAAGT TTAGCCAAGA GAATCAGAGA AAGATGCTGC ATTTTATAAT CAAAGCCCAA 960
 ACTCCTTTCT TATCTTGACC ATACTAATA ATATAATTTA TAAGCATTGC CATGGAAGGC 1020
 TTAATTGACT GAAATTACTT TAACATTTTG GAAATTGTTG TATATCACTA AAAGCATGAA 1080
 TTGGAAGTGC AATGAAAGTC AAATTACTT TAAAAAGAAA TTAATATGGC TTCACCAAGA 1140
 AGCAAAGTTC AACTTATTTT ATAATTGCCT ACATTTATCA TGGTCCTGAA TGTAGCGTGT 1200
 AAGCTTGTGT TTCTTGGGCA GTCTTTCTTG AAATTGAAGA GGTGAAATGG GGGTGGGGAG 1260
 TGGGAGGAAA GGTGACTTCC TCTGGTGTG ATTATAAAGC TTAATTTTAA TATCATTTTA 1320
 10 AAATGTCTTG GTCTTCTACT GCCTTGAAAA ATGACAATTG TGAACATGAT AGTTAAACTA 1380
 CCACTTTTT TAACCATAT TATGCAAAAT TTAGAAGAAA AGTTATTGGC ATGGTTGTTG 1440
 CATATAGTTA AACTGAGAGT AATTCATCTG TGAATCTGCT TTAATTACCT GGTGAGTAAC 1500
 TTAGAAAAGT GGTGTAAGT TGTACATGGA ATTTTTTGAA TATGCCTTAA TTTAGAAACT 1560
 GAAAAATATC TGGTTATATC ATTCTGGGTG TGTCTTACT GACACCAGGG GTCCGCTGCC 1620
 CCATGTGTCC TGGTGAGAAA ATATATGCCT GGCACAGCTT TTGTATAGAA AATTCTTGAG 1680
 15 AAGTAACTGT CCGCTAGAAG TCTGTCCAAA TTTAAATGT GTCCCATATT CTGGTTCTTG 1740
 AAAATAAGAT TCCAGAGCTC TTTGATCGCT TTTAATAAAC TGCAAGTTCA TTTTAAATGA 1800
 AGGGCCAGCA TATATACCTG CAAGATAATT TTCAGCTGCA AGGATTGAGC ACCAGTTATG 1860
 TTTGAATGAA CCCTCCTTTT CTCTGAGATT CTGGTCCCTG GAAATCCCTT TCTGCTAGTG 1920
 GTGAGCATGT AAGTGTAAAG TTTTAACTC GGGAGCAGGG CATAGGAAGA AAATGTCAGT 1980
 20 AGTGCTAATG CATTTTGCAC TAGAACGCTT CCGGAAAAATA TTCATGCTTG CCATCTGTTT 2040
 ATTTCTAAAT TTATATTCAT AAAGTTACAG TTTGATACAG GAATTATTAG GAGTAATTCT 2100
 TTTCTGTTTC TGTTTATAAT GAAGAACACT GTAGCTACAT TTTGAGAAAT TAACATCAAG 2160
 CCATCAAACC TGGGTATAGT GCAGAAAACG TGGCACACAC TGACCACACA TTAGGCTGTG 2220
 TCACCATGTG GTGGGTGACC TGCTGGAAGA ATCTAGCAT GCTACTTGGG GACATAATTT 2280
 25 CAGTGGGAAA TATGCCACTG ACCGATTTTT TTTTTTCTT CTTTGCAGTG GGGCTAGGAC 2340
 AGTTGATTCA ACAAGTATT TTTTCTTTT TTCTCAGTCC TAATTTGAAC AGGTCAAAGA 2400
 TGTGTTTCAGG CATTCAGGTT AACAGGTGTG TATGTAAAGT TAAAAATAGG CTTTTTAGGA 2460
 ACTCACTCTT TAGATATTTA CATCCAGCTT CTCATGTTAA ATATTTGTCC TTAAGGGTT 2520
 TGAGATGTAC ATCTTTTCAT TCGTATTTCT CATAGGCTAT GCCATGTGCG GAATTCAGT 2580
 30 TACCAATGTA ACATGCGCCA GCGGGCCAG CAATCTCCAT GTGTACTTAT TACAGTCTTA 2640
 TTTAACCAGG GGTCTTAACC ACTAACATTG TGACTTTGCT TTGAGACCTT TCCTCTCCTG 2700
 GGTACTGAGG TGCTATGAAG CCAACTGACA AAGATGCATC ACGTGTCTTA GGCTGATGCC 2760
 ACTACCGAT TGTGTTATTT GCAATTTGAG CCATTTAAAG ACCAATAAAC TTCCTTTTTT

Seq ID NO: 79 Protein sequence:
 Protein Accession #: XP_035787

40 1 11 21 31 41 51
 | | | | | |
 MAANKPKQGN SLALHKVIMV GSGGVGKSAL TLQFMYDEFV EDYEPTKADS YRKVVLDGE 60
 EVQIDILDTA GQEDYAAIRD NYFRSGEGFL CVFSITEMES FAATADFREQ ILRVKEDENV 120
 PFLLVGNKSD LEDKRQVSVE EAKNRAEQWN VNYVETSAKT RANVDKVFFD LMREIRARKM 180
 EDSKEKNGKK KRKSLAKRIR ERCCIL

Seq ID NO: 80 Nucleotide sequence:
 Nucleic Acid Accession #: NM_003467
 Coding sequence: 89..1147 (underlined sequences correspond to start and stop codons)

50 1 11 21 31 41 51
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 GTTTGTTGGC TGCGGCAGCA GGTAGCAAAG TGACGCCGAG GGCCTGAGTG CTCCAGTAGC 60
 CACCGCATCT GGAGAACCAG CGGTTACCAT GGAGGGGATC AGTATATACA CTTCAGATAA 120
 CTACACCGAG GAAATGGGCT CAGGGGACTA TGACTCCATG AAGGAACCTT GTTCCGTGA 180
 55 AGAAAATGCT AATTTCATAA AAATCTTCTT GCCCACCATC TACTCCATCA TCTTCTTAAC 240
 TGGCATTGTG GGCAATGGAT TGGTCATCCT GGTCACTGGG TACCAGAAGA AACTGAGAAG 300
 CATGACGGAC AAGTACAGGC TGCACCTGTC AGTGGCCGAC CTCCTCTTTG TCATCAGCT 360
 TCCCTTCTGG GCAGTTGATG CCGTGGCAAA CTGGTACTTT GGGAACTTCC TATGCAAGGC 420
 AGTCCATGTC ATCTACACAG TCAACCTCTA CAGCAGTGTC CTCATCCTGG CCTTCATCAG 480
 60 TCTGGACCGC TACCTGGCCA TCGTCCACGC CACCAACAGT CAGAGGCCAA GGAAGCTGTT 540
 GGCTGAAAAG GTGGTCTATG TTGGCGTCTG GATCCCTGCC CTCCTGTCTG CTATTCCCGA 600
 CTTCATCTTT GCGAACGTCA GTGAGGCAGA TGACAGATAT ATCTGTGACC GCTTCTACCC 660
 CAATGACTTG TGGGTGGTTG TGTTCAGTT TCAGCACATC ATGGTTGGCC TTATCCTGCC 720
 TGGTATTGTC ATCCTGTCTT GCTATTGCAT TATCATCTCC AAGCTGTAC ACTCCAAGGG 780
 65 CCACCAGAAG GCGAAGGCC CCAAGACCAC AGTCATCTCT ATCCTGGCTT TCTTCGCCTG 840
 TTGGCTGCCT TACTACATTG GGATCAGCAT CGACTCCTTC ATCCTCCTGG AAATCATCAA 900
 GCAAGGGTGT GAGTTTGAGA ACACTGTGCA CAAGTGGATT TCCATCACCG AGGCCCTAGC 960
 TTTCTTCCAC TGTTGTCTGA ACCCATCCT CTATGCTTTC CTGAGGCCA AATTTAAAC 1020
 CTTGCCCCAG CACGCACTCA CCTCTGTGAG CAGAGGGTCC AGCCTCAAGA TCCTCTCCAA 1080
 70 AGGAAAGCGA GGTGGACATT CATCTGTTTC CACTGAGTCT GAGTCTTCAA GTTTTCACTC 1140
 CAGCTAACAC AGATGTAATA GACTTTTTTT TATACGATAA ATAACCTTTT TTTAAGTTAC 1200
 ACATTTTTCG GATATAAAG ACTGACCAAT ATTGTACAGT TTTTATTGCT TGTGAGTTT 1260
 TTGTCTGTG TTTCTTTAGT TTTTGTGAAG TTTAATTGAC TTTATTTAT AAATTTTTTT 1320
 TGTTCATAT TGATGTGTGT CTAGGCAGGA CCTGTGGCCA AGTCTTAGT TGCTGTATGT 1380
 75 CTCGTGGTAG GACTGTAGAA AAGGGAACG AACATTCCAG AGCGTGTAGT GAATCACGTA 1440
 AAGCTAGAAA TGATCCCCAG CTGTTTATGC ATAGATAATC TCTCAATCC CGTGAACGT 1500

TTTTCCTGTT CTTAAGACGT GATTTTGCTG TAGAAGATGG CACTTATAAC CAAAGCCCAA 1560
 AGTGGTATAG AAATGCTGGT TTTTCAGTTT TCAGGAGTGG GTTGATTTC A GCACCTACAG 1620
 TGTACAGTCT TGTATTAAGT TGTTAATAAA AGTACATGTT AAACCTACTT AGTGTATATG

5 Seq ID NO: 81 Protein sequence:
 Protein Accession #: NP_003458

10 1 11 21 31 41 51
 MEGISIIYTS NYTEEMGSGD YDSMKEPCFR EENANFNKIF LPTIYSIIIFL TGIVGNGLVI 60
 LVMGYQKKLR SMTDKYRLHL SVADLLFVIT LPFWAVDAVA NWYFGNFLCK AVHVIYTVNL 120
 YSSVLILAFI SLDRLAIVH ATNSQRPRKL LAEKVVYVGV WIPALLLTIP DFIFANVSEA 180
 15 DDRYICDRFY PNDLWVVFQ PQHIMVGLIL PGIVILSCYC IISKLKSHSK GHQKRKALKT 240
 TVILILAFPA CWLPYYIGIS IDSFILLEII KQGEFENTV HKWISITEAL AFFHCCLNPI 300
 LYAFLGAKFK TSAQHALTSV SRGSSSLKILS KGKRGHSSV STESESSSFH SS

20 Seq ID NO: 82 Nucleotide sequence:
 Nucleic Acid Accession #: NM_014959
 Coding sequence: 314..1609 (underlined sequences correspond to start and stop codons)

25 1 11 21 31 41 51
 CTGGTTCTCA ACTTCTTTTG AAATAATGTT CATAGAGAAG GAGGGCTGTC TGAGATTCTGA 60
 GGGAAACAAG CTCTCAGGAC TTCCGGTCGC CATGATGGCT GTGGGCGGTA AACCGGGTTA 120
 GTGCAAGCAT CTGGGCCATC TTCAATGGTA AAAAAGATAC AGTAAAGACA TAAATACCAC 180
 ATTTGACAAA TGGAAAAAAA GGAGTGTCGA GAAAAGAGTA GCAGCAGTGA GGAAGAGCTG 240
 30 CCGAGACGGG TATACAGGGA GCTACCCTGT GTTCTGAGA CCCTTTGTGA CATCTCACAT 300
 TTTTTCGAAG AAGATGATGA GACAGAGGCA GAGCCATTAT TGTTCCGTGC TGTTCTGAG 360
 TGTCAACTAT CTGGGGGGGA CATTCCCAGG AGACATTGTC TCAGAAGAGA ATCAAATAGT 420
 TTCTCTTAT GCTTCTAAAG TCTGTTTGA GATCGAAGAA GATTATAAAA ATCGTCAGTT 480
 TCTGGGGCCT GAAGGAAATG TGGATGTTGA GTTGATTGAT AAGAGCACAA ACAGATACAG 540
 35 CGTTTGGTTC CCCACTGCTG GCTGGTATCT GTGGTCAGCC ACAGGCCTCG GCTTCCTGGT 600
 AAGGGATGAG GTCACAGTGA CGATTGCGTT TGGTTCCTGG AGTCAGCACC TGGCCCTGGA 660
 CCTGCAGCAC CATGAACAGT GGCTGGTGGG CGGCCCTTGG TTTGATGTCA CTGCAGAGCC 720
 AGAGGAGGCT GTCGCCGAGT TCCACCTCCC CCACCTCATC TCCCTCCAAG GTGAGGTGGA 780
 CGTCTCCTGG TTCTCTGTTG CCCATTTTAA GAATGAAGGG ATGGTCCTGG AGCATCCAGC 840
 40 CCGGGTGGAG CCTTCTATG CTGTCTCTGA AAGCCCCAGC TTCTCTCTGA TGGGCATCCT 900
 GCTGCGGATC CCGCATGGGA CTCGCCTCTC CATCCCCATC ACTTCCAACA CATTGATCTA 960
 TTATCACCCC CACCCCGAAG ATATTAAAGT CCACCTGTAC CTTGTCCCCA GCGACGCCTT 1020
 GCTAACAAAG GCGATAGATG ATGAGGAAGA TCGCTTCCAT GGTGTGCGCC TGCAGACTTC 1080
 GCCCCAATG GAACCCCTGA ACTTTGGTTC CAGTTATATT GTGTCTAATT CTGCTAACCT 1140
 45 GAAAGTAATG CCCAAGGAGT TGAATTGTC CTACAGGAGC CCTGGAGAAA TTCAGCACTT 1200
 CTCAAAATTC TATGCTGGGC AGATGAAGGA ACCCATTCAG CTTGAGATTA CTGAAAAAAG 1260
 ACATGGGACT TTGGTGTGGG ATACTGAGGT GAAGCCAGTG GATCTCCAGC TTGTAGCTGC 1320
 ATCAGCCCTC CCTCTTTTCT CAGGTGCAGC CTTTGTGAAG GAGAACCACC GGCAACTCCA 1380
 AGCCAGGATG GGGGACCTGA AAGGGGTGCT CGATGATCTC CAGGACAATG AGGTTCTTAC 1440
 50 TGAGAATGAG AAGGAGCTGG TGGAGCAGGA AAAGACACGG CAGAGCAAGA ATGAGGCCTT 1500
 GCTGAGCATG GTGGAGAAGA AAGGGGACCT GGCCCTGGAC GTGCTCTTCA GAAGCATTAG 1560
 TGAAAGGGAC CCTTACCTCG TGTCTATCT TAGACAGCAG AATTGTGTAAG ATGAGTCAGT 1620
 TAGGTAGTCT GGAAGAGAGA ATCCAGCGTT CTCATTGGAA ATGGATAAAC AGAAATGTGA 1680
 TCATTGATTT CAGTGTTCAG GACAGAAGAA GACTGGGTAA CATCTATCAC ACAGGCTTTT 1740
 55 AGGACAGACT TGTAACCTGG CATGTACCTA TTGACTGTAT CCTCATGCAT TTTCTCTCAAG 1800
 AATGTCTGAA GAAGGTAGTA ATATTCTTTT TAAATTTTTT CCAACCATTG CTTGATATAT 1860
 CACTATTTTA TCCATTGACA TGATTCTTGA AGACCCAGGA TAAAGGACAT CCGGATAGGT 1920
 GTGTTTATGA AGGATGGGGC CTGGAAGGCA AACTTTTCTT GATTAATGTG AAAAAAAT 1980
 CCTATGGACA CTCCGTTTGA AGTATCACCT TCTCATAACT AAAAGCAGAA AAGCTAACAA 2040
 60 AAGCTTCTCA GCTGAGGACA CTCAAGGCAT ACATGATGAC AGTCTTTTTT TTTTGTGAT 2100
 GTTAGGACTT TAACACTTTA TCTATGGCTA CTGTTATTAG AACAATGTAA ATGATTTTGC 2160
 TGAAAGAGAG CACAAAAATG GGAGAAATG CAAACATGAG CAGAAAAATAT TTTCCCACTG 2220
 GTGTGTAGCC TGCTACAAGG AGTTGTTGGG TTAATGTTC ATGGTCAACT CCAAGGAATA 2280
 CTGAGATGAA ATGTGGTAA TCAACTCCAC AGAACCACCA AAAAGAAAAAT GAGGGTAATT 2340
 65 CAGCTTATTC TGAGACAGAC ATTCTTGCCA ATGTACCATA CAAAAATAA GCCAACTCTG 2400
 ACATTGGAT TCTACCATAG ACTCTGTCTT TTTGTAGCCA TTTGAGTGT CTTTGTGATTA 2460
 ATGTTTTCGT GGCACACATA TTTCCATCCT TTTATGTTTA ATCTGTTTAA AACAAGTTCC 2520
 TAGTAGACAC CATCTGGTTG AGTCAGTTT TTTTATGGTG TATTTTGAAC CCATTCTGAT 2580
 AGTCTCTTTT AACTGGAAGA TTTCAATTAC TTACGTTAAT GTAATTATTA ATATGTTAGG 2640
 70 ATTTATCCTC AGTCAGCCAG TTTGTTATGT CTTTCTTATT CTACTGTTAT CACATTGTGA 2700
 CCACTTAAAG TGAATCTAG GCACTTTATC ACCATTTAGA TCCTATTACC TTTTCTCATC 2760
 TAGGATATAG TTATCTTCTA CATAATCTTT CTGTATCTTA AAACCATCA ATAAATTATT 2820
 ATATATTTTC TACTTTTAAT CACTCAGAAG ATTTAAAAAA CTCATGAGAA GAGTAATCTG 2880
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 75 GTTCTGCAAA TTTCCACTTC TTCTGATAGA CGTTTTTTAG TTCTTTTAGA GTGGTTCTGA 3000
 TAGGTACAGA TTCTCTTATT TTTTGTCTCC TCTGAGGACA TCTTTTCTC ACCTTCATTC 3060
 TCAGTGATGT TTTTGTCTTG TAGTATTTTT AGTTGACATT GTTTTCTGTT CAGCAGTTTC 3120

5 CTTTGTAGCTT CCGTATTTCC TGATGAGAAA TCTGCAGTCA TTCAAATTGT TGTTCCTCTG 3180
 TATGTAGTGT GTCAATTTTTC TGTCAGATTT CAAGGTATTT ATCTTTAGTT TTTAGCCATT 3240
 TCATTATGTT GGGGATGAGT TTCCTTGTTT TATTCCTTTT GGAATTTGCT CCAATTCATA 3300
 AATTTGCAGT TTTATGTCTT TTACCAAACT TAGAGGTTT CAGCCTAATT TCTAAAAATA 3360
 CTTTATTATTA GCCTGATTTT CATCTTTATA GGAAATAGTT TAAGTGATGA CAAGTTCCAA 3420
 TAGCTTATAT GCCCAGAAGG CCTTCAAAAT AAGAATTTTG AAAGAATACA GAAAACAAAC 3480
 TTTTATATACC TTCTCATGTC TTCTACTGTA AAATTCATAT GCTTTGCTAC TCTAAACCTA 3540
 GTTTTGAATC AACAGTCTTG AGAATAGATG AAAATTTTGA TGAATAGTGG AATTCTTTTA 3600
 10 AATGGAAACC TCTTACATGT GATTTTCCTT GCCATCTAGA AATAAACCAT AGTATTTATG 3660
 TTGAATCAAT CAATATTATA TTTTGTTTT TCCTCCTCT TCTGAGACTC TTATTGTGGA 3720
 AATGTTAGAC TTTTATGTTT TCCTAAATGT CCCTGATATT CTACTTATT AGAACATCTT 3780
 TTCATTTTTC CCATTATCTT GATTGGGTAA TTTTAATTG TCTATTTTCA AATTGCTGG 3840
 AGTGTTCACC TGTTGTGTC TGTGTCGTC CACTGAGTGC ATTCACCACC TTTTAAATT 3900
 TGGTCACTGT ATGTATCAGT TCTAAAATTT CCATTTTGT CTCTATATT TAAATTTCTT 3960
 15 GGCTTATATT CTATTTTCTT GCAAATGTGT CAGCATTTGC TTGTTTGAGC TTTTTTTTTT 4020
 TCAAGACAGG GTCTCAACTC TGTTACCCAG GCTGGAGTGC AGTGGTGCGA TCTCAGCTCA 4080
 CTGCAACCTC TCCTCCTGG TTCAAGCGAT TATTGTGCCT CAGCCTCCTG AGTAGCTGGG 4140
 ATTACAGGCA TGCACCACCA CAGCCCAGCT AATTTTGTG ATTTTATAGT GAGACAGAGT 4200
 TTTGTCTATG TGGCCAGGCT GGTTTTGAAC TCCTGGCCTC AAGTGATCCA CCCACCTCAG 4260
 20 CCTCCCAAAG TGCTGGGATT ACAGGCCAT ACACCTGGCA CATTGAGTA TTTTTTTTTT 4320
 TTTTTTTTTT TTGAGATGGA GTCTCGCTCT GTCATCTAGG CTGGAGTGCA GTGGTGTGAT 4380
 CTCAGCTCAC TGCAGCTCT GTCTCCCGGG CTCAAGCGAT TCTCTGCTC CAGCCTCCTG 4440
 AGTAGCTAGG ACTACAGGTG CATGCCAACA CGCCCGGCTA ATTTTAAATA AAAATATTTT 4500
 TAGTAGAGAC AGGGTTTCAC CATTTTGGCC AGGATGGTCT CGATCTCCTG ACCTCATGAT 4560
 25 CCACCCGCTT CGGCCCTTCA AAGTGCTGGG ATTACAGGCA TGAGCCACCG TGCCTGGCCT 4620
 CATTTGAGTA TTTTATAAT GTCTCTTTTA AAGTCTTTGT CAGATAATC CACTGTACAT 4680
 GTTATTCAGT GTTTGGTCT CACTGAGTGC TCATTTGCCA GACAAGTGGA GATTTTGTGA 4740
 GCTCATCCTT GTATTCTCAG TAGTCCGAT ATGTACCCTC GACATGTGAA TGTATCTTA 4800
 TGAGACTCTG TTTTATTGTT ATCCAACAGA AGATGTTTAT TATTATTG GCTTCTGTG 4860
 30 AACTGAGGTC TTAATATCAG CTCATTTTAA AAGTCTTTGC AGTGGTATTC GGATCTATCC 4920
 TGTGTGTGCC TATGAGATTG GGTGCACTGT ATCCTGTTAG CTCATTCTC AGGGCGTTTG 4980
 AATGTGAATT AGGACCAGCG CAATGAATGC TCAAGTTGGG GTTGGGCGT AGAATTCATA 5040
 AAAGTCTTTA TATGCTCAG

Seq ID NO: 83 Protein sequence:

Protein Accession #: NP_055774

40 1 11 21 31 41 51
 | | | | | |
 MMRQRQSHYC SVLFLSVNYL GGTFPGDICS EENQIVSSYA SKVCFEIEED YKNRQFLGPE 60
 GNVDVELIDK STNRYSVWFP TAGWYLSAT GLGFLVRDEV TVTIAFGSWS QHLALDLQHH 120
 EQWLVGGLPLF DVTAEPPEAV AEIHLPHFIS LQGEVDVSWF LVAHFKNEGM VLEHPARVEP 180
 45 FYAVLESFSPF SLMGILLRIA SGTRLSIPIT SNTLIYYHPH PEDIKFHLYL VPSDALLTKA 240
 IDDEEDRFHG VRLQTSPPME PLNFGSSYIV SNSANLKVMP KELKLSYRSP GEIQHFSKFY 300
 AGQMKEPIQL EITEKRHGT LVDTEVKPVD LQLVAASAPP PFSGAAPVKE NHRQLQARMG 360
 DLKGVLDLQ DNEVLTENEK ELVEQEKTRO SKNEALLSMV EKKGDLALDV LFRSISERDP 420
 50 YLVSYLQQN L

Seq ID NO: 84 Nucleotide sequence:

Nucleic Acid Accession #: NM_007036

Coding sequence: 56-610 (underlined sequences correspond to start and stop codons)

55 1 11 21 31 41 51
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 CTTCCACCA GCAAAGACCA CGACTGGAGA GCCGAGCCGG AGGCAGCTGG GAAACATGAA 60
 GAGCGTCTTG CTGCTGACCA CGCTCCTCGT GCCTGCACAC CTGGTGGCCG CCTGGAGCAA 120
 60 TAATTATGCG GTGGAAGTCC CTCAACACTG TGACAGCAGT GAGTGCAAAA GCAGCCCGCG 180
 CTGCAAGAGG ACAGTGCTCG ACGACTGTGG CTGCTGCCGA GTGTGCGCTG CAGGGCGGGG 240
 AGAAACTTGC TACCGCACAG TCTCAGGCAT GGATGGCATG AAGTGTGGCC CGGGGCTGAG 300
 GTGTCAAGCT TCTAATGGGG AGGATCCTTT TGGTGAAGAG TTTGGTATCT GCAAAGACTG 360
 TCCCTACGGG ACCCTCGGGA TGGATTGCAG AGAGACCTGC AACTGCCAGT CAGGCATCTG 420
 65 TGACAGGGGG ACCGGAAAAAT GCCTGAAATT CCCCTTCTTC CAATATTTCAG TAACCAAGTC 480
 TTCCAACAGA TTTGTTTCTC TCACGAGCA TGACATGGCA TCTGGAGATG GCAATATTGT 540
 GAGAGAAGAA GTTGTGAAGG AGAATGCTGC CGGGTCTCCC GTAATGAGGA AATGGTTAAA 600
 TCCACGCTGA TCCCGCTGT GATTTCTGAG AGAAGGCTCT ATTTTCGTGA TTGTTCAACA 660
 70 CACAGCCAAC ATTTTAGGAA CTTTCTAGAT ATAGCATAAG TACATGTAAT TTTTGAAGAT 720
 CCAAATTGTG ATGCATGGTG GATCCAGAAA ACAAAAAGTA GGATACTTAC AATCCATAAC 780
 ATCCATATGA CTGAACACTT GTATGTGTTT GTTAAATATT CGAATGCATG TAGATTGTGT 840
 AAATGTGTGT TATAGTAAC ACTGAAGAAC TAAAAATGCA ATTTAGGTAA TCTTACATGG 900
 AGACAGGTCA ACCAAAGAGG GAGCTAGGCA AAGCTGAAGA CCGCAGTGAG TCAAATTAGT 960
 75 TCTTTGACTT TGATGTACAT TAATGTTGGG ATATGGAATG AAGACTTAAG AGCAGGAGAA 1020
 GATGGGGAGG GGGTGGGAGT GGGAAATAAA ATATTTAGCC CTCCTTGGT AGGTAGCTTC 1080
 TCTAGAATTT AATTGTGCTT TTTTTTTTTT TTTGGCTTTG GAAAAAGTCA AAATAAACA 1140

5 ACCAGAAAAC CCCTGAAGGA AGTAAGATGT TTGAAGCTTA TGGAAATTGG AGTAACAAAC 1200
 AGCTTTGAAC TGAGAGCAAT TTCAAAGGC TGCTGATGTA GTTCCCGGT TACCTGTATC 1260
 TGAAGGACGG TTCTGGGGCA TAGGAAACAC ATACACTTCC ATAAATAGCT TTAACGTATG 1320
 CCACCTCAGA GATAAATCTA AGAAGTATTT TACCCACTGG TGGTTTGTGT GTGTATGAAG 1380
 GTAAATATTT ATATATTTTT ATAAATAAAT GTGTTAGTGC AAGTCATCTT CCCTACCCAT 1440
 ATTTATCATC CTCTTGAGGA AAGAAATCTA GTATTATTTG TTGAAAATGG TTAGAATAAA 1500
 AACCTATGAC TCTATAAGGT TTTCAAACAT CTGAGGCATG ATAAATTTAT TATCCATAAT 1560
 TATAGGAGTC ACTCTGGATT TCAAAAAATG TCAAAAAATG AGCAACAGAG GGACCTTATT 1620
 10 TAAACATAAG TGCTGTGACT TCGGTGAATT TTCAATTAA GGTATGAAA TAAGTTTTTA 1680
 GGAGGTTTGT AAAAGAAGAA TCAATTTTCA GCAGAAAACA TGTCAACTTT AAAATATAGG 1740
 TGAATTAGG AGTATATTTG AAAGAATCTT AGCACAAACA GGACTGTTGT ACTAGATGTT 1800
 CTTAGGAAAT ATCTCAGAAG TATTTTATTT GAAGTGAAGA ACTTATTAA GAATTATTTT 1860
 AGTATTTACC TGTATTTTAT TCTTGAAGTT GGCCAACAGA GTTGTGAATG TGTGTGGAAG 1920
 15 GCCTTTGAAT GTAAAGCTGC ATAAGCTGTT AGGTTTGTGT TTAAGAGGAC ATGTTTATTA 1980
 TTGTTCAATA AAAAGAACA AGATAC

Seq ID NO: 85 Protein sequence:

Protein Accession #: NP_008967.1

20 1 11 21 31 41 51
 MKSVLLLTLL LVPahlVAAW SNnyAVDCPQ HCDsSECKSS PRCKRTVLDD CGCCRVCAAG 60
 25 RGETCYRTVS GMDGMKCGPG LRCQPSNGED PFGEFEGICK DCPYGTFGMD CRETCNCQSG 120
 ICDRTGKGL KFFFFQYSVT KSSNRFVSLT EHDMAsgDGN IVREEVVKEN AAGSPVMRKW 180
 LNPR

Seq ID NO: 86 Nucleotide sequence:

Nucleic Acid Accession #: D86983

Coding sequence: 52-4491 (underlined sequences correspond to start and stop codons)

35 1 11 21 31 41 51
 AGCCGGCCGT GGTGGCTCCG TCGTCCGAG CGTCCGTCCG CGCCGTCCGC CATGGCCAAG 60
 CGCTCCAGGG GCCCGGGGCG CCGTGCCTG TTGGCGCTCG TGCTGTTCTG CGCCTGGGGG 120
 ACGCTGGCCG TGGTGGCCCA GAAGCCGGGC GCAGGGGTGTC CGAGCCGCTG CCTGTGCTTC 180
 CGCACCACCG TCGCTGTCAT GCATCTGCTG CTGGAGGCCG TGCCCGCCGT GGCGCCGCAG 240
 40 ACCTCCATCC TAGATCTTCG CTTTAACAGA ATCAGAGAGA TCCAACCTGG GGCATTCAGG 300
 CGGCTGAGGA ACTTGAACAC ATTGCTTCTC AATAATAATC AGATCAAGAG GATACCTAGT 360
 GGAGCATTGT AAGACTTGGA AAATTTAAAA TATCTCTATC TGTACAAGAA TGAGATCCAG 420
 TCAATTGACA GGCAAGCATT TAAGGGACTT GCCTCTCTAG AGCAACTATA CCTGCACTTT 480
 AATCAGATAG AAACTTTGGA CCCAGATTCTG TTCCAGCATC TCCGAAGCT CGAGAGGCTA 540
 45 TTTTTCGATA ACAACCGGAT TACACATTTA GTTCCAGGGA CATTTAATCA CTTGGAATCT 600
 ATGAAGAGAT TGCGACTGGA CTCAAACACA CTTCACCTCG ACTGTGAAAT CCTGTGGTTG 660
 CGGGATTGTC TGAAAACCTA CGCGGAGTCG GGGAAACGCG AGGCAGCGGC CATCTGTGAA 720
 TATCCAGAGC GCATCCAGGG ACGCTCAGTG GCAACCATCA CCCGGGAAGA GCTGAAGTGT 780
 GAAAGGCCCC GGATCACCTC CGAGCCCAG GACGCAGATG TGACCTCGGG GAACACCGTG 840
 50 TACTTCACCT GCAGAGCCGA AGGCAACCCC AAGCCTGAGA TCATCTGGCT GCGAAACAAT 900
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 TTTGTAATCC AGCCACAGAA TACAGAGGTG CTGGTTGGGG AGAGCGTCAC GCTGGAGTGC 1140
 55 AGCGCCACAG GCCACCCCCC CCGCGGATC TCTGGCGGGC TTTACATACA GAACGTCGTA 1200
 CCAGTTGACC CGCGGGTGAA CATCAGCCT TCTGGCGGGC TTTACATACA GAACGTCGTA 1260
 CAGGGGGACA GCGGAGAGTA TCGTGTCTCT GCGACCAACA ACATTGACAG CGTCCATGCC 1320
 ACCGCTTTCA TCATCGTCCA GGCTCTTCTT CAGTTCACTG TGACGCCTCA GGACAGAGTC 1380
 GTATTGAGG GCCAGACCGT GGATTTCAG TGTGAAGCCA AGGGCAACCC GCCGCCCGTC 1440
 60 ATCGCCTGGA CCAAGGGAGG GAGCCAGCTC TCCGTGGACC GCGGCCACCT GGTCTGTCA 1500
 TCGGGAACAC TTAGAATCTC TGGTGTGCCC CTCCACGACC AGGGCCAGTA CGAATGCCAG 1560
 GCTGTCAACA TCATCGGCTC CCAGAAGGTC GTGGCCCAAC TGAATGTGCA GCCCAGAGTC 1620
 ACCCCAGTGT TTGCCAGCAT TCCCAGCGAC ACAACAGTGG AGGTGGGCGC CAATGTGCAG 1680
 CTCCTGTGCA GCTCCCAGGG CGAGCCCAG CCAGCCATCA CCTGGAACAA GGATGGGGTT 1740
 65 CAGGTGACAG AAGTGGAAA ATTTACATC AGCCTGAAG GATTCTTGAC CATCAATGAC 1800
 GTTGGCCCTG CAGACGCAGG TCGTATGAG TGTGTGGCCC GGAACACCAT TGGGTGCGCC 1860
 TCGGTGAGCA TGTGTCTCAG TGTGAACGTT CCTGACGTCA GTCGAAATGG AGATCCGTTT 1920
 GTAGCTACCT CCATCGTGGG AGCGATTGCG ACTGTTGACA GAGCTATAAA CTCAACCCGA 1980
 ACACATTTGT TTGACAGCCG TCCTCGTTCT CCAAATGATT TGCTGGCCTT GTTCCGTAT 2040
 70 CCGAGGGATC CTTACACAGT TGAACAGGCA CGGGCGGGAG AAATCTTTGA ACGGACATTG 2100
 CAGCTCATT AGGAGCATGT ACAGCATGGC TTGATGGTCG ACCTCAACGG AACAAGTTAC 2160
 CACTACACG ACCTGGTGTG TCCACAGTAC CTGAACCTCA TCGCAACCT GTCGGGCTGT 2220
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 75 GAGCGCCTGC TGAAATCCGT GTACGAGAAT GGCTTCAACA CCCCTCGGG CATCAACCCC 2400
 CACCGACTGT ACAACGGGCA CGCCCTTCCC ATGCCGCGCC TGGTGTCCAC CACCCTGATC 2460
 GGGACGGAGA CCGTCACACC CGACGAGCAG TTCACCCACA TGCTGATGCA GTGGGGCCAG 2520

	TTCCTGGACC	ACGACCTCGA	CTCCACGGTG	GTGGCCCTGA	GCCAGGCACG	CTTCTCCGAC	2580
	GGACAGCACT	GCAGCAACGT	GTGCAGCAAC	GACCCCCCCT	GCTTCTCTGT	CATGATCCCC	2640
	CCCAATGACT	CCCGGGCCAG	GAGCGGGGCC	CGCTGCATGT	TCTTCGTGCG	CTCCAGCCCT	2700
	GTGTGCGGCA	GCGGCATGAC	TTCGCTGCTC	ATGAACTCCG	TGTACCCGCG	GGAGCAGATC	2760
5	AACCAGCTCA	CCTCCTACAT	CGACGCATCC	AACGTGTACG	GGAGCAGCGA	GCATGAGGCC	2820
	CGCAGCATCC	GCAGCCTGGC	CAGCCACCGC	GGCCTGCTGC	GGCAGGGCAT	CGTGCAGCGG	2880
	TCCGGGAAGC	CGCTGCTCCC	CTTCGCCACC	GGGCCGCCCA	CGGAGTGCAT	GCGGGACGAG	2940
	AACGAGAGCC	CCATCCCCTG	CTTCCTGGCC	GGGGACCACC	GCGCCAACGA	GCAGCTGGGC	3000
	CTGACCAGCA	TGCACACGCT	GTGGTTCGCG	GAGCACAACC	GCATTGCCAC	GGAGCTGCTC	3060
10	AAGCTGAACC	CGCACTGGGA	CGGCGACACC	ATCTACTATG	AGACCAGGAA	GATCGTGGGT	3120
	GCGGAGATCC	AGCACATCAC	CTACCAGCAC	TGGCTCCCGA	AGATCCTGGG	GGAGGTGGGC	3180
	ATGAGGACGC	TGGGAGAGTA	CCACGGCTAC	GACCCCGGCA	TCAATGCTGG	CATCTTCAAC	3240
	GCCTTCGCCA	CCGCGGCCCT	CAGGTTTGGC	CACACGCTTG	TCAACCCACT	GCTTTACCGG	3300
	CTGGACGAGA	ACTTCCAGCC	CATTGCACAA	GATCACCTCC	CCCTTCACAA	AGCTTTCTTC	3360
15	TCTCCCTTCC	GGATTGTGAA	TGAGGGCGCG	ATCGATCCGC	TTCTCAGGGG	GCTGTTCCGG	3420
	GTGGCGGGGA	AAATGCGTGT	GCCCTCGCAG	CTGCTGAACA	CGGAGCTCAC	GGAGCGGCTG	3480
	TTCTCCATGG	CACACACGGT	GGCTCTGGAC	CTGGCGGCCA	TCAACATCCA	GCGGGGCCGG	3540
	GACCACGGGA	TCCCACCCTA	CCACGACTAC	AGGGTCTACT	GCAATCTATC	GGCGGCACAC	3600
	ACGTTCCGAG	ACCTGAAAAA	TGAGATTAAA	AACCTTGAGA	TCCGGGAGAA	ACTGAAAAGG	3660
20	TTGTATGGCT	CGACACTCAA	CATCGACCTG	TTTCCGGCGC	TCGTGGTGGA	GGACCTGGTG	3720
	CCTGGCAGCC	GGCTGGGCCC	CACCCTGATG	TGTCTTCTCA	GCACACAGTT	CAAGCGCCTG	3780
	CGAGATGGGG	ACAGGTTGTG	GTATGAGAAC	CCTGGGGTGT	TCTCCCCGGC	CCAGCTGACT	3840
	CAGATCAAGC	AGACGTCGCT	GGCCAGGATC	CTATGCGACA	ACGCGGACAA	CATCACCCGG	3900
	GTGCAGAGCG	ACGTGTTTCA	GGTGGCGGAG	TTCCTTCACG	GCTACGGCAG	CTGTGACGAG	3960
25	ATCCCAGGG	TGGACCTCCG	GGTGTGGCAG	GACTGCTGTG	AAGACTGTAG	GACCAGGGGG	4020
	CAGTTCAATG	CCTTTTCTTA	TCATTTCCGA	GGCAGACGGT	CTCTTGAGTT	CAGCTACCAG	4080
	GAGGACAAGC	CGACCAAGAA	AACAAGACCA	CGGAAAATAC	CCAGTGTGGG	GAGACAGGGG	4140
	GAACATCTCA	GCAACAGCAC	CTCAGCCTTC	AGCACACGCT	CAGATGCATC	TGGGACAAAT	4200
	GACTTCAGAG	AGTTTGTCT	GGAAATGCAG	AAGACCATCA	CAGACCTCAG	AACACAGATA	4260
30	AAGAACTTG	AATCACGGCT	CAGTACCACA	GAGTGCCTGG	ATGCCGGGGG	CGAATCTCAC	4320
	GCCAACAACA	CCAAGTGGAA	AAAAGATGCA	TGCACCATTT	GTGAATGCAA	AGACGGGCAG	4380
	GTCACCTGCT	TGCTGGAAGC	TTGCCCCCCT	GCCACCTGTG	CTGTCCCCGT	GAACATCCCA	4440
	GGGGCCTGCT	GTCCAGTCTG	CTTACAGAAG	AGGGCGGAGG	AAAAGCCCTA	GGCTCCTGGG	4500
	AGGCTCCTCA	GAGTTTGTCT	GCTGTGCCAT	CGTGAGATCG	GGTGGCCGAT	GGCAGGGAGC	4560
35	TGCGGACTGC	AGACCAGGAA	ACACCCAGAA	CTCGTGACAT	TTCATGACAA	CGTCCAGCTG	4620
	GTGCTGTAC	AGAAGGCAGT	GCAGGAGGCT	TCCAACCAGA	GCATCTGCGG	AGAAGGAGGC	4680
	ACAGCAGGTG	CCTGAAGGGA	AGCAGGCAGG	AGTCCTAGCT	TCACGTTAGA	CTTCTCAGGT	4740
	TTTTATTAA	TTCTTTTAAA	ATGAAAAATT	GGTGCTACTA	TTAAATTGCA	CAGTTGAATC	4800
	ATTTAGGGCG	CTAAATTGGT	TTTGCCCTCCC	AACACCATT	CTTTTAAAT	AAAGCAGGAT	4860
40	ACCTCTATAT	GTCAGCCTTG	CCTTGTTTCA	ATGCCAGGAG	CCGGCAGACC	TGTCACCCCG	4920
	AGGTGGGGTG	AGTCTCGGAG	GGCTCACCAG	AATCGGGGTT	CCATCACAAG		4980
	CTATGTTTAA	AAAGAAAAAT	GGTGTTTGGC	AAACGGAAAC	GAACCTTTGA	TGAGAGCGTT	5040
	CACAGGGACA	CTGTCTGGGG	GTGCAGTGCA	AGCCCCGGGC	CTCTTCCCTG	GGAACTCTG	5100
45	AACCTCTCT	TCCTCTGGGC	TCTCTGTAAC	ATTTACCCAC	ACGTCAGCAT	CTAATCCCAA	5160
	GACAAACATT	CCCGCTGCTC	GAAGCAGCTG	TATAGCCTGT	GACTCTCCGT	GTGTGAGCTC	5220
	CTTCCACACC	TGATTAGAAC	ATTCTATAAG	CACATTAGA	AACAGATTG	CTTTCAGCTG	5280
	TCACTTGAC	ACATACTGCC	TAGTTGTGAA	CCAAATGTGA	AAAAACCTCC	TTCATCCCAT	5340
	TGTGTATCTG	ATACCTGCCG	AGGGCCAAGG	GTGTGTGTTG	ACAACGCCGC	TCCCAGCCGG	5400
50	CCCTGGTTGC	GTCCACGTCC	TGAACAAGAG	CCGCTTCCGG	ATGGCTCTTC	CCAAGGGAGG	5460
	AGGAGCTCAA	GTGTGCGGAA	CTGTCTAACT	TCAGGTTGTG	TGAGTGCCTT		

Seq ID NO: 87 Protein sequence:

Protein Accession #: BAA13219

	1	11	21	31	41	51	
55	SRPWWLRASE	RPSAPSAMAK	RSRGPGRRC	LALVLFCAWG	TLAVVAQKPG	AGCPSRCLCF	60
	RTTVRCMHLL	LEAVPAVAPQ	TSILDRLFNR	IREIQPGAPR	RLRNLNTLLL	NNNQIKRIPS	120
	GAFFEDLENLK	YLYLYKNEIQ	SIDRQAFKGL	ASLEQLYLHF	NQIETLDPDS	FQHLPKLERL	180
	FLHNNRITHL	VPGTFNHLES	MKRLRLDSNT	LHCDCEILWL	ADLLKTYAES	GNAQAAAICE	240
60	YPRRIQGRSV	ATITPEELNC	ERPRITSEBP	DADVTSGNTV	YFTCRAGNPN	KPEIIWLRNN	300
	NELSMKTDNR	LNLLDDGTLM	IQNTQETDQG	IYQCMANKVA	GEVKTQEVTL	RYFGSPARPT	360
	FVIQPNQTEV	LVGESVTLEC	SATGHPPPRI	SWTRGDRTP	PVDPRVNITP	SGGLVIQNVV	420
	QGDSGEYACS	ATNNIDSVHA	TAFIIVQALP	QFTVTPQDRV	VIEGQTVDFQ	CEAKGNPPPV	480
	IATWTKGSQL	SVDRRLVLVS	SGTLRISGVA	LHDQGYECQ	AVNIIGSQKV	VAHLTVQPRV	540
65	TPVFASIPSD	TTEVVGANVQ	LPCSSQGEPE	PAITWNKDG	QVTESGKFHI	SPEGFLTIND	600
	VGPADAGRYE	CVARNTIGSA	SVSMVLSVNV	PDVSRNGDPF	VATSIVEAIA	TVDRAINSTR	660
	THLFDSRPRS	PNDLLALFRY	PRDPYTVEQA	RAGEIFERTL	QLIQEHVQHG	LMVDLNGTSY	720
	HYNDLVSPQY	LNLIANLSGC	TAHRRVNNCS	DMCFHQKYRT	HDGTCNNLQH	PMWGLSLTAF	780
	ERLLKSVYEN	GFNTPRGINP	HRLYNGHALP	MPRLVSTTLI	GTETVTPDEQ	FTHMLMQWQ	840
70	FLDHDLDSTV	VALSQARFSD	GQHCSNVCSN	DPFCSVMIP	PNSDRARSGA	RCMFFVRSSP	900
	VCGSGMTSL	MNSVYPREI	NQLTSYIDAS	NVYGSTHEHA	RSIRDASHR	GLLRQGIQV	960
	SGKPLLPFAT	GPTECMRDE	NESPIPCFLA	GDHRANEQLG	LTSMHTLWFR	EHNRITATELL	1020
	KLNPWDGDT	IYYETRKIVG	AEIQHITYQH	WLPKILGEVG	MRTLGEYHGY	DPGINAGIFN	1080
	AFATAAFRFG	HTLVNPLLYR	LDENFQPIAQ	DHLPLHKAFF	SPFRIVNEGG	IDPLLRGLFG	1140
75	VAGKMRVPSQ	LLNTELTREL	FMSMAHTVALD	LAANIQQRGR	DHGIPPYHDY	RVYCNLSAAH	1200
	TFEDLKNEIK	NPEIREKLKR	LYGSTLNIDL	FPALVVEDLV	PGSRLGPTLM	CLLSTQPKRL	1260

RDGDRLWYEN PGVFSPAQLT QIKQTSRLARI LCDNADNITR VQSDVFRVAE FPHGYGSCDE 1320
 IPRVDLRVWQ DCCEDCRTRG QFNAFSVYHR GRRSLEFSYQ EDKPTKKTRP RKIPSVGRQG 1380
 EHLSNSTSAF STRSDASGTN DPREFVLEMQ KTITDLRTQI KKLESRLSTT ECV DAGGESH 1440
 ANNTKWKKDA CTICECKDQ VTCFVEACPP ATCAVPVNIP GACCPVCLQK RAEKPP

Seq ID NO: 88 DNA sequence

Nucleic Acid Accession #: NM_004834.1

Coding sequence: 80-3577 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
15	AATTCGAGGA	TCCGGGTACC	ATGGCACAGA	GCGACAGAGA	CATTTATTGT	TATTTGTTTT	60
	TTGGTGGCAA	AAAGGGAAAA	TGGCGAACGA	CTCCCCTGCA	AAAAGTCTGG	TGGACATCGA	120
	CCTCTCTCTC	CTGCGGGATC	CTGCTGGGAT	TTTTGAGCTG	GTGGAAGTGG	TTGGAATGG	180
	CACCTATGGA	CAAGTCTATA	AGGGTCGACA	TGTTAAAACG	GGTCAGTTGG	CAGCCATCAA	240
	AGTTATGGAT	GTCACGTAGG	ATGAAGAGGA	AGAAATCAAA	CTGGAGATAA	ATATGCTAAA	300
20	GAAATACTCT	CATCACAGAA	ACATTGCAAC	ATATTATGGT	GCTTTTCATCA	AAAAGAGCCC	360
	TCCAGGCAT	GATGACATC	TCTGGCTTGT	TATGGAGTTC	TGTGGGGCTG	GGTCCATTAC	420
	AGACCTTGTG	AAGAACACCA	AAGGGAACAC	ACTCAAAGAA	GACTGGATCG	CTTACATCTC	480
	CAGAGAAATC	CTGAGGGGAC	TGGCACATCT	TCACATTCAT	CATGTGATTC	ACCGGGATAT	540
	CAAGGGCCAG	AATGTGTGTC	TGACTGAGAA	TGCAGAGGTG	AAACTTGTGT	ACTTTGGTGT	600
25	GAGTGCTCAG	CTGGACAGGA	CTGTGGGGCG	GAGAAATACG	TTCATAGGCA	CTCCCTACTG	660
	GATGGCTCCT	GAGGTCATCG	CCTGTGATGA	GAACCCAGAT	GCCACCTATG	ATTACAGAAG	720
	TGATCTTTGG	TCTTGTGGCA	TTACAGCCAT	TGAGATGGCA	GAAGGTGCTC	CCCCTCTCTG	780
	TGACATGCGT	CCAATGAGAG	CACGTGTTCT	CATTCCCAGA	AACCTCCTC	CCCGGCTGAA	840
	GTCAAAAAAA	TGGTGAAGA	AGTTTCTTAG	TTTTATAGAA	GGGTGCCTGG	TGAAGAATTA	900
30	CATGCAGCGG	CCCTCTACAG	AGCAGCTTTT	GAAACATCCT	TTTATAAGGG	ATCAGCCAAA	960
	TGAAAGGCCA	GTTAGAATCC	AGCTTAAGGA	TCATATAGAT	CGTACCAGGA	AGAAGAGAGG	1020
	CGAGAAAGAT	GAAACTGAGT	ATGAGTACAG	TGGGAGTGAG	GAAGAAGAGG	AGGAAGTGCC	1080
	TGAACAGGAA	GGAGAGCCAA	GTTCCATTGT	GAACGTGCCT	GGTGAGTCTA	CTCTTCGCCG	1140
	AGATTTCCTG	AGACTGCAGC	AGGAGAACAA	GGAACGTTCC	GAGGCTCTTC	GGAGACAACA	1200
35	GTTACTACAG	GAGCAACAGC	TCCGGGAGCA	GGAAGAATAT	AAAAGGCCAA	TGCTGGCAGA	1260
	GAGACAGAA	CGGATTGAGC	AGCAGAAAGA	ACAGAGGCGA	CGGCTAGAAG	AGCAACAAAG	1320
	GAGAGAGCGG	GAGGCTAGAA	GGCAGCAGGA	ACGTGAACAG	CGAAGGAGAG	AACAAGAAGA	1380
	AAAGAGGCGT	CTAGAGGAGT	TGGAGAGAAG	GCGCAAGAGG	GAAGAGGAGA	GGAGACGGGC	1440
	AGAAGAAGAA	AAGAGGAGAG	TTGAAAGAGA	ACAGGAGTAT	ATCAGGCGAC	AGCTAGAAGA	1500
40	GGAGCAGCGG	CACCTGGAAG	TCCTTCAGCA	GCAGCTGCTC	CAGGAGCAGG	CCATGTTACT	1560
	GCATGACCAT	AGGAGGCCGC	ACCCGCAGCA	CTCGCAGCAG	CCGCCACCAC	CGCAGCAGGA	1620
	AAGGAGCAAG	CCAAGCTTCC	ATGCTCCCGA	GCCCAAAGCC	CACCTACGAGC	CTGCTGACCG	1680
	AGCGCGAGAG	GTTCCTGTGA	GAACAACATC	TCGCTCCCCT	GTTCTGTCCC	GTCGAGATTG	1740
	CCCCTGTCAG	GGCAGTGGGC	AGCAGAATAG	CCAGGCAGGA	CAGAGAAACT	CCACCAGTAT	1800
45	TGAGCCCAGG	CTTCTGTGGG	AGAGAGTGGG	GAAGCTGGTG	CCCAGACTTG	CGAGTGGCAG	1860
	CTCCTCAGGG	TCCAGCAACT	CAGGATCCCA	GCCCAGGTCT	CACCCTGGGT	CTCAGAGTGG	1920
	CTCCGGGGAA	CGCTTCAGAG	TGAGATCATC	ATCCAAGTCT	GAAGGCTCTC	CATCTCAGCG	1980
	CCTGGAAAAA	CGAGTGAAAA	AACCTGAAGA	TAAAAGGAA	GTTTTCAGAC	CCCTCAAGCC	2040
	TGCTGGCGAA	GTGGATCTGA	CCGCACTGGC	CAAAGAGCTT	CGAGCAGTGG	AAGATGTACG	2100
50	GCCACCTCAC	AAAGTAAACG	ACTACTCCTC	ATCCAGTGAG	GAGTCGGGGA	CGACGGATGA	2160
	GGAGGACGAC	GATGTGGAGC	AGGAAGGGGC	TGACGAGTCC	ACCTCAGGAC	CAGAGGACAC	2220
	CAGAGCAGCG	TATCTCTGTA	ATTTGAGCAA	TGGTGAACAG	GAATCTGTGA	AAACCATGAT	2280
	TGTCCATGAT	GATGTAGAAA	GTGAGCCGGC	CATGACCCCA	TCCAAGGAGG	GCACTCTAAT	2340
	CGTCCGCCAG	ACTCAGTCCG	CTAGTAGCAG	ACTCCAGAAA	CACAAATCTT	CCTCCTCCTT	2400
55	TACACCTTTT	ATAGACCCCA	GATTACTACA	GATTTCTCCA	TCTAGCGGAA	CAACAGTGAC	2460
	ATCTGTGGTG	GGATTTCCTT	GTGATGGGAT	GAGACCAGAA	GCCATAAGGC	AAGATCCTAC	2520
	CCGGAAAGGC	TCAGTGGTCA	ATGTGAATCC	TACCAACACT	AGGCCACAGA	GTGACACCCC	2580
	GGAGATTCTG	AAATACAAGA	AGAGGTTTAA	CTCTGAGATT	CTGTGTGCTG	CCTTATGGGG	2640
	AGTGAATTTG	CTAGTGGGTA	CAGAGAGTGG	CCTGATGCTG	CTGGACAGAA	GTGGCCAAGG	2700
60	GAAGGTCTAT	CCTCTTATCA	ACCGAAGACG	ATTTCAACAA	ATGGACGTAC	TTGAGGGCTT	2760
	GAATGTCTTG	GTGACAATAT	CTGGCAAAAA	GGATAAGTTA	CGTGTCTACT	ATTTGTCTCTG	2820
	GTTAAGAAAT	AAAATACTTC	ACAATGATCC	AGAAGTTGAG	AAGAAGCAGG	GATGGACAAC	2880
	CGTAGGGGAT	TTGGAAGGAT	GTGTACATTA	TAAAGTTGTA	AAATATGAAA	GAATCAAATT	2940
	TCTGTGTGAT	GCTTTGAAGA	GTTCTGTGGA	AGTCTATGCG	TGGGCACCAA	AGCCATATCA	3000
65	CAAAATTTATG	GCCTTTAAGT	CATTGAGAGA	ATTGGTACAT	AAGCCATTAT	TGGTGGATCT	3060
	CACGTGTGAG	GAAGGCCAGA	GGTTGAAAGT	GATCTATGGA	TCTGTGCTG	GATTCCATGC	3120
	TGTTGATGTG	GATTGAGGAT	CAGTCTATGA	CATTTATCTA	CCAACACATG	TAAGAAAGAA	3180
	CCCACACTCT	ATGATCCAGT	GTAGCATCAA	ACCCCATGCA	ATCATCATCC	TCCCCAATAC	3240
	AGATGGAAAT	GAGCTTCTGG	TGTGCTATGA	AGATGAGGGG	GTTTATGTAA	ACACATATGG	3300
70	AAGGATCACC	AAGGATGTAG	TTCTACAGTG	GGGAGAGATG	CCTACATCAG	TAGCATATAT	3360
	TCCATCCAAT	CAGACAATGG	GCTGGGGAGA	GAAGGCCATA	GAGATCCGAT	CTGTGGAAC	3420
	TGGTCACTTG	GATGGTGTGT	TCATGCACAA	AAGGGCTCAA	AGACTAAAAT	TCTTGTGTGA	3480
	ACGCAATGAC	AAGGTGTTCT	TTGCCCTCTGT	TCGGTCTGGT	GGCAGCAGTC	AGGTTTATTT	3540
	CATGACCTTA	GGCAGGACTT	CTCTCTGAG	CTGGTAGAAG	CAGTGTGATC	CAGGGATTAC	3600
	TGGCCTCCAG	AGTCTTCAAG	ATCCTGAGAA	CTTGGAATTC	CTTGTAAGTC	GAGCTCGGAG	3660
75	CTGCACCAG	GGCAACCAGG	ACAGCTGTGT	GTGCAGACCT	CATGTGTTGG	GTTCTCTCCC	3720
	CTCCTTCTCTG	TTCTCTTTAT	ATACCAGTTT	ATCCCCATTC	TTTTTTTTTT	TCTTACTCCA	3780

AAATAAATCA AGGCTGCAAT GCAGCTGGTG CTGTTTCAGAT TCCAAAAA AAAAAAACC 3840
ATGGTACCCG GATCCTCGAA TTCC

5 Seq ID No: 89 Protein sequence:
Protein Accession #: NP_004825.1

	1	11	21	31	41	51	
10							
	MANDSPAKSL	VDIDLSSLRD	PAGIFELVEV	VGNNGTYGQVY	KGRHVKTGQL	AAIKVMDVTE	60
	DEEEEIKLEI	NMLKKYSHHR	NIATYYGAFI	KKSPPGHDDQ	LWLVMFEFCGA	GSITDLVKNT	120
	KGNTLKEDWI	AYISREILRG	LAHLHIHHVI	HRDIKGQNVL	LTENAEVKLV	DFGVSAQLDR	180
	TVGRRNTFIG	TPYWMARPEVI	ACDENPDATY	DYRSDLWSCG	ITAIEMAEGA	PPLCDMHPMR	240
15	ALFLIPRNP	PRLKSKKWSK	KFFSFIEGCL	VKNYMQRPST	EQLLKHPFIR	DQPNRQVRI	300
	QLKDHIDRTR	KKRGEKDETE	YEYSGSEEEE	EEVPEQEGEP	SSIVNVPGES	TLRRDFLRLQ	360
	QENKERSEAL	RQQLLQEQQ	LREQEEYKRQ	LLAERQKRIE	QQKEQRRRLE	EQQRREREAR	420
	RQEREQRRR	EQEEKRRLEE	LERRRKEEEE	RRRAEBEKRR	VEREQEYIRR	QLEEEQRHLE	480
	VLQQLLQEQ	AMLLHDHRRP	HPQHSQQPPP	PQERSKPSF	HAPEPKAHYE	PADRAREVPV	540
20	RTTSRSPVLS	RRDSPLQSGS	QONSQAGQRN	STSIERLLW	ERVEKLVRP	SGSSSSGSSN	600
	SGSQPGSHPG	SQSGSGERFR	VRSSSKSEGS	PSQRLNNAVK	KPEDKKEVFR	PLKPAGEVDL	660
	TALAKELRAV	EDVRPPHKVT	DYSSSEESG	TTDEEDDDVE	QEGADESTSG	PEDTRAASSL	720
	RLNNGETESV	KTMIVHDDVE	SEPAMTPSKE	GTLIVRQTQS	ASSTLQKHKS	SSSFTPFIDP	780
	RLLSISPSSG	TTVTSVVGFS	CDGMRPEAIR	QDPTKGSV	NVNPTNTRPQ	SDTPEIRKYK	840
25	KRFNSEILCA	ALWGVNLLVG	TESGLMLLDR	SGQGVYPLI	NRRRFQQMDV	LEGLNVLVTI	900
	SGKKDKLRVY	YLSWLRNKIL	HNDPEVEKKQ	GWTTVGDLEG	CVHYKVVKYE	RIKFLVIALK	960
	SSVEYVAWAP	KPYHKFMAFK	SFGELVHKPL	LVDLTVEEGQ	RLKVIYGSCA	GFHAVDVDSG	1020
	SVYDIYLP	VRKNPHSMIQ	CSIKPHAI	LPNTDGMELL	VCYEDEGVYV	NTYGRITKDV	1080
30	VLQWGMPT	VAYIRSNQTM	GWGEKAIEIR	SVETGHL	DMGV	FMHKRAQLK	FLCERN
	FASVRS	GGSS	QVYFMT	LGRT	SLLSW		

Seq ID NO: 90 DNA sequence

Nucleic Acid Accession #: none found

35 Coding sequence: 2-71 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
40							
	<u>TT</u> ACTTCA	ATTCTTACA	CGGTATTTCA	AACAAACAGT	TTTGCTGAGA	GGAGCTTTTG	60
	TCTCTCCT <u>TA</u>	<u>AG</u> AAATGTT	TATAAAGCTG	AAAGGAAATC	AAACAGTAAT	CTTAAAAATG	120
	AAAACAAAAC	AACCCAAACAA	CCTAGATAAC	TACAGTGATC	AGGGAGCACA	GTTCAACTCC	180
	TTGTTATGTT	TTAGTCATAT	GGCCTACTCA	AACAGCTAAA	TAACAACACC	AGTGGCAGAT	240
	AAAAATCACC	ATTATCTTT	CAGCTATTAA	TCTTTTGAAT	GAATAAACTG	TGACAAACAA	300
45	ATTAACATTT	TTGAACATGA	AAGGCAACTT	CTGCACAATC	CTGTATCCAA	GCAAACCTTA	360
	AATTATCCAC	TTAATTATTA	CTTAATCTTA	AAAAAAATTA	GAACCCAGAA	CTTTTCAATG	420
	AAGCATTTGA	AAGTTGAAGT	GGAATTTAGG	AAAGCCATAA	AAATATAAAT	ACTGTTATCA	480
	CAGCACCAGC	AAGCCATAAT	CTTTATACCT	ATCAGTTCTA	TTTCTATTAA	CAGTAAAAAC	540
	ATTAAGCAAG	ATATAAGACT	ACCTGCCCAA	GAATTCAGTC	TTTTTTCATT	TTTGTTTTTC	600
50	TCAGTTCTGA	GGATGTTAAT	CGTCAAATTT	TCTTTGGACT	GCATTCTCTA	CTACTTTTTC	660
	CACAATGGTC	TCACGTTCTC	ACATTTGTTC	TCGCGAATAA	ATTGATAAAA	GGTGTTAAGT	720
	TCTGTGAATG	TCTTTTAAAT	TATGGGCATA	ATTGTGCTTG	ACTGGATAAA	AACTTAAGTC	780
	CACCCTTATG	TTTATAATAA	TTTCTTGAGA	ACAGCAAAC	GCATTTACCA	TCGTAAAACA	840
	ACATCTGACT	TACGGGAGCT	GCAGGGAAGT	GGTGAGACAG	TTCGAACGGC	TCCTCAGAAA	900
55	TCCAGTGACC	CAATTTCTAAA	GACCATAGCA	CCTGCAAGTG	ACACAACAAG	CAGATTTATT	960
	ATACATTTAT	TAGCCTTAGC	AGGCAATAAA	CCAAGAATCA	CTTTGAAGAC	ACAGCAAAAA	1020
	GTGATACACT	CCGCAGATCT	GAAATAGATG	TGTTCTCAGA	CAACAAAGTC	CCTTCAGAAT	1080
	CTTCATGTTG	CATAAATGTT	ATGAATATTA	ATAAAAGTT	GATTGAGA		

Seq ID No: 91 Protein sequence:

Protein Accession #: none found

	1	11	21	31	41	51
65						
	YTSIPYTVFQ	TNSFAERSFC	LSL			

Seq ID NO: 92 DNA sequence

Nucleic Acid Accession #: NM_003706.1

Coding sequence: 310-1935 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
75							
	CACGAGGCAG	GGGCCATTTT	ACCTCCAGGT	TGGCCCTGCT	CAGGACCAGG	AGGAAACACC	60

TCCAGCCCCG GACCTCCTCC CACAGGGGGA AAAGGAAAGC AGGAGGACCA CAGAAGCTTT 120
 GGCACCCGAG ATCCCCGAG TCTTCACCCG CGGAGATTCC GGCTGAAGGA GCTGTCCAGC 180
 GACTACACCG CTAAGCGCAG GGAGCCCCAAG CCTCCGCACC GGATTCCGGA GCACAAGCTC 240
 CACCGCGCAT GCGCACACGC CCCAGACCCA GGCTCAGGAG GACTGAGAAT TTTCTGACCG 300
 5 CAGTGCACCA TGGGAAGCTC TGAAGTTTCC ATAATTCTCT GGTCTCAGAA AGAAGAAAAG 360
 GCGGCCGTGG AGAGACGAAG ACTTCATGTG CTGAAAGCTC TGAAGAAGCT AAGGATTGAG 420
 GCTGATGAGG CCCCAGTTGT TGCTGTGCTG GGCTCAGGCG GAGGACTGCG GGCTCACATT 480
 GCCTGCCTTG GGGTCCTGAG TGAGATGAAA GAACAGGGCC TGTGGATGC CGTCACGTAC 540
 10 CTCGCAGGGG TCTCTGGATC CACTTGGGCA ATATCTTCTC TCTACACCAA TGATGGTGAC 600
 ATGGAAGCTC TCGAGGCTGA CCTGAAACAT CGATTTACCC GACAGGAGTG GGACTTGGCT 660
 AAGAGCCTAC AGAAAACCAT CCAAGCAGCG AGGTCTGAGA ATTACTCTCT GACCGACTTC 720
 TGGGCCTACA TGGTTATCTC TAAGCAAACC AGAGAACTGC CGGAGTCTCA TTTGTCCAAT 780
 ATGAAGAAGC CCGTGAAGA AGGGACACTA CCTACCCAA TATTTGCAGC CATTGACAA 840
 GACCTGCAAC CTCTCTGGCA GGAGGCAAGA GCACCAGAGA CCTGGTTCGA GTTCACCCCT 900
 15 CACCACGCTG GCTTCTCTGC ACTGGGGGCC TTTGTTTCCA TAACCCACTT CGGAAGCAAA 960
 TTCAAGAAGG GAAGACTGGT CAGAACTCAC CCTGAGAGAG ACCTGACTTT CCTGAGAGGT 1020
 TTATGGGGAA GTGCTCTTGG TAACACTGAA GTCATTAGGG AATACATTTT TGACCAGTTA 1080
 AGGAATCTGA CCCTGAAAGG TTTATGGAGA AGGGCTGTTG CTAATGTCAA AAGCATTGGA 1140
 20 CACCTTATTT TTGCCCGATT ACTGAGCTG CAAGAAAGT CACAAGGGGA ACATCCTCCC 1200
 CCAGAAGATG AAGCGGTGA GCCTGAACAC ACCTGGCTGA CTGAGATGCT CGAGAATTGG 1260
 ACCAGGACCT CCCTGGAAAA GCAGGAGCAG CCCCATGAGG ACCCCGAAAG GAAAGGCTCA 1320
 CTCAGTAAT TGATGGATT TGTGAAGAAA ACAGGCATTT GCGCTTCAAA GTGGGAATGG 1380
 GGGACCACT ACACCTTCCT GTACAAACAC GGTGGCATCC GGGACAAGAT AATGAGCAGC 1440
 CGGAAGCACC TCCACCTGGT GGATGCTGGT TTAGCCATCA ACACCTCCCT CCCACTCGTG 1500
 25 CTGCCCCCGA CGCGGGAGGT TCACCTCATC CTCTCCTTCG ACTTCAGTGC CGGAGATCCT 1560
 TTCGAGACCA TCCGGGCTAC CACTGACTAC TGCCGCCGCC ACAAGATCCC CTTTCCCCAA 1620
 GTAGAAGAGG CTGAGCTGGA TTTGTGGTCC AAGGCCCCCG CCAGCTGCTA CATCTGAAA 1680
 GGAGAACTG GACCAGTGGT GATACATTTT CCCCTGTTCA ACATAGATGC CTGTGGAGGT 1740
 GATATTGAGG CATGGAGTGA CACATACGAC ACATTCAAGC TTGCTGACAC CTACACTCTA 1800
 30 GATGTGGTGG TGCTACTCTT GGCATTAGCC AAGAAGAATG TCAGGGAAAA CAAGAAGAAG 1860
 ATCCTTAGAG AGTTGATGAA CGTGGCCGGG CTCTACTACC CGAAGGATAG TGCCCGAAGT 1920
 TGCTGCTTGG CATAAGATGAG CCTCAGCTTC CAGGGCACTG TGGGCTGTT GGTCTACTAG 1980
 GGCCCTGAAG TCCACCTGGC CTTCCTGTTT TCACTCCCT TCAGCCACAC GCTTCATGGC 2040
 35 CTTGAGTTCA CCTTGGCTGT CTAACAGGG CCAATCACCA GTGACCAGCT AGACTGTGAT 2100
 TTTGATAGCG TCATTAGAAA GAAGGTGTCC AAGGAGCTGA AGGTGGTGAA ATTTGTCTCTG 2160
 CAGGTCCCTC GGGAGATCCT GGAGCTGGAG CATGAGTGTC TGACAATCAG AAGCATCATG 2220
 TCCAATGTCC AGATGGCCAG AATGAATGTG ATAGTTCAGA CCAATGCCTT CCACTGCTCC 2280
 TTTATGACTG CACTTCTAGC CAGTAGCTCT GCACAAGTTA GCTCTGTAGA AGTAAGAACT 2340
 40 TGGGCTTAAA TCATGGGCTA TCTCTCCACA GCCAAGTGGG GCTCTGAGAA TACAACAAGT 2400
 GCTCAATAAA TGCTTGCTGA TTAGTGATG AAAAAA AAAA AAAA AAAA 2460
 AAAAAA AAAAAA AAAAAA AAAAAA

Seq ID No: 93 Protein sequence:

Protein Accession #: NP_003697.1

1 11 21 31 41 51
 50 MGSSEVSIIP GLQKEEKA AV ERRRLHVLKA LKKLRIEADE APVVAVLVSG GGLRAHIACL 60
 GVLSEMEQEQ LLDVITYLAG VSGSTWAISS LYTNDGDMEA LEADLKHRFT RQEWDLAKSL 120
 QKTIQARSE NYSLLDFWAY MVISKQTREL PESHLSNMKK PVEEGTLPYP IFAAIDNDLQ 180
 PSWQEARPE TWFEFTPHHA GFSAAGAFVS ITHFGSKFKK GRLVRTHPER DLTFRLGLWG 240
 55 SALGNTEVIR EYIFDQLRNL TLKGLWRRAV ANAKSIGHLI FARLLRLQES SQGEHPPPED 300
 EGGEPEHTWL TEMLENWTRT SLEKQEQPHE DPERKGSLSN LMDFVKKTGI CASKWEWGTT 360
 HNFLYKHGGI RDKIMSSRKH LHLVDAGLAI NTPFPLVLP TREVHLILSF DFSAGDPFET 420
 IRATTDYCRH HKIPFPQVEE AELDLWSKAP ASCYILKGET GPVVIHFPLF NIDACGGDIE 480
 AWSDTYDTFK LADTYTLDDV VLLLALAKKN VRENKKILR ELMNVAGLYY PKDSARSCL 540
 A

Seq ID NO: 94 DNA sequence

Nucleic Acid Accession #: AK027351

Coding sequence: 1-642 (underlined sequences correspond to start and stop codons)

65 1 11 21 31 41 51
 AGGGAAAAAA ACTCCATTAA AAAGCCCAGC TTTCTCCCAT GTTAGATGTG ACTTGAAAA 60
 70 TGAGAAAAGAT TTAGCAAAAT TCCACCGTAT CTTTGGCCAG GCTAGAGACA GGGAGAGCAG 120
 AGTAAACCC TCAGGCTGCT GAAATTTCTA GGCTGTTAGG AAGCCCTCG AATTCTGTGA 180
 AATATGAGGT TCTTAACTC ACACCTGAGAG CGGAAAGGGG CAGACCCTTT TCATAACTCC 240
 CTCAGATGTG TGTTACCTTT CTTTACCAGC ATGGTAAGCA ACAGGACATA TCCCAGCCTC 300
 GGACATGTCT GTATGATCCA AGGTACCCAA AGTCAGACAG AGTAAACTCA AGCCTGGCAC 360
 75 TGGCTTTCTG CCGCTTCTAG TGCTTTGGAA AAAGCAGGAG AAGCAATAGC AGCAGGAGTC 420
 CCCAGCAGCT GGAGCCGCAA GAATGAAGT CAAAGAGGGA ACTGACAGCA GCTGCGGCTG 480
 CAGGGGCAAC GACGAGAAGA AGATGTTGAA GTGTGTGGTG GTGGGGGACG GTGCCGTGGG 540

	GAAAACCTGC	CTGCTGATGA	GCTACGCCAA	CGACGCCTTC	CCAGAGGAAT	ACGTGCCAC	600
	TGTGTTTGAC	CACATATGCAG	TTACTGTGAC	TGTGGGAGGC	AAGCAACACT	TGCTCGGACT	660
	GTATGACACC	GCGGGACAGG	AGGACTACAA	CCAGCTGAGG	CCACTCTCCT	ACCCCAACAC	720
	GGATGTGTTT	TTGATCTGCT	TCTCTGTCGT	AAACCTTGCC	TCTTACCACA	ATGTCCAGGA	780
5	GGAAATGGGTC	CCCGAGCTCA	AGGACTGCAT	GCCTCACGTG	CCTTATGTCC	TCATAGGGAC	840
	CCAGATTGAT	CTCCGTGATG	ACCCAAAAAC	CTTGGCCCGT	TTGCTGTATA	TGAAAGAGAA	900
	ACCTCTCACT	TACGAGCATG	GTGTGAAGCT	CGCAAAAGCG	ATCGGAGCAC	AGTGCTACTT	960
	GGAAATGTTCA	GCTCTGACTC	AGAAAGGTCT	CAAAGCGGTT	TTTGATGAAG	CAATCCTCAC	1020
	CATTTTCCAC	CCCAAGAAAA	AGAAGAAACG	CTGTTCTGAG	GGTCACAGCT	GCTGTTCAAT	1080
10	TATCTGAGGT	TGTCTGGGAC	CTGCCTCCAC	CCCATCCAGG	GATGAGAATG	GCAGCCAATC	1140
	TCTGTGGCCA	AGCTCCAGCC	AAAAAGGAGG	GCACGACCAG	AAAGGAACCT	CCTTGCACG	1200
	GAGGCTTGCC	CCATCACCCCT	CTGAGCCCTC	CCAACACAGC	ACACTAGTCA	GCCCACTGCC	1260
	ACGACCTCCC	TGCCAGCCAG	AAGCATCCGT	ACTGCACGCT	GTCTGAGAAT	GCTGGGCCCTG	1320
	GATTGCAGAC	AGTGCCGCTG	CTGATCGCAT	CAAAAAACAA	GTCAAAGGCC	ATCTCACATT	1380
15	TTACAAATCC	CCAGCTCATG	AACGTGAAGC	TGATAGGAAA	TCACCCAGG	GAACCCGAAA	1440
	AAGAACTTG	ATTCCTCTAT	TGCTGGCCCT	ACTTGATGTC	TTTTATAAAA	CTTGGGACTA	1500
	CAATACTAAC	CTTTTTTCT	GAATCTGCTG	TTCTACCCAT	GTGTCTCACA	TTCTATTGTGTA	1560
	TTATTTCAG	AAATGTACTA	ATTTCCAGTT	CACCTCAGGC	TTACTAATCC	ATACCAAATT	1620
	AGCCTAAAG	CAAGGCATTT	TATATTCAAT	TCTATTTTCA	GCATGTTTCT	ACCAAAGCTA	1680
20	TTAGAACCAA	CACGTACCTC	TGAATGCCCG	ATTATAAGAA	GACATGAGAA	GACTTTAAAA	1740
	GTTTTGGAAA	TTTACAGAGC	CATGATTTTT	GAACCTAATT	GAAAGAAAAC	CATCTGAATT	1800
	GTTGCAGGTC	CACATTTTGT	CCAAAGATAC	ACTCTATAGA	TGCTTAGTAG	TGGCCTGATT	1860
	TTTTTCCATG	TATTGCCACG	ACAACTAAA	AATGAAGTGT	GTTTAAGAA	GTAGTATTTT	1920
	TGTTTTTCAT	CCAAGTTGAT	TGGGGGAAGA	ATATGGCAGG	ATCCATCTTT	TACAGTATTT	1980
	TGTATTCACT	AAAGTGGACA	TTCTGCTCC	TCCCTTCCCC	CATTGCATGC	CCTCTTCCTC	2040
25	CCTTGATTTT	ACTTTCTCTC	ATGCCCGGAT	CCTTTTATTC	TCCCCAGTTA	TAACCCAGTT	2100
	ATAAAAGAAA	GATCTGAGCA	TAAAGATACG	TGTTTAAAAA	TAACTAAAAA	TAAAGGAAAAG	2160
	TGCCCTTAATT	TTTCTATTGT	CTTCAACTGA	AAGTGCTTCT	CAGCTCGCCC	CATGTAAGTT	2220
	CTCATTTCCAT	GTAATGACA	TTTTCCAGTT	ACAACTGGTA	CTGAGATTTT	GCCTCTCTCT	2280
30	TTCTTTACTC	ATCCTCCCAA	ATGTCTTTGT	GGGAGCCATA	TCAGTGGATA	CCAAGCTCTG	2340
	TATCCATTGT	TCCCCTGCC	TCCACAATGT	GTGACATAGA	ACAGGGACTT	TGGCCCTGGG	2400
	AAAGCAAAAG	CTCCCACTAA	GGAATCCTGT	GCCCAATGAT	GTAAACAAT	TCCAAACATC	2460
	CAGGAATTTT	TGTATCATAG	AGCGAATTAC	TTCTATCTT	TTCATTAGAG	GCTATGAGGA	2520
	CTTCTAATTA	GTCTTAGTTG	CTTATAAGTG	CCCTGGAATC	ACCCAGGTAG	GCACCTAATT	2580
35	TTTTTTTCAG	TTGCATGAGC	AAAGTGCTTC	TTAGTAGTGT	GAAATTACAA	CAACTTTAAG	2640
	ACTTTCCAGA	TTCAAGCTCC	CACGTGTTGA	AAAAGCCAGC	CTTTCTAATC	TCTTCTGCTA	2700
	CTGGAATAAG	CACCTAAGAA	TTGCGTGATA	GCCAGGCACC	GTGGCTCATG	CCTGTAATCC	2760
	CAACACTTAG	GGAGGCTGAG	GTGGGTGGGC	CGCTTGAGCT	CAGGAGTTCA	AGACCAGCCT	2820
	GGGTAATATA	GTGAGATCCT	GTGTCTCTAT	AAAAAAATTA	AAAATTAGTC	AGTTGTAGTG	2880
40	ACACATACCT	GATGTCCCAG	CTACTCAGGA	GGCTGAGGTG	GAAGGATCAC	TTGAGCCAG	2940
	AAGGTAAGGC	TGCAGTGAGC	TGTGACTGTG	CCACTACACT	CCAGCCTGAG	TGACAGAGAA	3000
	AGAACCTGTC	AAAAAACAAC	CTACATTTC	AGTACTATTT	CCCTTCTCTC	3060	
	CCATCTAATT	GCTAAAGATT	TTCTTTCATA	CGCACACACT	CCAGTGACTG	GAAAAACGGG	3120
	AGTTTTCACT	CAAAGCTTGA	CATTTAGAGA	AAACAAGGAC	TTTCTGCCTT	TATAAATGGA	3180
45	AATCAACTGT	GTATGAACCTA	TAACTCTGCA	GAGGTTATGA	ATTCTATCCTT	TACAAACAAT	3240
	AATGAACCTT	TAGTCTCTGA	ATAAATGAAA	TGTTATTAGG	CAGCTTTGTT	GCATGATTGC	3300
	ATAGTTATAT	CTTGCTAACG	GGCCACTCAT	TTCTCACTGA	TGTGGATGAA	AAAATGAGAG	3360
	CAGTATGTTT	CCAGGTGTGT	GCACTCAACA	GGCAAAATAGC	TCCCGAGGTC	ACCACTTCCC	3420
	TAATGGGCCA	CAGGAAGTAA	GTTGATCTTG	ATGGGGAGAT	CACGTCACCC	AGAACAGCA	3480
50	ACTGGATAGA	GACTGTGTGT	AGTGTCTGGG	TAGAGCACAG	GCTCCAGGG	GTCTTAAGAG	3540
	CTAATTACTG	AATAAAACAA	TCTAGAACAA	AGCAA			

Seq ID No: 95 Protein sequence:

Protein Accession #: CAC06611.1

55

	1	11	21	31	41	51	
	MNCKEGTDSS	CGCRGNDEKK	MLKCVVVDG	AVGKTCLLMS	YANDAFPEEY	VPTVFDHYAV	60
60	TVTVGGKQHL	LGLYDTAGQE	DYNQLRPLSY	PNTDVFLICF	SVVNPASYHN	VQEEWVPELK	120
	DCMPHVPYVL	IGTQIDLRDD	PKTLARLLYM	KEKPLTYEHG	VKLAKAIGAQ	CYLECSALTQ	180
	KGLKAVPDEA	ILTIFHPKKK	KKRCSEGHSC	CSII			

65

Seq ID NO: 96 DNA sequence

Nucleic Acid Accession #: NM_003654.1

Coding sequence: 367-1602 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
	GGGGAGGGCG	CGGGAGGGCG	AGGATGCCGC	CGCGGCTGCT	GCCGCCGCCG	CCACCCGCGG	60
	GTCCCCGGCG	ACCCTACTCC	AGACCCGAGG	ATGGAGCCGG	CGCTGGGCGC	TGCAGCTGCT	120
	CCCGGCGCGT	CCCCGACCAG	GTAGCTGGTG	TCACTTCGGT	GTGGTTGGAA	GAAGACTTTC	180
	TCCCCAGCTG	CATTCCCGGA	GGCGCCCTTT	CGACCTGGAG	GCCGGGCTCTG	CTGGCCACAG	240
75	GGCTGCCGCA	CTGGCTGGGA	CTGCCAGCTG	GGCCTGGAGA	CGCTGGTGGC	TGTGGACTCC	300
	CCAGCTTGGA	GCAGTCCCTC	TTTGACCTCA	CCCCTTGGAG	AAGCAGCCCC	ATGAAGGTGC	360

	CCAGCCATGC	AATGTTCTCTG	GAAGGCCGTC	CTCCTCTCTTG	CCCTGGCCTC	CATTGCCATC	420
	CAGTACACGG	CCATCCGCAC	CTTCACCGCC	AAGTCCCTTC	ACACCTGCCC	CGGGCTGGCA	480
	GAGGCCGGGC	TGGCCGAGCG	ACTGTGCGAG	GAGAGCCCCA	CCTTCGCCTA	CAACCTCTCC	540
5	CGCAAGACCC	ACATCCTCAT	CCTGGCCACC	ACGCGCAGCG	GCTCCTCTCT	CGTGGGCCAG	600
	CTCTTCAACC	AGCACCTGGA	CGTCTTCTAC	CTGTTTGAGC	CCCTCTACCA	CGTCCAGAAC	660
	ACGCTCATCC	CCCCTTTTAC	CCAGGGCAAG	AGCCCGGCCG	ACCGCGGGGT	CATGCTAGGC	720
	GCCAGCCGCG	ACCTCCTGCG	GAGCCTCTAC	GACTGCGACC	TCTACTTCCT	GGAGAACTAC	780
	ATCAAGCCCG	CGCCGGTCAA	CCACACCACC	GACAGGATCT	TCCGCGCGCG	GGCCAGCCGG	840
10	GTCTCTGCT	CCCGGCCTGT	GTGCGACCCT	CCGGGGCCAG	CCGACCTGGT	CCTGGAGGAG	900
	GGGGACTGTG	TGCGCAAGTG	CGGGCTACTC	AACCTGACCG	TGGCGGCCGA	GGCGTGCCGC	960
	GAGCGCAGCC	ACGTGGCCAT	CAAGACCGTG	CGCGTGCCCG	AGGTGAACGA	CCTGCGCGCC	1020
	CTGGTGGAAG	ACCCGCGATT	AAACCTCAAG	GTCTATCCAG	TGGTCCGAGA	CCCCCGCGGC	1080
	ATTCTGGCTT	CGCGCAGCGA	GACCTTCCGC	GACACGTACC	GGCTCTGGCG	GCTCTGGTAC	1140
	GGCACCGGGA	GGAAACCCTA	CAACCTGGAC	GTGACGCAGC	TGACCACGGT	GTGCGAGGAC	1200
15	TTCTCCAAC	CCGTGTCCAC	CGGCCTCATG	CGGCCCCCGT	GGCTCAAGGG	CAAGTACATG	1260
	TTGGTGCCT	ACGAGGACCT	GGCTCGGAAC	CCTATGAAGA	AGACCGAGGA	GATCTACGGG	1320
	TTCCTGGGCA	TCCCGCTGGA	CAGCCACGTG	GCCCGCTGGA	TCCAGAACAA	CACGCGGGGC	1380
	GACCCCAACC	TGGGCAAGCA	CAAAATACGG	ACCGTGCGAA	ACTCGGCGGC	CACGGCCGAG	1440
	AAGTGGCGCT	TCCGCCTCTC	CTACGACATC	GTGGCCTTTG	CCCAGAACGC	CTGCCAGCAG	1500
20	GTGCTGGCCC	AGCTGGGCTA	CAAGATCGCC	GCCTCGGAGG	AGGAGCTGAA	GAACCCCTCG	1560
	GTCAGCCTGG	TGGAGGAGCG	GGACTTCCGC	CCCTTCTCGT	GACCCGGGCG	GTGCGGGTGG	1620
	GGGCGGGAGG	CGCAAGGTGT	CGGTTTTGAT	AAAATGGACC	GTTTTAACT	GTTGCCTTAT	1680
	TAACCCCTCC	CTCTCCCAAC	TCATCTTCGT	GTCTTCTCTG	CCCCAGCTC	ACCCCACTCC	1740
25	CTTCTGCCCC	TTTTTTGTCT	CTGAAATTG	CACTACGTCT	TGGACGGGAA	TCACTGGGGC	1800
	AGAGGGCGCC	TGAAGTAGGG	TCCCGCCCCC	CCACCCCAT	TCAGACACAT	GGATGTTGGG	1860
	TCTCTGTGCG	GACGGTGACA	ATGTTTACAA	GCACCACATT	TACACATCCA	CACACGCACA	1920
	CGGGCACTCG	CGAGGCGACT	TCTCAAGCTT	TTGAATGGGT	GAGTGGTCGG	GTATCTAGTT	1980
	TTTGCACTGT	CTTACTATTC	AAGGTAAGAG	GATACAAACA	AGAGGACCAC	TTGTCTCTAA	2040
30	TTTATGAATG	GTGTCCATCC	TTTCCCCATC	CCTGCCTCCT	GCCCCGTAGC	CCCATTTCCT	2100
	CCCTTAGAGC	AGCGAAACTG	CCCCCTCCTG	CCCGCCCTTG	CCTGTCCGGT	AGGCAGGTTT	2160
	TTACTGTGAG	GTGAACGTGG	ACCTGTTTCT	GTTTCCAGTC	TGTGGTGATG	CTGTCTGTCT	2220
	GTCTGAGTCT	CGTGCCGCGC	CCTGGACCAG	TGATGACTGA	TGAATCTTAT	GAGCTTCTGA	2280
	TTGATCTCGG	GGTCCATCTG	TGATATTCTT	TTGTGCCAAA	AAGAAAAAAA	AAGAGTGGAT	2340
35	CAGTTTGCTA	AATGAACATT	GAAATTGAAA	TGCTTTATCT	GTGTTTTCTG	TAAATAAAAG	2400
	AGTGCAATAA	TCACC					

Seq ID No: 97 Protein sequence:
Protein Accession #: NP_003645.1

40	1	11	21	31	41	51	
	MQCSWKAVLL	LALASIAIQY	TAIRTFTAKS	FHTCPGLAEA	GLAERLCEES	PTPAYNLSRK	60
	THILILATTR	SGSSFVQQLF	NQHLDVFYLF	EPLYHVQNTL	IPRFTQKSP	ADRRVMLGAS	120
45	RDLLRSLYDC	DLYFLENYIK	PPPVNHTTDR	IFRRGASRVL	CSRFPVCDPPG	PADLVLEEGD	180
	CVRKCGLLNL	TVAEACRER	SHVAIKTVRV	PEVNDLRALV	EDPRLNLKVI	QLVRDPRGIL	240
	ASRSETFRDT	YRLWRLWYGT	GRKPYNLDT	QLTTVCEDFS	NSVSTGLMRP	PWLKGYMLV	300
	RYEDLARNPM	KKTEEYIGFL	GIPLDSHVAR	WIQNNTRGDP	TLGKHXYGT	RNSAATAEKW	360
50	RFRLSYDIVA	FAQNACQQLV	AQLGYKIAAS	EEELKNPSVS	LVEERDFRPF	S	

Seq ID NO: 98 DNA sequence
Nucleic Acid Accession #: NM_002852.1

Coding sequence: 68-1213 (underlined sequences correspond to start and stop codons)

55	1	11	21	31	41	51	
	CTCAAACCTCA	GCTCACTTGA	GAGTCTCCTC	CCGCCAGCTG	TGGAAAGAAC	TTTGCGTCTC	60
	TCCAGCAATG	CATCTCCTTG	CGATCTCTGT	TTGTGCTCTC	TGGTCTGCAG	TGTTGGCCGA	120
60	GAACTCGGAT	GATTATGATC	TCATGTATGT	GAATTTGGAC	AACGAAATAG	ACAATGGACT	180
	CCATCCCACT	GAGGACCCCA	CGCCGTGCGA	CTGCGGTGAG	GAGCACTCGG	AATGGGACAA	240
	GCTCTTCATC	ATGCTGGAGA	ACTCGCAGAT	GAGAGAGCGC	ATGCTGCTGC	AAGCCACGGA	300
	CGACGTCTCT	CGGGGCGAGC	TGCAGAGGCT	CGGGGAGGAG	CTGGGCCCGC	TCGCGGAAAG	360
	CCTGGCGAGG	CGGTGCGCGC	CGGGGGCTCC	CGCAGAGGCC	AGGCTGACCA	GTGCTCTGGA	420
65	CGAGCTGCTG	CAGGCGACCC	GCGACGCGGG	CCGACGGCTG	GCGCGTATGG	AGGGCGCGGA	480
	GGCGCAGCGC	CCAGAGGAGG	CGGGGCGCGC	CCTGGCCGCG	GTGCTAGAGG	AGCTGCGGCA	540
	GACGCGAGCC	GACCTGACAG	CGGTGACAGG	CTGGGCTGCC	CGAGAGCTGG	TGCCGGCAGG	600
	TTGTGAAACA	GCTATTTTAT	TCCCAATGCG	TTCCAAGAAG	ATTTTGGGAA	GCGTGCATCC	660
	AGTGAGACCA	ATGAGGCTTG	AGTCTTTTAG	TGCCTGCATT	TGGGTCAAAG	CCACAGATGT	720
70	ATTAAACAAA	ACCATCCTGT	TTTCTATGCG	CACAAAGAGG	AATCCATATG	AAATCCAGCT	780
	GTATCTCAGC	TACCAATCCA	TAGTGTGTTG	GATGGGTGGA	GAGGAGAACA	AACTGGTTGC	840
	TGAAGCCATG	GTTTCCCTGG	GAAGGTGGAC	CCACCTGTGC	GGCACCTGGA	ATTACAGAGGA	900
	AGGGCTCACA	TCCTTGTGGG	TAAATGGTGA	ACTGGCGGCT	ACCACTGTTG	AGATGGCCAC	960
	AGGTCACATT	GTCTCTGAGG	GAGGAATCCT	GCAGATTGGC	CAAGAAAAGA	ATGGCTGCTG	1020
75	TGTGGGTGGT	GGCTTTGATG	AAACATTAGC	CTTCTCTGGG	AGACTCACAG	GCTTCAATAT	1080
	CTGGGATAGT	GTTCTTAGCA	ATGAAGAGAT	AAGAGAGACC	GGAGGAGCAG	AGTCTTGTCA	1140

CATCCGGGGG	AATATTGTG	GGTGGGGAGT	CACAGAGATC	CAGCCACATG	GAGGAGCTCA	1200
GTATGTTTCA	<u>TAAATGTTGT</u>	GAAACTCCAC	TTGAAGCCAA	AGAAAGAAAC	TCACACTTAA	1260
AACACATGCC	AGTTGGGAAG	GTCTGAAAAC	TCAGTGCATA	ATAGGAACAC	TTGAGACTAA	1320
TGAAAGAGAG	AGTTGAGACC	AATCTTTATT	TGTACTGGCC	AAATACTGAA	TAAACAGTTG	1380
AAGGAAAGAC	ATTGGAAAAA	GCTTTTGAGG	ATAATGTTAC	TAGACTTTAT	GCCATGGTGC	1440
TTTCAGTTTA	ATGCTGTGTC	TCTGTCAGAT	AAACTCTCAA	ATAATAAAAA	AGGACTGTAT	1500
TGTTGAACAG	AGGACAATT	GTTTTACTTT	TCTTTGGTTA	ATTTTGTTTT	GGCCAGAGAT	1560
GAATTTTACA	TTGGAAGAAT	AACAAAATAA	GATTTGTTGT	CCATTGTTCA	TTGTTATTGG	1620
TATGTACCTT	ATTACAAAAA	AAATGATGAA	AACATATTTA	TACTACAAGG	TGACTTAACA	1680
ACTATAAATG	TAGTTTATGT	GTTATAATCG	AATGTCACGT	TTTTGAGAAG	ATAGTCATAT	1740
AAGTTATATT	GCAAAGGGA	TTTGTATTAA	TTTAAGACTA	TTTTTGTAAG	GCTCTACTGT	1800
AAATAAAATA	TTTTATAAAA	CTAAAAAAA	AAAAAAA			

Seq ID No: 99 Protein sequence
Protein Accession #: NP_002843.1

1	11	21	31	41	51	
MHLLAILFCA	LWSAVLAENS	DDYDLMYVNL	DNEIDNGLHP	TEDPTPCDCG	QEHSEWDKLF	60
IMLENSQMRE	RMLLQATDDV	LRGELQRLRE	ELGRLAESLA	RPCAPGAPAE	ARLTSALDEL	120
LQATRDAGRR	LARMEGAEAQ	RPEEAGRALA	AVLEELRQTR	ADLHAVQGWA	ARSWLPAGCE	180
TAILFPMSRK	KIFGSVHPVR	PMRLESFSAC	IWVKATDVNL	KTILFSYGTK	RNPYEIQLYL	240
SYQSIWFFVG	GEENKLVAEA	MVSLGRWTHL	CGTWNSEGL	TSLWVNGELA	ATTVMEMATGH	300
IVPEGGILQI	GQEKNGCCVG	GGFDETLAFS	GRLTGFNIWD	SVLSNEEIRE	TGGAESCHIR	360
GNIVGWGVTE	IQPHGGAQYV	S				

Seq ID NO: 100 DNA sequence
Nucleic Acid Accession #: NM_007351.1

Coding sequence: 72-3758 (underlined sequences correspond to start and stop codons)

1	11	21	31	41	51	
CTGCTATCAA	AAAGGCCATA	AGGATTTTGT	CCCCAAATTT	CACATGAGCT	ACCTTGCTTC	60
AAACTACTGA	<u>GATGAAGGGG</u>	GCAAGATTAT	TTGTCCTTCT	TTCTAGTTTA	TGGAGTGGGG	120
GCAATGGGCT	TAACAACAGT	AAGCATTTCT	GGACTATACC	TGAGGATGGG	AACTCTCAGA	180
AGACTATGCC	TTCTGCTTCA	GTTCCCTCAA	ATAAAATACA	AAGTTTGCAA	ATACTGCCAA	240
CCACTCGGGT	CATGTCGGCG	GAGATAGCTA	CAACTCCAGA	GGCAAGAACT	TCTGAAGACA	300
GTCCTTCTAA	ATCAACACTG	CCTCCCTCAG	AAACAAGTGC	ACCTGCTGAG	GGTGTGAGAA	360
ATCAAACCTCT	CACATCCACA	GAGAAAGCAG	AAGGAGTGGT	CAAGTTACAG	AATCTTACCC	420
TCCCAACCAA	CGCTAGCATC	AAGTTCAATC	CTGGAGCAGA	ATCAGTGGTC	CTTTCCAATT	480
CTACACTGAA	ATTTCTTCAG	AGCTTTGCCA	GAAAGTCAAA	TGAACAAGCA	ACTTCTCTAA	540
ACACAGTTGG	AGGCACTGGA	GGCATTGGAG	GCGTTGGAGG	CACTGGAGGC	GTGGGAAATC	600
GAGCCCCACG	GGAAACATAC	CTCAGCCGGG	GTGACAGCAG	TTCCAGCCAA	AGAAGTGAAT	660
ACCAAAATAT	AAATTTTCGAA	ACAAGTAGAG	GAAAGAATTG	GTGTGCTTAT	GTACATACCA	720
GGTTATCTCC	CACAGTGACA	TTGGACAACC	AGGTCACTTA	TGTCCAGGTT	GGGAAAGGAC	780
CTTGTTGGCTG	GACCGGTGGA	TCCTGTCTTC	AGAGATCTCA	GAAGATATCC	AATCCTGTCT	840
ATAGGATGCA	ACATAAAATT	GTCACCTCAT	TGGATTGGAG	GTGCTGTCTT	GGATACAGTG	900
GGCCGAAATG	TCAACTAAGA	GCCCAGGAAC	AGCAAAAGTT	GATACACACC	AACCAGGCTG	960
AAAGTCATAC	AGCTGTTGGC	AGAGGAGTAG	CTGAGCAGCA	GCAGCAGCAA	GGCTGTGGTG	1020
ACCCAGAAAT	GATGCAAAAA	ATGACTGATC	AGGTGAACTA	CCAGGCAATG	AAACTGACTC	1080
TTCTGCAGAA	GAAGATTGAC	AATATTTCTT	TGACTGTGAA	TGATGTAAGG	AACACTTACT	1140
CCTCCCTTGA	AGGAAGAGTC	AGCGAAGATA	AAAGCAGAGA	ATTTCAATCT	CTTCTAAAAG	1200
GTCTAAATAT	CAAAAGCATT	AATGTACTGA	TAAGAGACAT	AGTAAGAGAA	CAATTTAAAA	1260
TTTTTCAAAA	TGACATGCAA	GAGACTGTAG	CACAGCTCTT	CAAGACTGTA	TCAAGTCTAT	1320
CAGAGGACCT	CGAAAGCACC	AGGCAAAATA	TTCAAAAAGT	TAATGAATCT	GTGGTTTCAA	1380
TAGCAGCCCA	GCAAAGTTT	GTTTGGTGC	AAGAGAATCG	GCCCCTTTG	ACTGATATAG	1440
TGGAACCTAAG	GAATCACATT	GTGAATGTAA	GGCAAGAAAT	GACTCTTACA	TGTGAGAAGC	1500
CTATTAAAGA	ACTAGAAGTA	AAGCAGACTC	ATTTAGAAGG	TGCTCTAGAA	CAGGAACACT	1560
CAAGAAGCAT	TCTGTATTAT	GAATCCCTCA	ATAAACTCT	TTCTAAATTG	AAGGAAGTAC	1620
ATGAGCAGCT	TTTATCAACT	GAACAGGTAT	CAGACCAGAA	GAATGCTCCA	GCTGCTGAGT	1680
CAGTTAGCAA	TAATGTCACT	GAGTACATGT	CTACTTTACA	TGAAAATATA	AAGAAGCAGA	1740
GTTTGTAGAT	GCTGCAATATG	TTTGAAGATT	TGCACATTCA	AGAAAGCAAG	ATTAACAATC	1800
TCACCGTCTC	TTTGAGATG	GAGAAAGAGT	CTCTCAGAGG	TGAATGTGAA	GACATGTTAT	1860
CCAAATGCAG	AAATGATTTT	AAATTTCAAC	TTAAGGACAC	AGAAGAGAAAT	TTACATGTGT	1920
TAAATCAAA	ATTGGCTGAA	GTTCTCTTTT	CAATGGACAA	TAAGATGGAC	AAAATGAGTG	1980
AGCAACTAAA	TGATTTGACT	TATGATATGG	AGATCCTTCA	ACCCTTGCTT	GAGCAGGGAG	2040
CATCACTCAG	ACAGACAATG	ACATATGAAC	AACCAAAGGA	AGCAATAGTG	ATAAGGAAAA	2100
AGATAGAAAA	TCTGACTAGT	GCTGTCAATA	GTCTAAATTT	TATTATCAAA	GAACCTACAA	2160
AAAGACACAA	CTTACTTAGA	AATGAAGTAC	AGGGTCGTGA	TGATGCCCTA	GAAAGACGTA	2220
TCAATGAATA	TGCCTTAGAA	ATGGAAGATG	GCCTCAATAA	GACAATGACT	ATTATAAATA	2280
ATGCTATTGA	TTTCACTCAA	GATAACTATG	CCCTAAAAGA	GACTTTAAGT	ACTATTAAAG	2340
ATAATAGTGA	GATCCATCAT	AAATGTACCT	CCGATATGGA	AACATTTTGT	ACATTATTTC	2400
CTCAGTTCCA	CCGTCTGAAT	GATTCTATTTC	AGACTTTGGT	CAATGACAAT	CAGAGATATA	2460

	ACTTTGTTTT	GCAAGTCGCC	AAGACCCTTG	CAGGTATTCC	CAGAGATGAG	AACTAAATC	2520
	AGTCCAACCT	CCAAAAGATG	TATCAAATGT	TCAATGAAAC	CACCTCCCAA	GTGAGAAAA	2580
	ACCAGCAAAA	TATGAGTCAT	TGGAAGAAA	AACTACTCTT	AACTACCAAG	ATTTCCAAAA	2640
5	ATTTTGAGAC	TCGGTTGCAA	GACATTGAGT	CTAAAGTTAC	CCAGACGCTC	ATACCTTATT	2700
	ATAATTCAGT	TAAAAAAGGC	AGTGTAGTTA	CAAATGAGAG	AGATCAGGCT	CTTCAACTGC	2760
	AAGTATTAAA	TTCCAGATT	AAGGCGTTGG	AAGCAAAATC	TATCCATCTT	TCAATTAACT	2820
	TC'TTTTCGCT	TAACAAAAC	CTCCACGAAG	TTTAAACAAT	GTGTCACAAT	GCTTCTACAA	2880
	GTGTGTCAGA	ACTGAATGCT	ACCATCCCTA	AGTGGATAAA	ACATTCCCTG	CCAGATATT	2940
10	AACTTCTTCA	GAAAGGTCTA	ACAGAAATTTG	TGGAACCAAT	AATTCAAATA	AAAACCTCAAG	3000
	CTGCCCTATC	TAATCAACT	TGTTGTATAG	ATCGATCGTT	GCCTGGTAGT	CTGGCAAATG	3060
	TTGTCAAGTC	TCAGAAGCAA	GTAATAATCAT	TGCCAAAGAA	AATTAACGCA	CTTAAGAAAC	3120
	CAACGGTAAA	TCTTACCACA	GTCCTGATAG	GCCGGACTCA	AAGAAACACG	GACAACATAA	3180
	TATATCCTGA	GGAGTATTCA	AGCTGTAGTC	GGCATCCGTG	CCAAAATGGG	GGCACGTGCA	3240
	TAAATGGAAG	AACTAGCTTT	ACCTGTGCCT	GCAGACATCC	TTTTACTGGT	GACAACTGCA	3300
15	CTATCAAGCT	TGTGGAAGAA	AATGCTTTAG	CTCCAGATTT	TTCCAAAGGA	TCTTACAGAT	3360
	ATGCACCCAT	GGTGGCATT	TTTGCATCTC	ATACGTATGG	AATGACTATA	CCTGGTCCTA	3420
	TCCTGTTTAA	TAACCTGGAT	GTCAATTATG	GAGCTTCATA	TACCCCAAGA	ACTGGAAAAT	3480
	TTAGAATTCC	GTATCTTGGA	GTATATGTTT	TCAAGTACAC	CATCGAGTCA	TTTAGTGCTC	3540
20	ATATTTCTCG	ATTTTTAGTG	GTTGATGGAA	TAGACAAGCT	TGCATTGAG	TCTGAAAATA	3600
	TTAACAGTGA	AATACACTGT	GATAGGGTTT	TAACTGGGGA	TGCCCTTATTA	GAATTAAATT	3660
	ATGGGCAGGA	AGTCTGGTTA	CGACTTGCAA	AAGGAACAAT	TCCAGCCAAG	TTTCCCCCTG	3720
	TTACTACATT	TAGTGGCTAT	TTATTATATC	GTACATAAGT	TAGTATGAAA	AACAGACTAT	3780
	CACCTTTATT	GAGAAACAGC	CAGTGTTTTC	ATTTATCTTT	GCTTGACAT	CTGCTCTGTT	3840
25	TTGGTTTTTC	TACAGGAAAT	GAAAATCAAC	TTGTTTTTTT	AATATGAGTA	AACTTGATG	3900
	TCTATTTTAT	AAAATTATTT	GAATATTGTT	TAATGTCTGA	ATATGAAAGA	GTTCTTGATC	3960
	CTAAAGAAAT	TTAGTGGCAC	AGAAAACAAA	GTGAATTTGT	TAGCATAATT	ATTCCTATT	4020
	TTATTTCTTC	ATTTTAAATG	ATTGCAATGG	AAAGTAATAT	TATAAAACGG	TAATTACAAC	4080
	ATATTATCAG	TCACAGTTT	CTTCCAATT	AAACACTTAA	CTTTTGTAT	TCCCTGTATA	4140
30	TAAATATATA	ACACACATT	TCTAGATTCA	CAAATTTAAA	TAAATTACTC	AAAAAATG	

Seq ID No: 101 Protein sequence:

Protein Accession #: NP_031377.1

	1	11	21	31	41	51	
35	MKGARLFLVLL	SSLWSGGIGL	NNSKHSWTIP	EDGNSQKTMF	SASVPPNKIQ	SLQILPTTRV	60
	MSAEIATPTE	ARTSEDSLLK	STLPPSETSA	PAEGVRNQTL	TSTKAEGVV	KLQNLTLPTN	120
	ASIKFNPGE	SVVLSNSTLK	FLQSFARKSN	EQATSLNTVG	GTGGIGGVGG	TGGVGNRAPR	180
40	ETYLNRDSS	SSQRTDYQKS	NFETTRGKNW	CAYVHTRLSP	TVTLDNQVTV	VPGGKGPCGW	240
	TGGSCPQRSQ	KISNPVYRMQ	HKIVTSLDWR	CCPGYSQPKC	QLRAQEQQSL	IHTNQAESHT	300
	AVGRGVAEQQ	QQQCGDPEV	MQKMTDQVNY	QAMKLTLLOK	KIDNISLTVN	DVRNTYSSLE	360
	GKVSSEKSR	FQSLKGLKLS	KSINVLIRDI	VREQFKIFQN	DMQETVAQLF	KTVSSLSDEL	420
	ESTRQIIQKV	NESVVSIAAQ	QKFVLVQENR	PTLTDIVELR	NHIVNVRQEM	TLTCEKPIKE	480
45	LEVKQTHLEG	ALEQEHRSRI	LYYESLNKTL	SKLKEVHEQL	LSTEQVSDQK	NAPAAESVSN	540
	NVTEYMTSLH	ENIKKQSLMM	LQMFEDLHIQ	ESKINNLTVS	LEMEKESLRG	ECEDMLSKCR	600
	NDFKFKLQKD	EENLHVLNQT	LAEVLFPMDN	KMDKMSEQLN	DLTYDMEILQ	PLLEQGGASLR	660
	QTMTEYQPK	AIIVIRKKIEN	LTSAVNSLNF	IKELTKRHN	LLRNEVQGRD	DALERRINEY	720
	ALEMEDGLNK	TMTIINNAID	FIQDNYALKE	TLSTIKDNSE	IHHKCTSDME	TILTFIPQPH	780
50	RLNDSIQTLV	NDNQRYNFVL	QVAKTLGAP	RDEKLNQSNF	QKMYQMFNET	TSQVRKYQQN	840
	MSHLEKLLLL	TTKISKNFET	RLQDIESKVT	QTLIPYYISV	KKGSVVTNER	DQALQLQVLN	900
	SRFKALEAKS	IHLISINFFSL	NKTLHEVLTM	CHNASTSVSE	LNATIPKWKI	HSLFDIQLLQ	960
	KGLTEFVEPI	IQIKTQAALS	NSTCCIDRSL	PGSLANVVKS	QKQVKSPLPK	INALKKPTVN	1020
	LTTVLIGRTQ	RNTDNIYPE	EYSSCSRHP	QNGGTCINGR	TSFTCACRHP	FTGDNCTIKL	1080
55	VEENALAPDF	SKGSYRYAPM	VAFFASHTYG	MTIPGPILFN	NLDVNYGASY	TPRTGKFRIP	1140
	YLGVVYFKYT	IESFSAHISG	FLVVDGIDKL	AFESENINSE	IHCDRVLTGD	ALLELNYGQE	1200
	VWLRLAKGTI	PAKFPVPTTF	SGYLLYRT				

Seq ID NO: 102 DNA sequence

Nucleic Acid Accession #: NM_000873.2

Coding sequence: 57-884 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
65	ATCTCCCTCC	AGGCAGCCCT	TGGCTGGTCC	CTGCGAGCCC	GTGGAGACTG	CCAGAGATGT	60
	CCTCTTTTCG	TTACAGGACC	CTGACTGTGG	CCCTCTTCAC	CCTGATCTGC	TGTCCAGGAT	120
	CGGATGAGAA	GGTATTCGAG	GTACACGTGA	GGCCAAAGAA	GCTGGCGGTT	GAGCCCAAAG	180
	GGTCCCTCGA	GGTCAACTGC	AGCACCACT	GTAACCAAGC	TGAAGTGGGT	GGTCTGGAGA	240
70	CCTCTCTAAA	TAAGATTCTG	CTGGACGAAC	AGGCTCAGTG	GAAACATTAC	TTGGTCTCAA	300
	ACATCTCCCA	TGACACGGTC	CTCCAATGCC	ACTTCACCTG	CTCCGGGAAG	CAGGAGTCAA	360
	TGAATTCCAA	CGTCAGCGTG	TACCAGCGCT	CAAGCAGGTT	CATCCTGACA	CTGCAACCCA	420
	CTTTGGTGGC	TGTGGGCAAG	TCCTTCACCA	TTGAGTGCAG	GGTGCCCAAC	GTGGAGCCCC	480
	TGGACAGCCT	CACCTCTCTC	CTGTTCCCGT	GCAATGAGAC	TCTGCACTAT	GAGACCTTCG	540
75	GGAAGGCAGC	CCCTGCTCCG	CAGGAGGCCA	CAGCCACATT	CAACAGCACG	GCTGACAGAG	600
	AGGATGGCCA	CCGCAACTTC	TCTGCTCGTG	CTGTGCTGGA	CTTGATGTCT	CGCGGTGGCA	660
	ACATCTTTCA	CAAACTACTCA	GCCCCGAAGA	TGTTGGAGAT	CTATGAGCCT	GTGTCGGACA	720

GCCAGATGGT CATCATAGTC ACGGTGGTGT CGGTGTTGCT GTCCCTGTTC GTGACATCTG 780
 TCCTGCTCTG CTTCATCTTC GGCCAGCACT TGCGCCAGCA GCGGATGGGC ACCTACGGGG 840
 TGCAGCGGGC TTGGAGGAGG CTGCCCCAGG CCTTCCGGCC ATAGCAACCA TGAGTGGCAT 900
 5 GGCCACCACC ACGGTGGTCA CTGGAACCTCA GTGTGACTCC TCAGGGTTGA GGTCCAGCCC 960
 TGGCTGAAGG ACTGTGACAG GCAGCAGAGA CTTGGGACAT TGCCTTTTCT AGCCCGAATA 1020
 CAAACACCTG GACTT

Seq ID No: 103 Protein sequence:
 Protein Accession #: NP_000864.1

1 11 21 31 41 51
 | | | | |
 15 MSSFGYRTLT VALFTLICCP GSDEKVFVEH VRPKKLAVEP KGSLEVNCSST TCNQPEVGGGL 60
 ETSLNKILLD EQAQWKHYLV SNISHDTVLQ CHFTCSGKQE SMNSNVSVYQ PPRQVILTLO 120
 PTLVAVGKSF TIECRVPTVE PLDSLTLFLF RGNETHYET FGKAAPAPQE ATATFNSTAD 180
 REDGHRNFSC LAVLDLMSRG GNIFHKHSAP KMLEIYEPVS DSQMVIIIVTV VSVLLSLFVT 240
 SVLLCFIFGQ HLRQQRMGTY GVRAAWRRRLP QAFRP

Seq ID NO: 104 DNA sequence
 Nucleic Acid Accession #: NM_001795.2
 Coding sequence: 121-2475 (underlined sequences correspond to start and stop codons)

25 1 11 21 31 41 51
 | | | | |
 GACGGTGGCG TGACAGGCTC CACAGAGCTC CACTCAGCT CAGGCCCTGG ACGGACAGGC 60
 AGTCCAACGG AACAGAAACA TCCCTCAGCC CCACAGGCAC GATCTGTTCC TCCTGGGAAG 120
 ATGCAGAGGC TCATGATGCT CCTCGCCACA TCGGGCGCCT GCCTGGGCCT GCTGGCAGTG 180
 30 GCAGCAGTGG CAGCAGCAGG TGCTAACCTT GCCCAACGGG ACACCCACAG CCTGTGCCCC 240
 ACCCACCAGG GCCAAAAGAG AGATTGGATT TGGAACCCAGA TGCACATTGA TGAAGAGAAA 300
 AACACCTCAC TTCCCCATCA TGTAGGCAAG ATCAAGTCAA GCGTGAGTCG CAAGAATGCC 360
 AAGTACCTCG TCAAAGGAGA ATATGTGGGC AAGGTCTTCC GGGTCGATGC AGAGACAGGA 420
 GACGTGTTCC CCATTGAGAG GCTGGACCGG GAGAATATCT CAGAGTACCA CCTCACTGCT 480
 35 GTCATTGTGG ACAAGGACAC TGGTGAAGAC CTGGAGACTC CTTCAGCTT CACCATCAAA 540
 GTTCATGACG TGAACGACAA CTGGCCTGTG TTCACGCATC GGTGTGTTCAA TGCCTCCGTG 600
 CCTGAGTCGT CGGCTGTGGG GACCTCAGTC ATCTCTGTGA CAGCAGTGGG TGCAGACGAC 660
 CCCACTGTGG GAGACACGCG CTCTGTCTATG TACCAAAATCC TGAAGGGGAA AGAGTATTTT 720
 GCCATCGATA ATTCTGGACG TATTATCACA ATAACGAAAA GCTTGGACCG AGAGAAGCAG 780
 40 GCCAGGTATG AGATCGTGGT GGAAGCGCGA GATGCCCAGG GCCTCCGGGG GGAAGTCCGG 840
 ACGGCCACCG TGCTGGTCACT CTGCAAGAGC ATCAATGACA ACTTCCCTCTT CTCACCCAG 900
 ACCAAGTACA CATTTGTCTG GCCTGAAGAC ACCCGTGTGG GCACCTCTGT GGGCTCTCTG 960
 TTGTGTTGAG ACCCAGATGA GCCCCAGAAC CGGATGACCA AGTACAGCAT CTTGCGGGGC 1020
 45 GACTACCAGG ACGCTTTCAC CATTGAGACA AACCCCGCCC ACAACGAGGG CATCATCAAG 1080
 CCCATGAAGC CTCTGGATTA TGAATACATC CAGCAATACA GCTTCATCGT CGAGGCCACA 1140
 GACCCACCA TCACCTCCG ATACATGAGC CCTCCCGCGG GAAACAGAGC CCAGGTCATT 1200
 ATCAACATCA CAGATGTGGA CGAGCCCCC ATTTTCCAGC AGCCTTTCTA CCCTTCCAG 1260
 CTGAAGGAAA ACCAGAAGAA GCCTCTGATT GGCACAGTGC TGGCCATGGA CCCTGATGCG 1320
 50 GCTAGGCATA GCATTGGATA CTCCATCCGC AGGACCAAGT ACAAGGGCCA GTTCTTCCGA 1380
 GTCAACAAA AGGGGGACAT TTACAATGAG AAAGAAGTGG ACAGAGAAGT CTACCCTTGG 1440
 TATAACCTGA CTGTGGAGGC CAAAGAAGT GATTCCACTG GAACCCACAG AGGAAAAGAA 1500
 TCCATTGTGC AAGTCCACAT TGAAGTTTGG GATGAGAATG ACAATGCCCC GGAGTTTGCC 1560
 AAGCCCTACC AGCCCAAAGT GTGTGAGAAC GCTGTCCATG GCCAGCTGGT CCTGCAGATC 1620
 55 TCCGCAATAG ACAAGGACAT AACACCAGCA AACGTGAAGT TCAAATTAC CTTGAATACT 1680
 GAGAACAAC TTAACCTCAC GGATAATCAC GATAACACGG CCAACATCAC AGTCAAGTAT 1740
 GGGCAGTTTG ACCGGGAGCA TACCAGGTC CACTTCTTAC CCGTGGTCAT CTCAGACAAT 1800
 GGGATGCCAA GTCGACGGGG CACCAAGCAG CTGACCGTGG CCGTGTGCAA GTGCAACGAG 1860
 CAGGGCGAGT TCACCTTCTG CGAGGATATG GCCGCCAGG TGGGCGTGAG CATCCAGGCA 1920
 60 GTGGTAGCCA TCTTACTCTG CATCCTCACC ATCAGAGTGA TCACCTGCT CATCTTCTCTG 1980
 CGGCGGCGGC TCCGGAAGCA GGCCCGCGCG CACGGCAAGA GCGTGCCGGA GATCCACGAG 2040
 CAGCTGGTCA CTFACGACGA GGAGGGCGCG GCGAGATGG ACACCACAG CTACGATGTG 2100
 TCGGTGCTCA ACTCGGTGCG CCGCGCGCGG GCCAAGCCCC CGCGGCCCGC GCTGGACGCC 2160
 CGGCCTTCCC TCTATGCGCA GGTGCAAGAG CCACCGAGGC ACGCGCCTGG GGCACACGGA 2220
 65 GGGCCCGGGG AGATGGCAGC CATGATCGAG GTGAAGAAGG ACGAGGCGGA CCACGACGGC 2280
 GACGGCCCCC CTTACGACAC GCTGCACATC TACGGCTACG AGGGCTCCGA GTCCATAGCC 2340
 GAGTCCCTCA GCTCCCTGGG CACCGACTCA TCCGACTCTG ACGTGGATTA CGACTTCTTT 2400
 AACGACTGGG GACCCAGGTT TAAGATGCTG GCTGAGCTGT ACGGCTCGGA CCCCCGGGAG 2460
 GAGCTGCTGT ATTAGCGGCG CGAGGTCAC CTGGGCTTGG GGACCCAAAC CCCCTGCAGC 2520
 70 CCAGGCCAGT CAGACGCCAG GCACCACAGC CTCCAAAAAT GGCAGTGAAT CCCCAGCCCA 2580
 GCACCCCTTC CTCGTGGGTC CCAAGAGACCT CATCAGCCTT GGGATAGCAA ACTCCAGGTT 2640
 CCTGAAATAT CCAGGAATAT ATGTCAAGTGA TGAATATTCT CAAATGCTGG CAAATCCAGG 2700
 CTGTGTTTCT GTCTGGGCTC AGACATCCAC ATAACCTGT CACCCACAGA CCGCCGTCTA 2760
 ACTCAAAGAC TTCCTCTGGC TCCCCAAGGC TGCAAAGCAA AACAGACTGT GTTTAACTGC 2820
 75 TGCAAGGCTCT TTTTCTAGGG TCCCTGAAGC CCCTGGTAAG GCTGGTGAGG TCCTGGTGCC 2880
 TATCTGCTGT GAGGCAAGG CTGGACAGC TTGACTTGTG GGGCAGGATT CTCTGCAGCC 2940
 CATTCCCAAG GGAGACTGAC CATCATGCCC TCTCTCGGGA GCCCTAGCCC TGCTCCAAT 3000

CCATACTCCA CTCCAAGTGC CCCACCACTC CCCAACCCCT CTCCAGGCCT GTCAAGAGGG 3060
 AGGAAGGGGC CCCATGGCAG CTCCTGACCT TGGGTCCTGA AGTGACCTCA CTGGCCTGCC 3120
 ATGCCAGTAA CTGTGCTGTA CTGAGCACTG AACCACATTC AGGGAAATGG CTTATTAAAC 3180
 5 TTTGAAGCAA CTGTGAATTC ATTCTGGAGG GGCAGTGGAG ATCAGGAGTG ACAGATCACA 3240
 GGGTGAGGGC CACCTCCACA CCCACCCCT CTGGAGAAGG CCTGGAAGAG CTGAGACCTT 3300
 GCTTTGAGAC TCCTCAGCAC CCCTCCAGTT TTGCCTGAGA AGGGGCAGAT GTTCCCGGAG 3360
 CAGAAGACGT CTCCCCTTCT CTGCCTCACC TGGTCGCCAA TCCATGCTCT CTTTCTTTTC 3420
 TCTGTCTACT CCTTATCCCT TGGTTTAGAG GAACCAAGA TGTGGCCTTT AGCAAACTG 3480
 10 GACAATGTCC AAACCCACTC ATGACTGCAT GACGGAGCCG AGCCATGTGT CTTACACCT 3540
 CGCTGTTGTC ACATCTCAGG GAACTGACCC TCAGGCACAC CTTGCAGAAG GCAAGGCCCT 3600
 GCCCTGCCCA ACCTCTGTGG TCACCCATGC ATCTTCCACT GGAACGTTTC ACTGCAACA 3660
 CACCTTGGAG AAGTGGCATC AGTCAACAGA GAGGGGCAGG GAAGGAGACA CCAAGCTCAC 3720
 CCTTCGTCAT GGACCGAGGT TCCCACTCTG GGCAAGCCC CTCACACTGC AAGGGATTGT 3780
 15 AGATAACACT GACTTGTGTTG TTTTAAACAA TAACTAGCTT CTATAATGA TTTTCTTACT 3840
 AATGATACTT ACAAGTTTCT AGCTCTCACA GACATATAGA ATAAGGGTTT TTGCATAATA 3900
 AGCAGGTTGT TATTAGGTTT AACAAATATTA ATTCAGGTTT TTAGTTGGA AAAACAATTC 3960
 CTGTAACCTT CTATTTCTA TAATTGTAGT AATTGCTCTA CAGATAATGT CTATATATTG 4020
 GCCAACTGG TGCATGACAA GTACTGTATT TTTTATACC TAAATAAAGA AAAATCTTTA 4080
 20 GCCTGGGCAA CAAAAA

Seq ID No: 105 Protein sequence
 Protein Accession #: NP_001786.1

25 1 11 21 31 41 51
 | | | | |
 MQRLLMMLLAT SGACLGLLAV AAVAAAGANP AQRDTHSLLP THRRQKRDWI WNQMHIIDEEK 60
 NTSLPHHVVGK IKSSVSRKNA KYLLKGEYVG KVFRVDAETG DVFAIERLDR ENISEYHLTA 120
 30 VIVDKDTGEN LETPSSFTIK VHDVNDNWPV FTHRLFNASV PESSAVGTSV ISVTAVDADD 180
 PTVGDHASVM YQILKGEYF AIDNSGRIIT ITKSLDREKQ ARYEIVVEAR DAQGLRGDSG 240
 TATVLVTLQD INDNFPFFFTQ TKYTFVVPED TRVGTSVGSGL FVEDPDEPQN RMTKYSILRG 300
 DYQDAFTIET NPAHNEGIK PMKPLDYEYI QQYSFIVEAT DPTIDLRYMS PPAGNRAQVI 360
 INITDVDEPP IFQPPFYHFO LKENQKKPLI GTVLAMDPDA ARHSIGYSIR RTSKQGFRR 420
 35 VTKKGDYNE KELDREVYPW YNLTVEAKEL DSTGTPTGKE SIVQVHIEVL DENDNAPEFA 480
 KPYQPKVCEN AVHGQLVLQI SAIDKDITPR NVKFKFTLNT ENNFTLTDNH DNTANITVKY 540
 GQFDREHTKV HFLPVVISDN GMPSTGTST LTVAVCKCNE QGEFTFCEDM AAQGVVSIQA 600
 VVAILLCILT ITVITLLIFL RRRLRKQARA HGKSVPEIHE QLVTVDEEGG GEMDTTSYDV 660
 SVLNSVRRGG AKPPRPALDA RPSLYAQVQK PPRHAPGAHG GPGEMAAMIE VKKDEADHDG 720
 40 DGPPYDTLHI YGYEGSEsia ESLSSLTGDS SDSVDYDFL NDWGPFRFKML ABLYGSDPRE 780
 ELLY

Seq ID NO: 106 DNA sequence
 Nucleic Acid Accession #: none found
 Coding sequence: 1-474 (underlined sequences correspond to start and stop codons)

45 1 11 21 31 41 51
 | | | | |
 ACAGTACTCT GTGCAAAAAA CCTGGTGAAA AAGGATTTTT TCCGACTTCC TGATCCATTT 60
 GCTAAGGTGG TGGTTGATGG ATCTGGGCAA TGCCATTCTA CAGATACTGT GAAGAATACG 120
 50 CTTGATCCAA AGTGGAAATCA GCATTATGAC CTGTATATTG GAAAGTCTGA TTCAGTTACG 180
 ATCAGTGTAT GGAATCACA GAAGATCCAT AAGAAACAAG GTGCTGGATT TCTCGGTTGT 240
 GTTCGTCTTC TTTCCAATGC CATCAACCGC CTCAAAGACA CTGTTATCA GAGGTTGGAT 300
 TTATGCAAA CCGGGCCAAA TGACAATGAT ACAGTTAGAG GACAGATAGT AGTAAGTCTT 360
 55 CAGTCCAGAG ACCGAATAGG CACAGGAGGA CAAGTTGTGG ACTGCAGTCG TTTATTTGAT 420
 AACGATTTAC CAGACGGAGC TCATTATTTG TGGACTTGGA AAGATAGATG TTAATGACTG 480
 GAAGGTAAAC ACCCGGTTAA AACACTGTAC ACCAGACAGC AACATTGTCA AATGGTTCTG 540
 GAAAGCTGTG GAGTTTTTTG ATGAAGAGCG ACGAGCAAGA TTGCTTCAGT TTGTGACAGG 600
 ATCCTCTCGA GTGCCTCTGC AGGGCTTCAA AGCATTGCAA GGTGCTGCAG GCCCGAGACT 660
 60 CTTTACCATA CACCAGATTG ATGCCTGCAC TAACAACCTG CCGAAAGCCC ACCTGTGCTT 720
 CAATCGAATA GACATTCCAC CCTATGAAAG CTATGAAAAG CTATATGAAA AGCTGCTAAC 780
 AGCCATTGAA GAAACATGTG GATTGTGCTG GGAATGACAA GCTTCAAGGA TTTACCCAGG 840
 AC

Seq ID No: 107 Protein sequence
 Protein Accession #: none found

70 1 11 21 31 41 51
 | | | | |
 TVLCAKNLVK KDFRLPDPF AKVVVDGSGQ CHSTDIVKNT LDPKWNQHYD LYIGKSDSVT 60
 ISVWNHKKIH KQAGAGFLGC VRLLSNAINR LKDTGYQRLD LCKLGPNDND TVRGQIVVSL 120
 QSRDRIGTGG QVVDCSRFLD NDLPDGAHYL WTWKDRRC

Seq ID NO: 108 DNA sequence
 Nucleic Acid Accession #: NM_002318.1
 Coding sequence: 248-2572 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
5	ACTCCAGCGC	GCGGCTACCT	ACGCTTGGTG	CTTGCTTTCT	CCAGCCATCG	GAGACCAGAG	60
	CCGCCCCCTC	TGCTCGAGAA	AGGGGCTCAG	CGGCGGCGGA	AGCGGAGGGG	GACCACCGTG	120
	GAGAGCGCGG	TCCAGCCCG	GCCACTGCGG	ATCCCTGAAA	CCAAAAAGCT	CCTGCTGCTT	180
	CTGTACCCCG	CCTGTCCCTC	CCAGCTGCGC	AGGGCCCCCT	CGTGGGATCA	TCAGCCCGAA	240
	GACAGGGATG	GAGAGGCCTC	TGTGCTCCCA	CCTCTGCAGC	TGCTTGGCTA	TGCTGGCCCT	300
10	CCTGTCCCCC	CTGAGCCTGG	CACAGTATGA	CAGCTGGCCC	CATTACCCCG	AGTACTTCCA	360
	GCAACCGGCT	CCTGAGTATC	ACCAGCCCCA	GGCCCCCGCC	AACGTGGCCA	AGATTTCAGT	420
	GCGCCTGGCT	GGGCAGAAAG	GGAGCACAG	CGAGGGCCCG	GTGGAGGTGT	ACTATGATGG	480
	CCAGTGGGGC	ACCGTGTGCG	ATGACGACTT	CTCCATCCAC	GCTGCCACG	TCGTCTGCCG	540
	GGAGCTGGGC	TATGTGGAGG	CCAAGTCTTG	GACTGCCAGC	TCCTCTACG	GCAAGGGAGA	600
15	AGGGCCCATC	TGGTTAGACA	ATCTCCACTG	TACTGGCAAC	GAGGCGACCC	TTGCAGCATG	660
	CACCTCCAAT	GGCTGGGGCG	TCACTGACTG	CAAGCACACG	GAGGATGTCG	GTGTGGTGTG	720
	CAGCGACAAA	AGGATTCCCT	GGTTCAAATT	TGACAAATCG	TTGATCAACC	AGATAGAGAA	780
	CCTGAATATC	CAGGTGGAGG	ACATTCCGAT	TCGAGCCATC	CTCTCAACCT	ACCGCAAGCG	840
	CACCCAGTGT	ATGGAGGGCT	ACGTGGAGGT	GAAGGAGGGC	AAGACCTGGA	AGCAGATCTG	900
20	TGACAAGCAC	TGGACGGCCA	AGAATTCCCG	CGTGGTCTCG	GGCATGTTTG	GCTTCCCTGG	960
	GGAGAGGACA	TACAATACCA	AAGTGTACAA	AATGTTTGCC	TCACGGAGGA	AGCAGCGCTA	1020
	CTGGCCATTG	TCCATGGACT	GCACCGGCAC	AGAGGCCAC	ATCTCCAGCT	GCAAGCTGGG	1080
	CCCCCAGGTG	TCACTGGACC	CCATGAAGAA	TGTACCTGCG	GAGAATGGGC	TGCCGGCCGT	1140
	GGTGAGTTGT	GTGCCTTGGC	AGGTCTTCAG	CCCTGACGGA	CCCTCGAGAT	TCCGGAAAGC	1200
25	ATACAAGCCA	GAGCAACCCC	TGGTGCAGCT	GAGAGGCGGT	GCCTACATCG	GGGAGGGCCG	1260
	CGTGGAGGTG	CTCAAAAATG	GAGAATGGGG	GACCGTCTGC	GACGACAAGT	GGGACCTGGT	1320
	GTCCGGCAGT	TGGTCTGCGA	GAGAGCTGGG	CTTTGGGAGT	GCCAAAGAGG	CAGTCACTGG	1380
	CTCCCGACTG	GGGCAAGGGA	TCGGACCCAT	CCACCTCAAC	GAGATCCAGT	GCACAGGCAA	1440
	TGAGAAGTCC	ATTATAGACT	GCAAGTTCAA	TGCCGAGTCT	CAGGGCTGCA	ACCACGAGGA	1500
30	GGATGCTGGT	GTGAGATGCA	ACACCCCTAG	CATGGGCTTG	CAGAAGAAGC	TGCGCCTGAA	1560
	CGGCGGCCGC	AATCCCTACG	AGGGCCGAGT	GGAGGTGCTG	GTGGAGAGAA	ACGGGTCCCT	1620
	TGTGTGGGGG	ATGGTGTGTG	GCCAAAACCT	GGGCATCGTG	GAGGCCATGG	TGGTCTGCCG	1680
	CCAGCTGGGC	CTGGGATTCC	CCAGCAACGC	CTTCCAGGAG	ACCTGGTATT	GGCACGGAGA	1740
	TGTCAACAGC	AACAAAGTGG	TCATGAGTGG	AGTGAAGTGC	TCGGGAACGG	AGCTGTCCCT	1800
35	GGCGCACTGC	CGCCACGACG	GGGAGGACGT	GGCCTGCCCC	CAGGGCGGAG	TGCAGTACGG	1860
	GGCCGGAGTT	GCCTGTCTAG	AAACCGCCCC	TGACCTGGTC	CTCAATGCGG	AGATGGTGCA	1920
	GCAGACACCC	TACCTGGAGG	ACCGGCCCAT	GTTTATGCTG	CAGTGTGCCA	TGGAGGAGAA	1980
	CTGCCTCTCG	CGCTCAGCCG	CGCAGACCGA	CCCCACCACG	GGCTACCGCC	GGCTCCTGCG	2040
	CTTCTCCTCC	CAGATCCACA	ACAATGGCCA	GTCCGACTTC	CGGCCCAAGA	ACGGCCGCCA	2100
40	CGCGTGGATC	TGGCAGCACT	GTACAGGCA	CTACCACAGC	ATGGAGGTGT	TCACCCACTA	2160
	TGACCTGCTG	AACCTCAATG	GCACCAAGGT	GGCAGAGGGC	CACAAGGCCA	GCTTCTGCTT	2220
	GGAGGACACA	GAATGTGAAG	GAGACATCCA	GAAGAATTAC	GAGTGTGCCA	ACTTCGGCGA	2280
	TCAGGGCATC	ACCATGGGCT	GCTGGGACAT	GTACCGCCAT	GACATCGACT	GCCAGTGGGT	2340
	TGACATCACT	GACGTGCCCC	CTGGAGACTA	CCTGTTCCAG	GTTGTTATTA	ACCCCAACTT	2400
45	CGAGGTTGCA	GAATCCGATT	ACTCCAACAA	CATCATGAAA	TGCAGGAGCC	GCTATGACGG	2460
	CCACCGCATC	TGGATGTACA	ACTGCCACAT	AGGTGGTTCC	TTCAGCGAAG	AGACGGAAAA	2520
	AAAGTTTGAG	CACCTTCAGC	GGCTCTTAAA	CAACCAAGCT	TCCCCGAGT	AAAGAAGCCT	2580
	CCGTGGTCAA	CTCCTGTCTT	CAGGCCACAC	CACATCTTCC	ATGGGACTTC	CCCCCAACAA	2640
	CTGAGTCTGA	ACGAATGCCA	CGTGCCCTCA	CCCAGCCCGG	CCCCCACCCT	GTCCAGACCC	2700
50	CTACAGCTGT	GTCTAAGCTC	AGGAGGAAAG	GGACCCCTCC	ATCATTTCAT	GGGGGCTGCT	2760
	ACCTGACCTT	TGGGGCCTGA	GAAGGCCTTG	GGGGGGTGGG	GTTTGTCCAC	AGAGCTGCTG	2820
	GAGCAGCACC	AAGAGCCAGT	CTTGACCGGG	ATGAGGCCCA	CAGACAGGTT	GTCATCAGCT	2880
	TGTCCCATTC	AAGCCACCGA	GCTCACCACA	GACACAGTGG	AGCCGCGCTC	TTCTCCAGTG	2940
	ACACGTGGAC	AAATGCGGGC	TCATCAGCCC	CCCCAGAGAG	GGTCAGGCCG	AACCCCATTT	3000
55	CTCCTCTCT	TAGGTCAATT	TCAGCAAACT	TGAATATCTA	GACCTCTCTT	CCAATGAAAC	3060
	CCTCCAGTCT	ATTATAGTCA	CATAGATAAT	GGTGCCACGT	GTTTCTGAT	TTGGTGAGCT	3120
	CAGACTTGGT	GCTTCCCTCT	CCACAACCCC	CACCCCTTGT	TTTTCAAGAT	ACTATTATTA	3180
	TATTTTCACA	GACTTTTGAA	GCACAAATTT	ATTGGCATTT	AATATTGGAC	ATCTGGGCCC	3240
	TTGGAAGTAC	AAATCTAAGG	AAAAACCAAC	CCACTGTGTA	AGTGACTCAT	CTTCTGTGTG	3300
60	TGCCAATTCT	GTGGGTTT	GATTCAACGG	TGCTATAACC	AGGGTCTCTG	GTGACAGGGC	3360
	GCTCACTGAG	CACCATGTGT	CATCACAGAC	ACTTACACAT	ACTTGAAACT	TGGAATAAAA	3420
	GAAAGATTTA	TG					

Seq ID No: 109 Protein sequence:
Protein Accession #: NP_002309.1

	1	11	21	31	41	51	
70	MERPLCSHLC	SCLAMLALLS	PLSLAQYDSW	PHYPEYFQQP	APEYHQPPAP	ANVAKIQLRL	60
	AGQKRKHSEG	RVEVYYDQGW	GTVCDDDFSI	HAAHVVCREL	GVVEAKSWTA	SSSYGKGEGP	120
	IWLNLHCTG	NEATLAACTG	NGWGVTDCKH	TEDVGVVCS	KRIPGFKFDN	SLINQIENLN	180
	IQVEDIRIRA	ILSTYRKRTG	VMEGYVEVKE	GKTWKQICDK	HWTAKNSRVV	CGMFGFPGER	240
	TYNTKVYKMF	ASRRKQRYWP	FSMDCTGTEA	HISSCKLGPQ	VSLDPMKNVT	CENGLPAVVS	300
75	CVPGQVFSPD	GPSRFRKAYK	PEQPLVRLRG	GAYIGGRVVE	VLKNGEWGTV	CDKWDLVSA	360
	SVVCRELGFG	SAKEAVTGSR	LQGIGIPIHL	NEIQCTGNEK	SIIDCKFNAE	SQGCNHEEDA	420

GVRCNTPAMG LQKKLRINGG RNPYEGRVEV LVERNGSLVW GMVCGQNWGI VEAMVVCRL 480
 GLGFASNAFQ ETWYWHGDVN SNKVVMGSKV CSGTELSLAH CRHDGEDVAC PQGGVQYAG 540
 VACSETAPDL VLNAEMVQQT TYLEDPRMFM LQCAMEENCL SASAAQTDPT TGYRRLLRFS 600
 5 SQIHNNQSD FRPKNGRHAW IWHDCRRHYH SMEVFTHYDL LNLNGTKVAE GHKASFCLD 660
 TECEGDIQKN YECANFGDQG ITMGCWDMYR HDIDCQWVDI TDVPPGDYLF QVVINPNFEV 720
 AESDYSNNIM KCRSRYDHR IWMYNCHIGG SFSEETEKKF EHFSGLLNQ LSPQ

Seq ID NO: 110 DNA sequence

Nucleic Acid Accession #: none found, CAT_73007_3

Coding sequence: 1-495 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
15	<u>GGG</u> ACGCGTG	GGTCGACCCA	CGCGTCCGCC	CACGCGTCCG	TATGGACAGA	GCCTCCACTG	60
	GCTGCTGCCT	GCCCGCCACA	TACCCAGCTG	ACATGGGCAC	CGCAGGAGCC	ATGCAGCTGT	120
	CTGGGTGATC	CTGGGCTTCC	TCCTGTTCCG	AGGCCACAAC	TCCAGCCCA	CAATGACCCA	180
	ACCTCTAGCT	CTCAGGAGG	CCTTGCGGT	CTAAGTCTGA	CCACAGAGCC	AGTTTCTTCC	240
	ACCCAGGATA	CATCCCTTCC	TCAGAGGCTA	ACAGGCCAAG	CCATCTGTCC	AGCACTGGTA	300
20	CCCAGGCGCA	GGTGTCCCA	GCAGTGAAG	AGACGGAGG	ACAAGCAGAG	ACACATTTCA	360
	ACTGTTCCCC	CCAATTCAAC	CACCATGAGC	CTGAGCATGA	GGGAAGATGC	GACCATCCTG	420
	CCAGCCCCAC	GTCAGAGACT	GTGCTCACTG	TGGCTGCATT	TGGGATGGAG	TCGGGTGGAG	480
	GCCCCTCTG	GCTAGGGGG	GGCAGGCTGA	GAGCTCACCT	GTTCAGCAGA	GAAGTGGAAC	540
	CACCTTTGCTC	CTGGAGCCTG	TCTACCACAG	TGTTATCAGC	TTTATTGTCA	TCCTGGTGGT	600
25	GTGGTGATCA	TCCTAGTTGG	TGTGGTCAGC	CTGAGGGTTC	AGTGTCCGAA	GAGCAAGGAG	660
	TCTGAAGATC	CCAGAACCTG	GGAGTACAGG	GCGTGTCTGA	CAAGCTGGTC	ACAGACCATG	720
	GCGAGAACGA	CAGCATCGCC	CATTATCACA	TGGAAGACAT	CACACGACTT	AGGGCAACAC	780
	GCACTCAGCA	GCGAGCATCA	AAGGAGCCTA	CGCATGGCCC	AGACTGAGAG	CAAGCACAAA	840
	GGG						

Seq ID No: 111 Protein sequence:

Protein Accession #: none found, CAT_73007_3

	1	11	21	31	41	51	
35	RTRGSTHASA	HASVWTEPPL	AAACPPHTQL	TWAPQEPESC	LGDPGLPPVP	RPQLPAHNDP	60
	TSSSQGGLGG	LSLTTEPVSS	TQDTSLPQRL	TGQAICPALV	PRRRCPQQWK	RRRHKQRHIS	120
	TVPNSTTMS	LSMREDATIL	PAPRQLCSL	WLHLGWSRVE	AHSG		

Seq ID NO: 112 DNA sequence

Nucleic Acid Accession #: NM_005424.1

Coding sequence: 37-3453 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
45	CGCTCGTCCT	GGTCGGCCTG	GGTCGGCCTC	TGGAGTATGG	TCTGGCGGGT	GCCCCCTTTC	60
	TGCTCCCCA	TCCTCTTCTT	GGCTTCTCAT	GTGGGCGCGG	CGGTGGACCT	GACGCTGCTG	120
50	GCCAACCTGC	GGCTCACGGA	CCCCCAGCGC	TTCTTCTCTGA	CTTGCCTGTC	TGGGGAGGCC	180
	GGGGCGGGGA	GGGGCTCGGA	CGCTTGGGGA	CGCCCCCTGC	TGCTGGAGAA	GGACGACCGT	240
	ATCGTGCGCA	CCCCGCCCCG	GCCACCCCTG	CGCCTGGCGC	GCAACGGTTC	GCACAGGTGC	300
	ACGCTTCGCG	GCTTCTCCAA	GCCCTCGGAC	CTCGTGGGCG	TCTTCTCTCTG	CGTGGGCGGT	360
	GCTGGGGCGC	GGCGCACGCG	CGTCATCTAC	GTGCACAACA	GCCCTGGAGC	CCACCTGCTT	420
55	CCAGACAAGG	TCACACACAC	TGTGAACAAA	GGTGACACCG	CTGTACTTTC	TGCACGTGTG	480
	CACAAGGAGA	AGCAGACAGA	CGTGATCTGG	AAGAGCAACG	GATCCTACTT	CTACACCCTG	540
	GACTGGCATG	AAGCCCAGGA	TGGGCGGTTC	CTGCTGCAGC	TCCCAAATGT	GCAGCCACCA	600
	TCGAGCGGCA	TCTACAGTGC	CACCTTACCTG	GAAGCCAGCC	CCCTGGGCAG	CGCCTTCTTT	660
	CGGCTCATCG	TGCGGGGTTG	TGGGGCTGGG	CGCTGGGGGC	CAGGCTGTAC	CAAGGAGTGC	720
60	CCAGGTGTGC	TACATGGAGG	TGTCTGCCAC	GACCATGACG	GCGAATGTGT	ATGCCCCCTT	780
	GGCTTCACTG	GCACCCGCTG	TGAACAGGCC	TGCAGAGAGG	GCCGTTTTGG	GCAGAGCTGC	840
	CAGGAGCAGT	GCCCAGGCAT	ATCAGGCTGC	CGGGGCCTCA	CCTTCTGCCT	CCCAGACCCC	900
	TATGGCTGCT	CTTGTGGATC	TGGCTGGAGA	GGAAGCCAGT	GCCAAGAAGC	TTGTGCCCTT	960
	GGTCATTTTG	GGGCTGATTG	CCGACTCCAG	TGCCAGTGTG	AGAATGGTGG	CACCTTGTGAC	1020
65	CGGTTCACTG	GTTGTGTCTG	CCCCTCTGGG	TGGCATGGAG	TGCACTGTGA	GAAGTCAGAC	1080
	CGGATCCCCC	AGATCCTCAA	CATGGCCTCA	GAAGTGGAGT	TCAACTTAGA	GACGATGCCC	1140
	CGGATCAACT	GTGCAGCTGC	AGGGAACCCC	TTCCCCGTGC	GGGGCAGCAT	AGAGCTACGC	1200
	AAGCCAGACG	GCACTGTGCT	CCTGTCCACC	AAGGCCATTG	TGGAGCCAGA	GAAGACCACA	1260
	GCTGAGTTTC	AGGTGCCCCG	CTTGGTTCTT	GCGGACAGTG	GCTTCTGGGA	GTGCCGTGTG	1320
70	TCCACATCTG	GCGGCCAAGA	CAGCCGGCGC	TTCAAGGTCA	ATGTGAAAGT	GCCCCCGGTG	1380
	CCCCTGGCTG	CACCTCGGCT	CCTGACCAAG	CAGAGCCGCC	AGCTTGTGGT	CTCCCCGTG	1440
	GTCTCGTTCT	CTGGGGATGG	ACCCATCTCC	ACTGTCCGCC	TGCACTACCC	GCCCCAGGAC	1500
	AGTACCATGG	ACTGGTCGAC	CATTGTGGTG	GACCCAGTGC	AGAACGTGAC	GTTAATGAAC	1560
	CTGAGGCCAA	AGACAGGATA	CAGTGTTCGT	GTGCAGCTGA	GCCGGCCAGG	GGAAGGAGGA	1620
75	GAGGGGGCCT	GGGGGCCTCC	CACCTCATGT	ACCACAGACT	GTCCTGAGCC	TTTGTTCAG	1680
	CCGTGGTTGG	AGGGCTGGCA	TGTGGAAGGC	ACTGACCGGC	TGCGAGTGAG	CTGGTCCTTG	1740
	CCCTTGGTGC	CCGGGCCACT	GGTGGGCGAC	GTTTCTCTGC	TGCGCCTGTG	GGACGGGACA	1800

CGGGGGCAGG AGCGGCGGGA GAACGTCTCA TCCCCCAGG CCCGCACTGC CCTCCTGACG 1860
 GGACTCACGC CTGGCACCCA CTACCAGCTG GATGTGCAGC TCTACCACTG CACCCTCCTG 1920
 GGCCCGGGCT CGCCCCCTGC ACACGTGCTT CTGCCCCCCA GTGGGCTCC AGCCCCCGA 1980
 CACCTCCACG CCCAGGCCCT CTCAGACTCC GAGATCCAGC TGACATGGAA GCACCCGAG 2040
 5 GCTCTGCCTG GGCCAATATC CAAGTACGTT GTGGAGGTGC AGGTGGCTGG GGGTGCAGGA 2100
 GACCCACTGT GGATAGACGT GGACAGGCCT GAGGAGACAA GCACCATCAT CCGTGGCCTC 2160
 AACGCCAGCA CGCGCTACCT CTTCCGCTG CGGGCCAGCA TTCAGGGGCT CGGGGACTGG 2220
 AGCAACACAG TAGAAGAGTC CACCTGGGC AACGGGCTGC AGGCTGAGGG CCCAGTCCAA 2280
 GAGAGCCGGG CAGCTGAAGA GGGCCTGGAT CAGCAGCTGA TCCTGGCGGT GGTGGGCTCC 2340
 10 GTGTCTGCCA CCTGCCTCAC CATCCTGGCC GCCCTTTTAA CCTGGTGTG CATCCGAGA 2400
 AGCTGCCTGC ATCGGAGACG CACCTTCACC TACCAGTCAG GCTCGGGCGA GGAGACCATC 2460
 CTGCAGTTCA GCTCAGGGAC CTTGACACTT ACCCGGCGGC CAAAACCTGA GCCCGAGCCC 2520
 CTGAGCTACC CAGTGCTAGA TTGGGAGGAC ATCACCTTTG AGGACCTCAT CGGGGAGGGG 2580
 AACTTCGGCC AGGTCATCCG GGCCATGATC AAGAAGGACG GGCTGAAGAT GAACGCAGCC 2640
 15 ATCAAATATG TGAAAGAGTA TGCCTCTGAA AATGACCATC GTGACTTTGC GGGAGAACTG 2700
 GAAGTTCTGT GCAAATTGGG GCATCACCCC AACATCATCA ACCTCCTGGG GGCCTGTAAG 2760
 AACCGAGGTT ACTTGTATAT CGCTATTGAA TATGCCCCCT ACGGGAACCT GCTAGATTTT 2820
 CTGCGGAAAA GCCGGGTCTT AGAGACTGAC CCAGCTTTTG CTGAGAGCA TGGACAGCC 2880
 TCTACCTTTA GCTCCCGGCA GCTGCTGCGT TTCGCCAGTG ATGCGGCCAA TGGCATGCAG 2940
 20 TACCTGAGTG AGAAGCAGTT CATCCACAGG GACCTGGCTG CCGGAAATGT GCTGGTCGGA 3000
 GAGAACCTAG CCTCCAAGAT TGCAGACTTC GGCCTTTCTC GGGGAGAGGA GGTATTATGT 3060
 AAGAAGACGA TGGGGCGTCT CCTGTGCGC TGGATGGCCA TTGAGTCCCT GAACTACAGT 3120
 GTCTATACCA CCAAGAGTGA TGTCTGGTCC TTTGGAGTCC TTCTTTGGGA GATAGTGAGC 3180
 CTTGGAGGTA CACCCTACTG TGGCATGACC TGTGCCGAGC TCTATGAAAA GCTGCCCCAG 3240
 25 GGCTACCGCA TGGAGCAGCC TCGAAACTGT GACGATGAAG TGTACGAGCT GATGCGTCAG 3300
 TGCTGGCGGG ACCGTCCTTA TGAGCGACCC CCCTTTGCCC AGATTGCGCT ACAGCTAGGC 3360
 CGCATGCTGG AAGCCAGGAA GGCCTATGTG AACATGTCGC TGTITGAGAA CTTCACTTAC 3420
 GCGGCGATTG ATGCCACAGC TGAGGAGGCC TGAGCTGCCA TCCAGCCAGA ACCTGGCTCT 3480
 GCTGGCCGGA GCAAATCTCT CTGTCTAACC TGTGACCACT CTGACCCCTA CAGCCTCTGA 3540
 30 CTTAAGCTGC CTCAAGGAAT TTTTAACT TAAGGGAGAA AAAAAGGAT CTGGGGATGG 3600
 GGTGGGCTTA GGGGAACCTG GTTCCCATGC TTTGTAGGTG TCTCATAGCT ATCCTGGGCA 3660
 TCCTTCTTTC TAGTTCACTG GCGCCACAGG TGTGTTTCCC ATCCCACTGC TCCCCCAACA 3720
 CAAACCCCCA CTCCAGCTCC TTCGCTTAAG CCAGCACTCA CACCACTAAC ATGCCCTGTT 3780
 CAGCTACTCC CACTCCCGGC CTGTCACTCA GAAAAAATA AATGTTCTAA TAAGCTCCAA 3840
 35 AAAAA

Seq ID No: 113 Protein sequence
 Protein Accession #: NP_005415.1

40 1 11 21 31 41 51
 | | | | |
 MVWRVPPFL PILFLASHVG AAVDLTLLAN LRLTDPQRF LTCVSGEAGA GRGSDAWGPP 60
 LLLLEKDDRIV RTPPGPPLRL ARNGSHQVTL RGFSPKPSDLV GVFSVCGGAG ARRTRVIYVH 120
 NSPGAHLPLD KVTHTVNKG TAVLSARVHK EKQTDVIWKS NGSYFYTLDW HEAQDGRFLL 180
 45 QLPNVQPPSF GIYSATYLEA SPLGSAFFRL IVRGCGAGRW GPGCTKECPG CLHGGVCHDH 240
 DGEVCVPPGF TGTRCEQACR EGRFGQSCQE QCPGISGCRG LTFCLPDPYG CSCGSGWRGS 300
 QCQEACAPGH FGADCRLOQC CQNGGTCDFR SGCVCPSGWH GVHCEKSDRI PQILNMASEL 360
 EFNLETMPRI NCAAGNPPF VRGSIELRKP DGTVLLSTKA IVEPEKTTAE FEVPRVLVAD 420
 SGFWECRVST SGGQDSRRFK VNVKVPVPL AAPRLLTQKS RQLVVSPLVS FSGDGPSTV 480
 50 RLHYRPQDST MDWSTIVDP SENVTLMNLR PKTGYSVRVQ LSRPGEKGEG AWGPPTLMTT 540
 DCPELLQPW LEGWHVEGT RLRVSWSLPL VPGPLVGDGF LLRLWDGTRG QERRENVSSP 600
 QARTALLTGL TPGTHYQLDV QLYHCTLLGP ASPPAHVLLP PSGPPAPRHL HAQALSDSEI 660
 QLTWKHPEAL PGISKYVVE VQVAGGAGDP LWIDVDRPEE TSTIIRGLNA STRYLFMRRA 720
 SIQGLGDWSN TVEESTLNG LQAEQPVQES RAAEGLDQO LILAVVGSVS ATCLTILAL 780
 55 LTLVCIRRS LHRRTFTYQ SGSGETILQ FSSGTLTLTR RPKLQPEPLS YPVLEWEDIT 840
 FEDLIGENF QGVIRAMIK DGLKMNAIK MLKEYASEND HRDFAGELEV LCKLGHHPNI 900
 INLLGACKNR GYLIAIEYA PYGNLLDFLR KSRVLETDPA FAREHGTAST LSSRQLLRFA 960
 SDAANGMQYL SEKQFIHRDL AARNVLVGEN LASKIADFGL SRGEEVYVK TMGRLPVRWM 1020
 60 AIESLNYSVY TTKSDVWSFG VLLWEIVSLG GTPYCGMTCA ELYEKLFGY RMEQPRNCDD 1080
 EYVBLMRQW RDRPYERPPF AQIALQLGRM LEARKAYVNM SLFENFTYAG IDATAEEA

Seq ID NO: 114 DNA sequence

Nucleic Acid Accession #: NM_002632.1

Coding sequence: 322-771 (underlined sequences correspond to start and stop codons)

65 1 11 21 31 41 51
 | | | | |
 GGGATTCGGG CCGCCAGCT ACGGGAGGAC CTGGAGTGGC ACTGGGCGCC CGACGGACCA 60
 TCCCGGGGAC CCGCTGCCC CTCGGCGCCC CGCCCGCCC GGCCGCTCCC CGTCGGGTTC 120
 CCCAGCCACA GCCTTACCTA CGGGCTCCTG ACTCCGCAAG GCTTCCAGAA GATGCTCGAA 180
 CCACCGGCG CGGCTCGGG GCAGCAGTGA GGGAGGCGTC CAGCCCCCA CTCAGCTCTT 240
 CTCTCTCTGT GCCAGGGGCT CCGCGGGGTA TGAGCATGGT GGTTTTCCCT CGGAGCCCCC 300
 TGGCTCGGGA CGTCTGAGAA GATCCGGT ATGAGGCTGT TCCCTTGCTT CCTGCAGCTC 360
 75 CTGGCCGGGC TGGCGCTGCC TGCTGTGCC CCCCAGCAGT GGGCCTTGTC TGCTGGGAAC 420
 GGCTCGTCAG AGGTGGAAGT GGTACCCTTC CAGGAAGTGT GGGGCCGCG CTAAGTCCGG 480

5 GCGCTGGAGA GGCTGGTGGA CGTCGTGTCC GAGTACCCCA GCGAGGTGGA GCACATGTTC 540
 AGCCCATCCT GTGTCTCCCT GCTGCGCTGC ACCGGCTGCT GCGGCGATGA GAATCTGCAC 600
 TGTGTGCCCG TGGAGACGGC CAATGTACAC ATGCAGCTCC TAAAGATCCG TTCTGGGGAC 660
 CGGCCCTCCT ACGTGGAGCT GACGTTCTCT CAGCACGTTT GCTGCGAATG CCGGCTCTGT 720
 CCGGAGAAGA TGAAGCCGGA AAGGTGCGGC GATGCTGTTT CCCGGAGGTA ACCCACCCCT 780
 TGGAGGAGAG AGACCCCGCA CCCGGCTCGT GTATTTATTA CCGTCACACT CTTCAAGTGAC 840
 TCCTGCTGGT ACCTGCCCTC TATTTATTAG CCAACTGTTT CCCTGCTGAA TGCCTCGCTC 900
 CCTTCAAGAC GAGGGGACAG GAAGGACAGG ACCCTCAGGA ATTCAAGTGC TTCAACAACG 960
 10 TGAGAGAAAG AGAGAAGCCA GCCACAGACC CCTGGGAGCT TCCGCTTTGA AAGAAGCAAG 1020
 ACACGTGGCC TCGTAGAGGG CAAGCTAGGC CCCAGAGGCC CTGGAGGTCT CCAGGGGCCT 1080
 GCAGAAGGAA AGAAGGGGGC CCTGCTACCT GTTCTTGGGC CTAGGCTCT GCACAGACAA 1140
 GCAGCCCTTG CTTTCGGAGC TCCTGTCCAA AGTAGGGATG CGGATTCTGC TGGGGCCGCC 1200
 ACGGCTGGT GGTGGGAAGG CCGGCAGCGG GCGGAGGGGA TTCAGCCACT TCCCCCTCTT 1260
 CTTCTGAAGA TCAGAACATT CAGCTCTGGA GAACAGTGGT TGCCTGGGGG CTTTGGCCAC 1320
 15 TCCTTGTCCC CCGTGATCTC CCCTCACACT TTGCCATTG CTGTACTGG GACATTGTTC 1380
 TTTCCGGCCG AGGTGCCACC ACCCTGCCCC CACTAAGAGA CACATACAGA GTGGGCCCCG 1440
 GGCTGGAGAA AGAGTGCCTT GGATGAGAAA CAGCTCAGCC AGTGGGGATG AGGTCAACAG 1500
 GGGAGGAGCC TGTGCGTCCC AGCTGAAGGC AGTGGCAGGG GAGCAGGTTT CCAAGGGCC 1560
 20 CTGGCACCCC CACAAGCTGT CCCTGCAGGG CCATCTGACT GCCAAGCCAG ATTCTCTTGA 1620
 ATAAAGTATT CTAGTGTGGA AACGC

Seq ID No: 115 Protein sequence:

Protein Accession #: NP_002623.1

25 1 11 21 31 41 51
 | | | | |
 MPVMRLFPFC LQLLAGLALP AVPPQWALS AGNGSSEVEV VPFQEVWGRS YCRALERLVD 60
 VVSEYPSVEE HMFSPSCVSL LRCTGCCGDE NLHCVPVETA NVTMQLLKIR SGDRPSYVEL 120
 TFSQHVRCEB RPLREKMKPE RCGDAVPRR

Seq ID NO: 116 DNA sequence

Nucleic Acid Accession #: NM_007361.1

Coding sequence: 1-4131 (underlined sequences correspond to start and stop codons)

35 1 11 21 31 41 51
 | | | | |
 ATGGAGGGGG ACCGGGTGGC CGGGCGGCCG GTGCTGTCGT CGTTACCAGT GCTACTGCTG 60
 CTGCAGTTGC TAATGTTGCG GGCCGCGGCG CTGCACCCAG ACGAGCTCTT CCCACACGGG 120
 40 GAGTCGTGGT GGGACCACTT CCTGCAGGAA GGCAGCAGCG TAAAGCTCAG CCGTGGTGAA 180
 GCTGGCGAAT CCCGTGCACT TCTTACGAAG CCCGATTGAG CAACCTCTAC GTGGGCACCA 240
 ACGGCATCAT CTCCACTCAG GACTTCCCCA GGGAAACGCA GTATGTGGAC TATGATTTC 300
 CCACCGACTT CCCGGCCATC GCCCTTTTTC TGGCGGACAT CGACACGAGC CACGGCAGAG 360
 GCCGAGTCCT GTACCGAGAG GACACCTCCC CCGCAGTGCT GGGCCTGGCC GCCCGCTATG 420
 45 TGCGCGCTGG CTTCCCGCGC TCTGCGCGCT TTTTACCCCC ACCCAGCCCT TCCTGGCCAC 480
 CTGGGAGCAG GTAGGCGCTT ACGAGGAGGT CAAACGCGGG CGCTGCCCTC GGGAGAGCTG 540
 AACACTTTCC AGGCAGTTT GGCATCTGAT GGGTCTGATA GCTACGCCCT CTTTCTTTAT 600
 CCTGCCAAGC GCGTGCAGTT CCTTGGAAAC CGCCCCAAG AGTCTTACAA TGTCCAGCTT 660
 CAGCTTCCAG CTCGGGTGGG CTTCTGCCGA GGGGAGGCTG ATGATCTGAA GTCAGAAGGA 720
 50 CCATATTTCA GCTTGACTAG CACTGAACAG TCTGTGAAAA ATCTCTATCA ACTAAGCAAC 780
 CTGGGGATCC CTGGAGTGTG GGCTTTCCAT ATCGGCAGCA CTTCCCCGTT GGACAATGTC 840
 AGGCCAGCTG CAGTTGGAGA CCTTTCCGCT GCCCACTCTT CTGTTCCCTT GGGACGTTCC 900
 TTCAGCCATG CTACAGCCCT GGAAAGTGAC TATAATGAGG ACAATTTGGA TTACTACGAT 960
 GTGAATGAGG AGGAAGCTGA ATACCTTCCG GGTGAACCCAG AGGAGGCATT GAATGGCCAC 1020
 55 AGCAGCATTG ATGTTTCTTT CCAATCCAAA GTGGATACAA AGCCTTTAGA GGAATCTTCC 1080
 ACCTTGGATC CTCACACCAA AGAAGGAACA TCTCTGGGAG AGGTAGGGGG CCCAGATTTA 1140
 AAAGGCCAAG TTGAGCCCTG GGATGAGAGA GAGACCAGAA GCCCAGCTCC ACCAGAGGTA 1200
 GACAGAGATT CACTGGCTCC TTCCTGGGAA ACCCCACCAC CGTACCCCGA AAACGGAAGC 1260
 ATCCAGCCCT ACCCAGATGG AGGGCCAGTG CCTTCGGAAA TGGATGTTCC CCCAGCTCAT 1320
 60 CCTGAAGAAG AAATGTTTCT TCGAAGTTAC CCTGCTTCAG GTCACACTAC ACCCTTAAGT 1380
 CGAGGGACGT ATGAGGTGGG ACTGGAAGAC AACATAGGTT CCAACACCGA GGTCTTCACG 1440
 TATAATGCTG CCAACAAGGA AACCTGTGAA CACAACCACA GACAATGCTC CCGGCATGCC 1500
 TTCTGCACGG ACTATGCCAG TGGCTTCTGC TGCCACTGCC AATCCAAGTT TTATGGAAAT 1560
 GGGAGCACT GTCTGCCTGA GGGGGCACCT CACCGAGTGA ATGGGAAAGT GAGTGGCCAC 1620
 65 CTCACGTTGG GCCATACACC CGTGCACTTC ACTGATGTGG ACCTGCATGC GTATATCGTG 1680
 GGCATGATG GCAGAGCCTA CACGGCCATC AGCCACATCC CACAGCCAGC AGCCCAAGGC 1740
 CTCCTCCCCC TCACACCAAT TGGAGGCCTG TTTGGCTGGC TCTTTGCTTT AGAAAAACCT 1800
 GGCTCTGAGA ACGGCTTCAG CCTCGCAGGT GCTGCCTTTA CCCATGACAT GGAAGTTACA 1860
 TTCTACCCGG GAGAGGAGAC GGTTCGTATC ACTCAAACTG CTGAGGGACT TGACCCAGAG 1920
 70 AACTACCTGA GCATTAAGAC CAACATCAA GGCCAGGTGC CTTACGTCCC AGCAAATTTT 1980
 ACAGCCCACA TCTCTCCCTA CAAGGAGCTG TACCACTACT CCGACTCCAC TGTGACCTCT 2040
 ACAAGTTTCA GAGACTACTC TCTGACTTTT GGTGCAATCA ACCAAACATG GTCCTACCGC 2100
 ATCCACCAGA ACATCACTTA CCAGGTGTGC AGGCACGCCC CCAGACACCC GTCCTTCCCC 2160
 ACCACCCAGC AGCTGAACCT GGACCGGGTC TTTGCCTTGT ATAATGATGA AGAAAGAGTG 2220
 75 CTTAGATTGG CTGTGACCAA TCAAATTGGC CCGGTCAAAG AAGATTGAGA CCCCACTCCG 2280
 GTGAATCCTT GCTATGATGG GGTGACACAA CAGCACGGTG CCATCCAGGG 2340
 ACAGGTGTAG ATTACACCTG TGAGTGCGCA TCTGGGTACC AGGGAGATGG ACGGAACCTG 2400

	GTGGATGAAA	ATGAATGTGC	AACTGGCTTT	CATCGCTGTG	GCCCCAACTC	TGTATGTATC	2460
	AACTTGCCCTG	GAAGCTACAG	GTGTGAGTGC	CGGAGTGGTT	ATGAGTTTGC	AGATGACCGG	2520
	CATACTTGCA	TCTTGATCAC	CCCACCTGCC	AACCCCTGTG	AGGATGGCAG	TCATACCTGT	2580
5	GCTCCTGCTG	GGCAGGCCCG	GTGTGTTTAC	CATGGAGGCCA	GCACGTTTCTG	CTGTGCTTGC	2640
	CTGCCTGGTT	ATGCCCGCGA	TGGGCACACG	TGCACTGATG	TAGATGAATG	CTCAGAAAAC	2700
	AGATGTCACC	CTGCAGCTAC	CTGTCTACAA	ACTCCTGGTT	CCTTCTCCTG	CCGTGTGCAA	2760
	CCCGGATATT	ATGGGGATGG	ATTTCAGTGC	ATACCTGACT	CCACCTCAAG	CCTGACACCC	2820
	TGTGAACAAC	AGCAGCGCCA	TGCCCAGGCC	CAGTATGCCT	ACCCCTGGGGC	CCGGTTCCAC	2880
	ATCCCCCAAT	GCGACGAGCA	GGGCAACTTC	CTGCCCCCTAC	AGTGTTCATG	CAGCACTGGT	2940
10	TTCTGCTGGT	GCGTGGACCC	TGATGGTCAT	GAACTTCCTG	GTACCCAGAC	TCCACCTGGC	3000
	TCCACCCCGC	CTCACTGTGG	ACCATCACCA	GAGCCCAACC	AGAGGCCCCC	GACCATCTGT	3060
	GAGCGCTGGA	GGGAAAACCT	GCTGGAGCAC	TACGGTGGCA	CCCCCGGAGA	TGACCAGTAC	3120
	GTGCCCCAGT	GCGATGACCT	GGGCCACTTC	ATCCCCCTGC	AGTGCCACGG	AAAGAGCGAC	3180
	TTCTGCTGGT	GTGTGGACAA	AGATGGCAGA	GAGGTGCAGG	GCACCCGCTC	CCAGCCAGGC	3240
15	ACCACCCCTG	CGTGTATACC	CACCGTCGCT	CCACCCATGG	TCCGGCCCCC	GCCCCGGCCA	3300
	GATGTGACCC	CTCCATCTGT	GGGCACCTTC	CTGCTCTATA	CTCAGGGCCA	GCAGATGGC	3360
	TACTTACCCC	TCAATGGCAC	CAGGCTTCAG	AAGGATGCAG	CTAAGACCTT	GCTGTCTCTG	3420
	CATGGCTCCA	TAATCGTGGG	AATTGATTAC	GACTGCCGGG	AGAGGATGGT	GTACTGGACA	3480
	GATGTTGCTG	GACGGACAAT	CAGCCGTGCC	GGTCTGGAAC	TGGGAGCAGA	GCCTGAGACG	3540
20	ATCGTGAATT	GAGGTCTGAT	AAGCCCTGAA	GGACTTGCCA	TAGACCACAT	CCGCAGAACCA	3600
	ATGTACTGGA	CGGACAGTGT	CCTGGATAAG	ATAGAGAGCG	CCCTGCTGGA	TGGCTCTGAG	3660
	CGCAAGGTCC	TCTTCTACAC	AGATCTGGTG	AATCCCCCGT	CCATCGCTGT	GGATCCAATC	3720
	CGAGGCAACT	TGTACTGGAC	AGACTGGAAT	AGAGAAGCTC	CTAAAATTGA	AACGTCTCT	3780
	TTAGATGGAG	AAAACAGAA	AATTCTGATC	AATACAGACA	TTGGATTGCC	CAATGGCTTA	3840
25	ACCTTTGACC	CTTCTCTTAA	ACTGCTCTGC	TGGGCAGATG	CAGGAACCAA	AAAACCTGGG	3900
	TGTACACTAC	CTGATGGAAC	TGGACGGCGT	GTCATTCAAA	ACAACCTCAA	GTACCCCTTC	3960
	AGCATCGTAA	CTCTGTGACA	TCACTTCTAC	CACACAGACT	GGAGGAGGGA	TGGTGTGTA	4020
	TCAGTAAATA	AACATAGTGG	CCAGTTTACT	GATGAGTATC	TCCAGAACCA	ACGATCTCAC	4080
	CTCTACGGGA	TAACCTGCAGT	CTACCCCTAC	TGCCCAACAG	GAGAAAGTA	AGTACAGTAA	4140
30	TGTAAAGGAA	GACTTGGAGT	TTACAATCAC	AACCTGGACC	CTAAAGAACA	GTGACTGCAA	4200
	AGGCAAAAGAA	AGTAAAAAAG	GAATTGGCCA	TTAGACGTTT	CTGAGCATCC	AAGATGAACA	4260
	TTTTGTAGTG	CAAAAAGACT	TTTGTGAAAA	GCTGATACCT	CAATCTTTAC	TACTGTATTT	4320
	TTAAAAATGA	AGGTTGTTAT	TGCAAGTTTA	AAAAGGTAAC	AGAATTTTAA	CTGTTGCTTA	4380
	TTAAAGCAAC	TTCTTGTAAA	CATTTATCAT	TAATATTTAA	AAGATCAAA	TCATTCAACT	4440
35	AAGAATTAGA	GTTTAAAGCT	CTAAACCTGA	TTTTTGCCAT	GGATTCCTTC	TGGCCAAGAA	4500
	ATTAAAGCAC	ATGTGATCAA	TATAACAATA	TAATCCTAAA	CCTTGACAGT	TGGAGAAGCC	4560
	AATGCAGAAC	TGATGGGAAA	GGACCAATTA	TTTATAGTTT	CCCAACAAAA	GTTCTAAGAT	4620
	TTTTTACCTC	TGCATCAGTG	CATTTCTATT	TATATCAAAA	GGTGCTAAAA	TGATTCAATT	4680
	TGCATTTTCT	GATCCTGTAG	TGCCTCTATA	GAAGTACCCA	CAGAAAGTAA	AGTATCACAT	4740
40	TTATAAATAC	CAAAGATGTA	ACAATTTTAA	AATTTTCTAG	ATTACTCCAA	TAAAGTGTTT	4800
	TAAGTTTAAA	AAAAAAAAAA	AAAAAAAAAA				

Seq ID No: 117 Protein sequence
Protein Accession #: NP_031387.1

	1	11	21	31	41	51	
	MEGDRVAGRP	VLSSLPVLLL	LQLMLRAAA	LHPDELFPHG	ESWWDQLLQE	GDDVKLSRGE	60
50	AGESPALLTK	PDSATSTWAP	TASSPLRTSP	GKRSMTWMTIS	PPTSRRPSPLF	WRTSTRATAE	120
	AESCERTTPP	PCWAWPPAM	CALASRALRA	FYPHPRLPGH	LGAGRRRLRG	QTRALPSGEL	180
	NTFQAVLASD	GSDSYALFLY	PANGLQFLGT	RPKESYNVQL	QLPARVGFPCR	GEADDLKSEG	240
	PYFSLTSTEQ	SVKNLYQLSN	LGIIPGVWAFH	IGSTSPLDNV	RPAAVGDLA	AHSSVPLGRS	300
	FSHATALESD	YNEDNLDYYD	VNEEEAEYLP	GEPEEALNGH	SSIDVSFQSK	VDTKPLEESS	360
55	TLDPHTKEGT	SLGEVGGPDL	KQQVEPWDER	ETRSPAPPEV	DRDSLAPSWE	TPPPYPENG	420
	IQPYPDGGPV	PSEMDVPPAH	PEEEIVLRSY	PASGHTTPLS	RGTYEVGLED	NIGSNTTEVFT	480
	YNAANKETCE	HNHRQCSRHA	FCTDYATGFC	CHCQSKFYGN	GKHCLPEGAP	HRVNGKVS	540
	LHVGHTPVHF	TDVDLHAYIV	GNDGRAYTAI	SHIPQPAQA	LLPLTPIGGL	FGWLFALKEP	600
	GSENGFSLAG	AAFTHDMEVT	FYPGEETVRI	TQTAEGLDPE	NYLSIKTNIQ	GQVPYVPANF	660
60	TAHISPYKEL	YHYSDSVTFS	TSSRDYSLTF	GAINQTWSYR	IHQNTYQVC	RHAPRHPSFP	720
	TTQQLNVDRV	FALYNDEERV	LRFAVTNQIG	PVKEDSDPTP	VNPDYDGS	CDTTARCHPG	780
	TGVDYTCECA	SGYQDGRNC	VDENECATGF	HRCGPNSVCI	NLPGSYRCEC	RSGYEFADDR	840
	HTCILITPPA	NPCEDGSHTC	APAGQARCVH	HGGSTFSCAC	LPGYAGDGHQ	CTDVDECSN	900
	RCHPAATCYN	TPGSFSCRCQ	PGYGDGFQ	IPDSTSSLTP	CEQQQRHAQA	QYAYPGARFH	960
65	IPQCDEQGNF	LPLQCHGSTG	FCWCVDPDGH	EVPGTQTPPG	STPPHCGPS	EPTQRPPTIC	1020
	ERWRENLEH	YGGTPRDDQY	VPQCDDLGHF	IPQCHGKSD	FCWCVDKDR	EVQGRSQPG	1080
	TTPACITPVA	PPMVRPTPRP	DVTPPSVGT	LLYTQGGQIG	YLPLNGTRLQ	KDAAKTLLSL	1140
	HGSIIIVGIDY	DCRERMVYWT	DVAGRTISRA	GLELGAEPET	IVNSGLISPE	GLAIDHIRRT	1200
	MYWTDVLDK	IESALLDGSE	RKVLFTYDLV	NPRAIAVDPI	RGNLYWTDWN	REAPKIETSS	1260
70	LDGENRRILI	NTDIGLPNGL	TFDPFSKLLC	WADAGTKKLE	CTLDPGTGR	VIQNNLKYPF	1320
	SIVSYADHFI	HTDWRDGVV	SVNKHSGQFT	DEYLPEQRSH	LYGITAVYPI	CPTGRK	

Seq ID NO: 118 DNA sequence

Nucleic Acid Accession #: NM_003088.1

Coding sequence: 112-1593 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
	GCGGAGGGTG	CGTGCGGGCC	GCGGCAGCCG	AACAAAGGAG	CAGGGGCGCC	GCCGCAGGGA	60
5	CCCCCACC	ACCTCCCGGG	GCCGCGCAGC	GGCCTCTCGT	CTACTGCCAC	CATGACCGCC	120
	AACGGCACAG	CCGAGGCGGT	GCAGATCCAG	TTCGGCCTCA	TCAACTGCGG	CAACAAGTAC	180
	CTGACGGCCG	AGGCGTTTCG	GTTCAAGGTG	AACGCGTCCG	CCAGCAGCCT	GAAGAAGAAG	240
	CAGATCTGGA	CGCTGGAGCA	GCCCCCTGAC	GAGGCGGGCA	GCGCGGCCGT	GTGCCTGCGC	300
	AGCCACCTGG	GCCGCTACCT	GCGGCGGAC	AAGGACGGCA	ACGTGACCTG	CGAGCGCGAG	360
10	GTGCCCCGTC	CCGACTGCCG	TTTCTCATC	GTGGCGCAGC	ACGACGGTCG	CTGGTCTGCTG	420
	CAGTCCGAGG	CGCACC GGCG	CTACTTCGGC	GGCACCAGAG	ACCGCCTGTC	CTGCTTCGCG	480
	CAGACGGTGT	CCCCCGCCGA	GAAGTGGAGC	GTGCACATCG	CCATGCACCC	TCAGGTCAAC	540
	ATCTACAGTG	TCAACCGTAA	GCGCTACGCG	CACCTGAGCG	GCGGCGCGC	CGACGAGATC	600
	GCCGTGGACC	GCGACGTGCC	CTGGGCGGTC	GACTCGCTCA	TCACCTCTGC	CTTCCAGGAC	660
	CAGCGCTACA	CGGTGCAGAC	CGCCGACCAC	CGCTTCCTGC	GCCACGACGG	GCGCCTGGTG	720
15	GCGCGCCCCG	AGCCGGCCAC	TGGCTACACG	CTGGAGTTC	GCTCCGGCAA	GGTGGCCTTC	780
	CGCGACTGCG	AGGGCCGTTA	CCTGGCGCCG	TCGGGGCCCA	GCGGCACGCT	CAAGGCGGGC	840
	AAGGCCACCA	AGGTGGGCAA	GGACGAGCTC	TTTGCTCTGG	AGCAGAGCTG	CGCCAGGTC	900
	GTGCTGCAGG	CGGCCAACGA	GAGGAACGTG	TCCACGCGCC	AGGGTATGGA	CCTGTCTGCC	960
20	AATCAGGACG	AGGAGACCGA	CCAGGAGACC	TTCCAGCTGG	AGATCGACCG	CGACACCAA	1020
	AAGTGTGCCT	TCCGTACCCA	CACGGGCAAG	TACTGGACGC	TGACGGCCAC	CGGGGGCGTG	1080
	CAGTCCACCG	CCTCCAGCAA	GAATGCCAGC	TGCTACTTTG	ACATCGAGTG	GCGTGACCGG	1140
	CGCATCACAC	TGAGGGCGGT	CAATGGCAAG	TTTGTGACCT	CCAAGAAGAA	TGGGCAGCTG	1200
	GCCGCTCGG	TGGAGACAGC	AGGGGACTCA	GAGCTCTTCC	TCATGAAGCT	CATCAACCGC	1260
25	CCCATCATCG	TGTTCCGCGG	GGAGCATGGC	TTCATCGGCT	GCCGCAAGGT	CACGGGCACC	1320
	CTGGACGCCA	ACCCTCCAG	CTATGACGTC	TTCCAGCTGG	AGTTCAACGA	TGGCGCCTAC	1380
	AACATCAAAG	ATCCACAGG	CAAATACTGG	ACGGTGGGCA	GTGACTCCG	GGTCACCAGC	1440
	AGCGGCGACA	CTCCTGTGGA	CTTCTTCTTC	GAGTTCTGCG	ACTATAACAA	GGTGGCCATC	1500
	AAGGTGGGCG	GGCGCTACCT	GAAGGGCGAC	CACGCAGGCG	TCCTGAAGGC	CTCGGCGGAA	1560
30	ACCGTGGACC	CCGCTCGCT	CTGGGAGTAC	TAGGGCCGGC	CCGTCTTCC	CCGCCCCCTG	1620
	CCACATGGCG	GCTCCTGCCA	ACCCTCCCTG	CTAACCCCTT	CTCCGCCAGG	TGGGCTCCAG	1680
	GGCGGGAGGC	AAGCCCCCTT	GCCTTTCAAA	CTGGAAACCC	CAGAGAAAAC	GGTGCCCCCA	1740
	CCTGTCGCCC	CTATGGACTC	CCCCTCTCTC	CCTCCGCCCC	GGTTCCCTAC	TCCCCCTCGG	1800
	TCAGCGGCTG	CGGCTTGGCC	CTGGGAGGGA	TTTCAGATGC	CCCTGCCCTC	TTGTCTGCCA	1860
35	CGGGGCGAGT	CTGGCACCTC	TTTCTTCTGA	CCTCAGACGG	CTCTGAGCCT	TATTTCTCTG	1920
	GAAGCGGCTA	AGGGACGGTT	GGGGGCTGGG	AGCCCTGGGC	GTGTAGTGTA	ACTGGAATCT	1980
	TTTGCCTCTC	CCAGCCACCT	CCTCCAGGCC	CCCCAGGAGA	GCTGGGCACA	TGTCCCAAGC	2040
	CTGTCACTGG	CCCTCCCTGG	TGCACTGTCC	CCGAAACCCC	TGCTTGGGAA	GGGAAGCTGT	2100
	CGGGAGGGCT	AGGACTGACC	CTTGTGGTGT	TTTTTTGGGT	GGTGGCTGGA	AACAGCCCTT	2160
40	CTCCACGTC	GGAGAGGCTC	AGCCTGGCTC	CCTTCCCTGG	AGCGGCAGGG	CGTGACGGCC	2220
	ACAGGGTCTG	CCCGCTGCAC	GTTCTGCCAA	GGTGGTGGTG	GCGGGCGGGT	AGGGGTGTGG	2280
	GGGCCGTCTT	CCTCCTGTCT	CTTTCCTTTC	ACCCTAGCCT	GACTGGAAGC	AGAAAATGAC	2340
	CAAATCAGTA	TTTTTTTTTA	TGAAATATTA	TTGTCTGGAG	CGTCCCAGGC	AAGCCTGGCT	2400
	GATAGTAGCA	GTGATCTGGC	GGGGGCGGTC	TCAGCACCTC	CCCCAGGGGG	TGCATCTCAG	2460
45	CCCCCTCTTT	CCGTCTCTCC	CGTCCAGCCC	CAGCCCTGGG	CCTGGGCTGC	CGACACCTGG	2520
	GCCAGAGCCC	CTGCTGTGAT	TGGTGCTCCC	TGGGCTCTCC	GGGTGGATGA	AGCCAGGCGT	2580
	CGCCCCCTCC	GGGAGCCCTG	GGGTGAGCCG	CCGGGGCCCC	CCTGCTGCCA	GCCTCCCCCG	2640
	TCCCCAACAT	GCATCTCACT	CTGGGTGTCT	TGGTCTTTTA	TTTTTTGTAA	GTGTATTG	2700
50	TATAACTCTA	AACGCCCATG	ATAGTAGCTT	CAAACCTGGA	ATAGCGAAAT	AAAATAACTC	2760
	AGTCTGCG						

Seq ID No: 119 Protein sequence:
Protein Accession #: NP_003079.1

	1	11	21	31	41	51	
	MTANGTAEAV	QIQFGLINCG	NKYLTAEAFG	FKVNASASSL	KKKQIWTLEQ	PPDEAGSAAV	60
55	CLRSHLGRYL	AADKDGNVTC	EREVPGPDCR	FLIVAHDDGR	WSLQSEAHRR	YFGGTEDRLS	120
	CFAQTVSPA	KWSVHIAMHP	QVNIYSVTRK	RYAHLASARE	DEIAVD RDVP	WGVDSLITLA	180
60	FQDQRYSVQT	ADHRFLRHDG	RLVARPEPAT	GYTLEFRSGK	VAFRDCEGRY	LAPSGPSGTL	240
	KAGKATKVGK	DELFALEQSC	AQVVLQAANE	RNVSTRQGM	LSANQDEETD	QETFQLEIDR	300
	DTKKCAFRT	TGKYWTLTAT	GGVQSTASSK	NASCYFDIEW	RDRRITLRAS	NGKPVTSKKN	360
	GQLAASVETA	GDSEFLMKL	INRPIIVFRG	EHGFIGCRKV	TGTL DANRSS	YDVFQLEFND	420
65	GAYNIKDSTG	KYWTVGSDSA	VTSSGDPVD	FFFEFC DYNK	VAIKVGGRYL	KGDHAGVLKA	480
	SAETVDPASL	WEY					

Seq ID NO: 120 DNA sequence
Nucleic Acid Accession #: NM_006404.1
Coding sequence: 25-741 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
75	CAGGTCCGGA	GCCTCAACTT	CAGGATGTTG	ACAACATTGC	TGCCGATACT	GCTGCTGTCT	60
	GGCTGGGCGT	TTTG TAGCCA	AGACGCCTCA	GATGGCCTCC	AAAGACTTCA	TATGCTCCAG	120
	ATCTCCTACT	TCCGCGACCC	CTATCAGCTG	TGGTACCAGG	GCAACGCGTC	GCTGGGGGGA	180

CACCTAACGC ACGTGCTGGA AGGCCCAGAC ACCAACACCA CGATCATTCA GCTGCAGCCC 240
 TTGCAGGAGC CCGAGAGCTG GGCGCGCAGC CAGAGTGGCC TGCAGTCCTA CCTGCTCCAG 300
 TTCCACGGCC TCGTGCCTCT GGTGCACACG GAGCGGACCT TGGCCTTTCC TCTGACCATC 360
 CGCTGCTTCC TGGGCTGTGA GCTGCCTCCC GAGGGCTCTA GAGCCCATGT CTTCTTCGAA 420
 GTGGCTGTGA ATGGGAGCTC CTTTGTGAGT TTCCGGCCCG AGAGAGCCTT GTGGCAGGCA 480
 GACACCCAGG TCACCTCCGG AGTGGTCACC TTCACCTGCG AGCAGCTCAA TGCCTACAAC 540
 CGCACTCGGT ATGAAGTGGC GGAATTCCTG GAGGACACCT GTGTGCAGTA TGTGCAGAAA 600
 CATATTTCCG CGGAAAACAC GAAAGGGAGC CAAACAAGCC GCTCCTACAC TTCGCTGGTC 660
 CTGGGCGTCC TGGTGGGCGG TTTCATCATT GCTGGTGTGG CTGTAGGCAT CTTCTGTGTC 720
 ACAGGTGGAG GCGCATGTGA ATTACTCTCC AGCCCCGTCA GAAGGGGCTG GATTGATGGA 780
 GGTGTGGCAG GGAAGTTTTC AGCTCACTGT GAAGCCAGAC TCCCCAAGT AAACACCAGA 840
 AGGTTTGGAG TGACAGCTCC TTTCTTCTCC CACATCTGCC CACTGAAGAT TTGAGGGAGG 900
 GGAGATGGAG AGGAGAGGTG GACAAAGTAC TTGGTTTGCT AAGAACCCTAA GAACGTGTAT 960
 GCTTTGCTGA ATTAGTCTGA TAAGTGAATG TTTATCTATC TTTGTGGAAA ACAGATAATG 1020
 GAGTTGGGSC AGGAAGCCTA TGCGCCATCC TCCAAAGACA GACAGAATCA CCTGAGGCGT 1080
 TCAAAAGATA TAACCAATA AACAAAGTCAT CCACAATCAA AATACAACAT TCAATACTTC 1140
 CAGGTGTGTC AGACTTGGGA TGGGACGCTG ATATAATAGG GTAGAAAGAA GTAACACGAA 1200
 GAAGTGGTGG AAATGTAAAA TCCAAGTCAT ATGGCAGTGA TCAATTATTA ATCAATTAAT 1260
 AATATTAATA AATTCTTAT ATTT

Seq ID No: 121 Protein sequence:
 Protein Accession #: NP_006395.1

1 11 21 31 41 51
 MLTTLPLILL LSGWAFCSQD ASDGLQRLHM LQISYFRDPY HVWYQGNASL GGHLTHVLEG 60
 PDTNTTIIQL QPLQEPESWA RTQSGLQSYL LQFHGLVRLV HQERTLAPPL TIRCFGLGCEL 120
 PPEGSRAHV FEVAVNGSSF VSFRPERALW QADTQVTSKV VTFTLQQLNA YNRTRYELRE 180
 FLEDTCVQYV QKHISAENTK GSQTSRSYTS LVLGVLVGGF IIAGVAVGIF LCTGGRRC

Seq ID NO: 122 DNA sequence
 Nucleic Acid Accession #: none found
 Coding sequence: 2-505 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 CGAGAAGCTG GGAGAGACAC CACTTGTCCC TGAACAAGAC AATTCAGTAA CATCTATTCC 60
 TGAGATTCCT CGATGGGGAT CACAGAGCAC GATGTCTACC CTTCAAATGT CCCTTCAAGC 120
 CGAGTCAAAG GCCACTATCA CCCCATCAGG GAGCGTGATT TCCAAGTTTA ATTCTACGAC 180
 TTCCTCTGCC ACTCCTCAGG CTTTCGACTC CTCCTCTGCC GTGGTCTTCA TATTGTGTAG 240
 CACAGCAGTA GTAGTGTGG TGATCTTGAC CATGACAGTA CTGGGGCTTG TCAAGCTCTG 300
 CTTTCACGAA AGCCCCCTCT CCCAGCCAAG GAAGGAGTCT ATGGGCCCGC CGGGCCTGGA 360
 GAGTGATCCT GAGCCCGCTG CTTTGGGCTC CAGTCTTGCA CATTGCACAA ACAATGGGGT 420
 GAAAGTCGGG GACTGTGATC TGCGGGACAG AGCAGAGGGT GCCTTGCTGG CGGAGTCCCC 480
 TCTTGGCTCT AGTGATGAT AGGGAAACAG GGGACATGGG CACTCCTGTG AACAGTTTTT 540
 CACTTTTGTAT GAAACGGGGA ACCAAGAGGA ACTTACTTGT GTAACGTACA ATTTCTGCAG 600
 AAATCCCCCT TCCTCTAAAT TCCCTTTACT CCACTGAGGA GCTAAATCAG AACTGCACAC 660
 TCCTTCCTCT ATGATAGAGG AAGTGGAAGT GCCTTTAGGA TGGTGATACT GGGGGACCGG 720
 GTAGTGTCTG GGAGAGATAT TTTCTTATGT TTATTCGGAG AATTGTGAGA AGTGATTGAA 780
 CTTTTCAGAA CATTGGAAAC AAATAGAACA CAATATAATT TACATTAAAA AATAATTTCT 840
 ACCAAAATGG AAAGGAAATG TTCTATGTTG TTCAGGCTAG GAGTATATTG GTTCGAAATC 900
 CCAGGGAAAA AAATAAAAT AAAAAATTAA AGGATTGTTG ATAAAA

Seq ID No: 123 Protein sequence:
 Protein Accession #: none found

1 11 21 31 41 51
 EKLGETPLVP EQDNSVTSIP EIPRWGSQST MSTLQMSLQA ESKATITPSG SVISKFNSTT 60
 SSATPQAFDS SSAVVVFIVS TAVVVLVILT MTVLGLVKLC PHESPSSQPR KESMGPPGLE 120
 SDPEPAALGS SSAHCTNNGV KVGDCDLRDR AEGALLAES LGSSDA

Seq ID NO: 124 DNA sequence
 Nucleic Acid Accession #: NM_006500.1
 Coding sequence: 27-1967 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 ACTTGCCTCT CGCCCTCCGG CCAAGCATGG GGCTTCCCAG GCTGGTCTGC GCCTTCTTGC 60
 TCGCCGCTCT CTGCTGCTGT CCTCGCGTCG CGGGTGTGCC CGGAGAGGCT GAGCAGCTCT 120
 CGCTGAGCT GGTGGAGGTG GAAGTGGGCA GCACAGCCCT TCTGAAGTGC GGCCTCTCCC 180
 AGTCCCAAG CAACCTCAGC CATGTGCACT GGTTTTCTGT CCACAAGGAG AAGCGGACGC 240
 TCATCTTCCG TGTGCGCCAG GGCCAGGGCC AGAGCGAACC TGGGGAGTAC GAGCAGCGGC 300
 TCAGCCTCCA GGACAGAGGG GCTACTCTGG CCCTGACTCA AGTCACCCCC CAAGACGAGC 360

	GCATCTTCTT	GTGCCAGGGC	AAGCGCCCTC	GGTCCCAGGA	GTACCGCATC	CAGCTCCGCG	420
	TCTACAAAGC	TCCGGAGGAG	CCAAACATCC	AGGTCAACCC	CCTGGGCATC	CCTGTGAACA	480
	GTAAAGGAGC	TGAGGAGGTC	GCTACCTGTG	TAGGGAGGAA	CGGGTACCCC	ATTCTCAAG	540
5	TCATCTGGTA	CAAGAAATGGC	CGGCCCTCTG	AGGAGGAGAA	GAACCGGGTC	CACATTCAAGT	600
	CGTCCCAGAC	TGTGGAGTCG	AGTGGTTTGT	ACACCTTGCA	GAGTATTCTG	AAGGCACAGC	660
	TGGTTAAAGA	AGACAAAGAT	GCCCAGTTTT	ACTGTGAGCT	CAACTACCGG	CTGCCCAGTG	720
	GGAAACCACAT	GAAGGAGTCC	AGGGAAGTCA	CCGTCCCTGT	TTTCTACCCG	ACAGAAAAAG	780
	TGTGGCTGGA	AGTGGAGCCC	GTGGGAATGC	TGAAGGAAGG	GGACCGCGTG	GAAATCAGGT	840
10	GTTTGGCTGA	TGGCAACCCCT	CCACCACACT	TCAGCATCAG	CAAGCAGAAC	CCCAGCACCA	900
	GGGAGGCAGA	GGAAGAGACA	ACCAACGACA	ACGGGGTCTT	GGTGTCTGGAG	CCTGCCCGGA	960
	AGGAACACAG	TGGGCGCTAT	GAATGTCAGG	CCTGGAACCT	GGACACCATG	ATATCGCTGC	1020
	TGAGTGAACC	ACAGGAACCTA	CTGGTGAAC	ATGTGTCTGA	CGTCCGAGTG	AGTCCCGCAG	1080
	CCCCTGAGAG	ACAGGAAGGC	AGCAGCCTCA	CCCTGACCTG	TGAGGCAGAG	AGTAGCCAGG	1140
15	ACCTCGAGTT	CCAGTGGCTG	AGAGAAGAGA	CAGACCAGGT	GCTGGAAAGG	GGGCCTGTGC	1200
	TTCAGTTGCA	TGACCTGAAA	CGGGAGGCAG	GAGGCGGCTA	TCGCTGCGTG	CGCTCTGTGC	1260
	CCAGCATACC	CGGCCTGAAC	CGCACACAGC	TGGTCAAGCT	GGCCATTTTT	GGCCCCCTT	1320
	GGATGGCATT	CAAGGAGAGG	AAGGTGTGGG	TGAAAGAGAA	TATGGTGTGG	AATCTGTCTT	1380
	GTGAAGCGTC	AGGGCACCCT	CGGCCACCA	TCTCTGGAA	CGTCAACGGC	ACGGCAAGTG	1440
20	AACAAGACCA	AGATCCACAG	CGAGTCTCTG	GCACCCTGAA	TGTCCTCGTG	ACCCCGGAGC	1500
	TGTTGGAGAC	AGGTGTTGAA	TGCACGGCCT	CCAACGACCT	GGGCAAAAAC	ACCAGCATCC	1560
	TCTTCTCGGA	GCTGGTCAAT	TTAACCACCC	TCACACCAGA	CTCCAACACA	ACCACTGGCC	1620
	TCAGCACTTC	CACTGCCAGT	CCTCATACCA	GAGCCAACAG	CACCTCCACA	GAGAGAAAGC	1680
	TGCCGGAGCC	GGAGAGCCGG	GGCGTGGTCA	TGCTGGCTGT	GATTGTGTGC	ATCCTGGTCC	1740
25	TGGCGGTGCT	GGGCGCTGTC	CTCTATTTCC	TCTATAAGAA	GGGCAAGCTG	CCGTGCAGGC	1800
	GCTCAGGGAA	GCAGGAGATG	ACGCTGCCCT	CGTCTCGTAA	GACCGAACTT	GTAGTTGAAG	1860
	TTAAGTCAGA	TAAGCTCCCA	GAAGAGATGG	GCCTCCTGCA	GGGCAGCAGC	GGTGACAAGA	1920
	GGGCTCCGGG	AGACCAGGGA	GAGAAATACA	TCGATCTGAG	GCATTAGCCC	CGAATCACTT	1980
	CAGCTCCCTT	CCCTGCCTGG	ACCATTCCCA	GCTCCTGCT	CACCTTTCTC	TCAGCCAAG	2040
30	CCTCCAAAGG	GACTAGAGAG	AAGCCTCCTG	CTCCCCCTAC	CTGCACACCC	CCTTTCAGAG	2100
	GGCCACTGGG	TTAGGACCTG	AGGACCTCAC	TTGGCCCTGC	AAGCCGCTTT	TCAGGGACCA	2160
	GTCCACCACC	ATCTCCTCCA	CGTTGAGTGA	AGCTCATCCC	AAGCAAGGAG	CCCCAGTCTC	2220
	CCGAGCGGGT	AGGAGAGTTT	CTTGCCAGAAC	GTGTTTTTTC	TTTACACACA	TTATGGCTGT	2280
	AAATACCTGG	CTCCTGCCAG	CAGCTGAGCT	GGGTAGCCTC	TCTGAGCTGG	TTTCTGCCC	2340
35	CAAAGGCTGG	CTTCCACCAT	CCAGGTGCAC	CACCTGAAGT	AGGACACACC	GGAGCCAGGC	2400
	GCCTGTCTAT	GTTGAAGTGC	GCTGTTCACA	CCGCTCCCG	AGAGCACCCC	AGCGGCATCC	2460
	AGAAGCAGCT	GCAGTGTGTC	TGCCACCACC	CTCCTGTCTG	CCTCTTCAAA	GTCTCCTGTG	2520
	ACATTTTTTC	TTGGTCCAGA	AGCCAGGAAC	TGGTGTCAAT	CCTTAAAAGA	TACGTGCCGG	2580
	GGCCAGGTGT	GGTGGCTCAC	GCCTGTAATC	CCAGCACTTT	GGGAGGCCGA	GGCGGGCGGA	2640
40	TCACAAAGTC	AGGACGAGAC	CATCCTGGCT	AACACGGTGA	AACCCTGTCT	CTACTAAAAA	2700
	TACAAAAAAA	AATTAGCTAG	GGTAGTGGT	TGGCACCTAT	AGTCCCAGCT	ACTCGGAAGG	2760
	CTGAAGCAGG	AGAATGGTAT	GAATCCAGGA	GGTGGAGCTT	GCAGTGAGCC	GAGACCGTGC	2820
	CACTGCACTC	CAGCCTGGGC	AACACAGCGA	GACTCCGCTC	CGAGGAAAAA	AAAAGAAAAG	2880
	ACGCGTACCT	GCGGTGAGGA	AGCTGGGCGC	TGTTTTCGAG	TTCAGGTGAA	TTAGCCTCAA	2940
45	TCCCCGTGTT	CACTTGTCTC	CATAGCCCTC	TTGATGGATC	ACGTAAAACT	GAAAGGCAGC	3000
	GGGGAGCAGA	CAAAGATGAG	GTCTACACTG	TCCTTCATGG	GGATTAAAGC	TATGGTTATA	3060
	TTAGCACCAA	ACTTCTACAA	ACCAAGCTCA	GGGCCCCAAC	CCTAGAAGGG	CCCAAATGAG	3120
	AGAATGGTAC	TTAGGGATGG	AAAAACGGGC	CTGGCTAGAG	CTTCGGGTGT	GTGTGTCTGT	3180
	CTGTGTGTAT	GCATACATAT	GTGTGTATAT	ATGGTTTTGT	CAGGTGTGTA	AATTTGCAAA	3240
50	TTGTTTCCTT	TATATATGTA	TGTATATATA	TATATGAAAA	TATATATATA	TATGAAAAAT	3300
	AAAGCTTAAT	TGTCCCGAAA	AATCATACAT	TGCTTTTTTA	TTCTACATGG	GTACCACAGG	3360
	AACCTGGGGG	CCTGTGAAAC	TACAACCAAA	AGGCACACAA	AACCGTTTCC	AGTTGGCAGC	3420
	AGAGATCAGG	GGTTACCTCT	GCTTCTGAGC	AAATGGCTCA	AGCTCTACCA	GAGCAGACAG	3480
	CTACCCTACT	TTTCAGCAGC	AAAACGTCCC	GTATGACGCA	GCACGAAGGG	CCTGGCAGGC	3540
55	TGTTAGCAGG	AGCTATGTCC	CTTCTATCG	TTTCCGTCCA	CTT		

Seq ID No: 125 Protein sequence
 Protein Accession #: NP_006491.1

60	1	11	21	31	41	51	
	MGLPRLVCAF	LLAACCCCPR	VAGVPGEAEQ	PAPELVEVEV	GSTALLKCGL	SQSQGNLSHV	60
	DWFSVHKEKR	TLIFRVRQGG	QSEPEGEYEQ	RLSLQDRGAT	LALTQVTPQD	ERIFLCQGR	120
65	PRSQEYRIQL	RVYKAPPEEPN	IQVNLGIPV	NSKEPEEVAT	CVGRNGYPIPI	QVIWYKNGRP	180
	LKEEKNRVHI	QSSQTVESG	LYTLQSLKLA	QLVKEDKDAQ	FYCELYRLP	SGNHMKESRE	240
	VTVPVFPYTE	KVWLEVEPVG	MLKEGDRVEI	RCLADGNPPP	HFSISKQNP	TREAEETTIN	300
	DNGVLVLEPA	RKEHSGRYEC	QAWNLDTMIS	LLSEPQELLV	NYVSDVRVSP	AAPERQEGSS	360
	LTLTCEAESS	QDLEFPWLRE	ETDQVLERGP	VLQLHDLKRE	AGGGYRCVAS	VPSIPGLNRT	420
70	QLVKLAIFGP	PWMAFKERKV	WVKENMVLNL	SCEASGHPRP	TISWNVNGTA	SEQDQDPQRV	480
	LSTLNVLVTP	ELLETVGECT	ASNDLGKNTS	ILFLELVNLT	TLTPDSNTTT	GLSTSTASPH	540
	TRANSTSTER	KLPEPESRGV	VIVAVIVCIL	VLAVLGAVLY	FLYKKGKLP	RRSGKQSEITL	600
	PPSRKTELTV	EVKSDKLPEE	MGLLQSSSGD	KRAPGDQGEK	YIDLRLH		

Seq ID NO: 126 DNA sequence
 Nucleic Acid Accession #: NM_001955.1

Coding sequence: 337-975 (underlined sequences correspond to start and stop codons)

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      AGCTCTCCAC CACCGCCGCG TCGCCTGCA GACGCTCCGC TCGTGCCTT CTCTCCTGGC 180
      AGGCGCTGCC TTTTCTCCCC GTTAAAGGGC ACTTGGGCTG AAGGATCGCT TTGAGATCTG 240
10     AGGAACCCGC AGCGCTTTGA GGGACCTGAA GCTGTTTTTC TTCTTTTTCC TTTGGGTTCA 300
      GTTTGAACGG GAGGTTTTTT ATCCCTTTTT TTCAGAAATG ATTATTTGCT CATGATTTTC 360
      TCTCTGCTGT TTGTGGCTTG CCAAGGAGCT CCAGAAACAG CAGTCTTAGG CGCTGAGCTC 420
      AGCGCGGTGG GTGAGAACGG CGGGGAGAAA CCCACTCCCA GTCCACCCTG GCGGCTCCGC 480
      CGGTCCAAGC GCTGCTCTCG CTCGTCCCTG ATGGATAAAG AGTGTGTCTA CTTCTGCCAC 540
15     CTGGACATCA TTTGGGTCAA CACTCCCGAG CACGTTGTTC CGTATGGACT TGAAGCCCT 600
      AGGTCCAAGA GAGCCTTGGA GAATTTACTT CCCACAAAGG CAACAGACCG TGAGAATAGA 660
      TGCCAAATGTG CTAGCCAAAA AGACAAGAAG TGCTGGAATT TTTGCCAAGC AGGAAAAGAA 720
      CTCAGGGCTG AAGACATTAT GGAGAAAGAC TGGAAATAAT ATAAGAAAGG AAAAGACTGT 780
      TCCAAGCTTG GGAAGAAAGT TATTATATCAG CAGTTAGTGA GAGGAAGAAA AATCAGAAGA 840
20     AGTTCAGAGG AACACCTAAG ACAAACCCAG TCGGAGACCA TGAGAAACAG CGTCAAATCA 900
      TCTTTTCATG ATCCCAAGCT GAAAGGCAAG CCCTCCAGAG AGCGTTATGT GACCCACAAC 960
      CGAGCACATT GGTGACAGAC TTCGGGGCCT GTCTGAAGCC ATAGCTCCA CGGAGAGCCC 1020
      TGTGGCCGAC TCTGCACTCT CCACCCTGGC TGGGATCAGA GCAGGAGCAT CCTCTGCTGG 1080
      TTCTGACTG GCAAAGGACC AGCGTCTCTG TTCAAACAT TCCAAGAAAG GTTAAGGAGT 1140
25     TCCCCAACCC ATCTTCACTG GCTTCCATCA GTGGTAACTG CTTTGGTCTC TTCTTTCATC 1200
      TGGGGATGAC AATGGACCTC TCAGCAGAAA CACACAGTCA CATTGGAATT C

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Seq ID No: 127 Protein sequence:

Protein Accession #: NP_001946.1

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35     KECVYFCHLD IIVWNTPEHV VPYGLGSPRS KRALENLLPT KATDRENRCQ CASQKDKKCW 120
      NFCQAGKELR AEDIMEKDWK NHKKGKDCSK LGKKCIYQQL VRGRKIRRSS BEHLRQTRSE 180
      TMRNSVKSSF HDPKLKGKPS RERYVTHNRA HW

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Seq ID NO: 128 DNA sequence

Nucleic Acid Accession #: NM_001721.1

Coding sequence: 34-2061 (underlined sequences correspond to start and stop codons)

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      CTTTTTGTGT TGACCAAAAC AAACCTTTCC TACTATGAAT ATGACAAAAT GAAAAGGGGC 180
      AGCAGAAAAG GATCCATTGA AATTAAGAAA ATCAGATGTG TGGAGAAAAG AAATCTCGAG 240
      GAGCAGACGC CTGTAGAGAG ACAGTACCCA TTTCAGATTG TCTATAAAGA TGGGCTTCTC 300
      TATGTTCTATG CATCAAATGA AGAGAGCCGA AGTCAGTGGT TGAAGGCATT ACAAAAAGAG 360
      ATAAGGGGTA ACCCCCACCT GCTGGTCAAG TACCATAGTG GGTTCCTCGT GGACGGGAAG 420
55     TTCCTGTGTT GCCAGCAGAG CTGTAAAGCA GCCCCAGGAT GTACCCTCTG GGAAGCATAT 480
      GCTAATCTGC ATACTGCAGT CAATGAAGAG AAACACAGAG TTCCCACCTT CCCAGACAGA 540
      GTGCTGAAGA TACCTCGGGC AGTTCCTGTT CTCAAAATGG ATGCACCATC TTCAAGTACC 600
      ACTCTAGCCC AATATGACAA CGAATCAAAG AAAAATATAT GCTCCAGGCC ACCATCTTCA 660
      AGTACCAGTC TAGCGCAATA TGACAGCAAC TCAAAGAAAA TCTATGGCTC CCAGCCAAAC 720
60     TTCAACATGC AGTATATTCC AAGGGAAGAC TTCCCTGACT GGTGGCAAGT AAGAAAACCTG 780
      AAAAGTAGCA GCAGCAGTGA AGATGTTGCA AGCAGTAACC AAAAAGAAAG AAATGTGAAT 840
      CACACCACCT CAAAGATTTC ATGGGAATTC CCTGAGTCAA GTTCATCTGA AGAAGAGGAA 900
      AACCTGGATG ATTATGACTG GTTTGCTGGT AACATCTCCA GATCACAATC TGAACAGTTA 960
      CTCAGACAAA AGGGAAGAAAG AGGAGCATTT ATGGTTAGAA ATTCGAGCCA AGTGGGAATG 1020
65     TACACAGTGT CCTTATTTAG TAAGGCTGTG AATGATAAAA AAGGAACTGT CAAACATTAC 1080
      CACGTGCATA CAAATGCTGA GAACAAATTA TACCTGGCAG AAAACTACTG TTTTGATTCC 1140
      ATTCCAAGGC TTATTCAATTA TCATCAACAC AATTGAGCAG GCATGATCAC ACGGCTCCGC 1200
      CACCCTGTGT CAACAAGGCG CAACAAGGTC CCCGACTCTG TGTCCCTGGG AAATGGAATC 1260
      TGGGAACCTGA AAAGAGAAGA GATTACCTTG TTGAAGGAGC TGGGAAGTGG CCAGTTTGGA 1320
70     GTGGTCCAGC TGGGCAAGTG GAAGGGGCGAG TATGATGTTG CTGTTAAGAT GATCAAGGAG 1380
      GGCTCCATGT CAGAAGATGA ATCTTTTCAG GAGGCCCAGA CTATGATGAA ACTCAGCCAT 1440
      CCCAAGCTGG TTAATTTCTA TGGAGTGTGT TCRAAGGAAT ACCCATATA CATAGTGAAT 1500
      GAATATATAA GCAATGGCTG CTTGCTGAAT TACCTGAGGA GTCACGGAAG AGGACTTGAA 1560
      CCTTCCAGC TCCTAGAAAT GTGCTACGAT GTCTGTGAAG GCATGGCCTT CTTGGAGAGT 1620
75     CACCAATTCA TACACCGGGA CTTGGCTGCT CGTAACTGCT TGGTGGACAG AGATCTCTGT 1680
      GTGAAAGTAT CTGACTTTGG AATGACAAGG TATGTTCTTG ATGACCAGTA TGTCAGTTCA 1740

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 5 CACGAGCTTC CAGAAAAGCG TCCCACATTT CAGCAACTCC TGTCTTCCAT TGAACCACTT 2040
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 CTGGCCAGCA TTTTCATTCA TTTTAAGGAA AGTAGGAAGG CATAAGTAAT TTTAGCTAGT 2160
 TTTTAATAGT GTTCTCTGTA TTGTCTATTA TTTAGAAATG AACAAGGCAG GAAACAAAAG 2220
 10 ATTCCTTGA AATTTAGATC AAATTAGTAA TTTTGTTTTA TGCTGCTCCT GATATAACAC 2280
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 AAAGACTGAG CAGAACTGAA AAATTACTTA TTGGATATTC ATTCCTTTCT TTATATTGTC 2400
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Seq ID No: 129 Protein sequence
 Protein Accession #: NP_001712.1

1 11 21 31 41 51
 20 MDTKSILEEL LLKRSQKKK MSPNNYKERL FVLTKTNLSY YEYDKMKRGS RKGSIEIKKI 60
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 HSGFFVDGKF LCCQQSCKAA PGCTLWEAYA NLHTAVNEEK HRVPTFPDRV LKIPRAVPVL 180
 KMDAPSSSTT LAQYDNESKK NYGSQPPSSS TSLAQYDSNS KKIYGSQPNF NMQYIPREDF 240
 25 PDWQVQRKLL SSSSSSEVAS SNQKERNVNH TTSKISWEFP SSSSSSEEEEN LDDYDWFAGN 300
 ISRSQSEQLL RQKGKEGAFM VRNSSQVGMV TVSLFSKAVN DKKGTVKHYH VHTNAENKLY 360
 LAENYCFDSI PKLIHYHQHN SAGMITRLRH PVSTKANKVP DSVSLNGNIW ELKREBITLL 420
 KELGSGQFGV VQLGKWKQGY DVAVKMIKEG SMSEDEFFQE AQTMMKLSHP KLVKFYGVCS 480
 KEYPIIYIVT YISNGCLLMY LRSHGKGLEP SQLLEMCYDV CEGMAPLESH QFIHRDLAAR 540
 30 NCLVDRDLCV KVSDFGMTRY VLDDQYVSSV GTKFPVKWSA PEVFHYFKYS SKSDVWAFGI 600
 LMWEVFSLGK QPYDLYDNSQ VVLKVSQGHR LYRPHLASDT IYQIMYSCWH ELPEKRPTFQ 660
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Seq ID NO: 130 DNA sequence
 Nucleic Acid Accession #: NM_012072.2
 Coding sequence: 149-2107 (underlined sequences correspond to start and stop codons)

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 40 AAAGCCCTCA GCCTTTGTGT CTTCTCTGTC GCCGGAGTGG CTGCAGCTCA CCCCTCAGCT 60
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 45 GCTGCTGCTC CTGACCCAGC CCGGGGCGGG GACGGGAGCT GACACGGAGG CGGTGGTCTG 240
 CGTGGGGACC GCCTGTACCA CGGCCCACTC GGGCAAGCTG AGCGCTGCCG AGGCCAGAA 300
 CCACTGCAAC CAGAACGGGG GCAACCTGGC CACTGTGAAG AGCAAGGAGG AGGCCAGCA 360
 CGTCCAGCGA GTACTGGCCC AGCTCCTGAG CGGGGAGGCA GCCCTGACGG CGAGGATGAG 420
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 50 GAAGGGCTTC AGCTGGGTGG GCGGGGGGGA GGACACGCCT TACTCTAACT GGCACAAGGA 540
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 GCTCCTTCCC AACCCTCTGC CCAAGTGGTC TGAGGGCCCC TGTTGGAGCC CAGGCTCCCC 660
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 GGCCCTGGGG GGCCCAAGTC AGGTGACCTA CACCACCCCC TTCCAGACCA CCAGTTCTCT 780
 55 CTTGGAGGCT GTGCCCTTTG CCTCTGCGGC CAATGTAGCC TGTGGGGAAG GTGACAAGGA 840
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 CTGCTGAAAG TGAGGTGGCC CTAGAGACAC TAGAGTCACC AGCCACCATC CTCAGAGCTT 2160

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10	AGCACAAAGT	TTGCTAAATG	TGATACTGTT	GACATCCTCC	AGAATGGCCA	GAAGTGCAAT	2700
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15	TGTGATCAAC	ACTAACAAAG	AAACAAATTC	AAGGACAACC	TGTCTTTGAG	CCAGGGCAGG	3000
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25	TGAGTATCTC	TGGGAGGGCT	CATGTCTCCT	GTGGGCTTTT	TACCACCACT	GTGCAGGAGA	3660
	ACAGACAGAG	GAAATGTGTC	TCCTCCCAAG	GCCCCAAAGC	CTCAGAGAAA	GGGTGTTTCT	3720
	GGTTTTGCGCT	TAGCAATGAG	TCGGTCTCTG	AGGTGACACT	CTGGAGTGGT	TGAAGGGCCA	3780
	CAAGGTGCAG	GGTTAATACT	CTTGCCAGTT	TTGAAATATA	GATGCTATGG	TTTCTAGTTG	3840
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35	CACCTTAAATA	AATGCAAATG	CAACATTTCT	CCCTCTGGGC	CTTGAAAATC	CTTGCCCTTA	4200
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	GCCCAGGCC	ATCGTCTGTT	CTCTGAATGC	AGCCCTGTTT	TCAACAACAG	GGAGGTCTATG	4380
	GAACCCCTCT	GTGGAACCCA	CAAGGGGAGA	AATGGGTGAT	AAAGAATCCA	GTTCTCTCAA	4440
	ACCTTCCCTG	GCAGGCTGGG	TCCCTCTCCT	GCTGGGTGGT	GCTTCTCTCT	GCACACCACT	4500
40	CCCACACCG	GGGGAGAGCC	AGCAACCCAA	CCAGACAGCT	CAGGTTGTGC	ATCTGATGGA	4560
	AACCACTGGG	CTCAAAACAG	TGCTTTATTC	TCTGTTTTAT	TTTTGCTGTT	ACTTTGAAGC	4620
	ATGGAATTC	TTGTTTGGGG	GATCTTGGGG	CTACAGTAGT	GGGTAAACAA	ATGCCACCCG	4680
	GCCAAGAGGC	CATTAAACAA	TCGTCTTGT	CCTGAGGGGC	CCCAGCTTGC	TCGGGCGTGG	4740
45	CACAGTGGGG	AATCCAAGGG	TCACAGTAGT	GGGAGAGGTG	CACCCTGCCA	CCTGCTAACT	4800
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	CATGGGGACG	GGGGAAGTTT	TCACTTGGAG	ATGGACACCA	AGACAATGAA	GATTTGTTGT	4920
	CCAAATAGGT	CAATAATTCT	GGGAGACTCT	TGGAAAAAAC	TGAATATATT	CAGGACCAAC	4980
	TCTCTCCCTC	CCCTCATCCC	ACATCTCAAA	GCAGACAATG	TAAAGAGAGA	ACATCTCACA	5040
	CACCCAGCTC	GCCATGCCTA	CTCATCTCCT	AATTTTCAGT	GCCATCACTG	CTCTTCTCTT	5100
50	CTTCTTTGTC	ATTTGAGAAA	GGATGCAGGA	GGACAATTCC	CACAGATAAT	CTGAGGAATG	5160
	CAGAAAAACC	AGGGCAGGAC	AGTTATCGAC	AATGCATTAG	AACTTGGTGA	GCATCCTCTG	5220
	TAGAGGGACT	CCACCCCTGC	TCAACAGCTT	GGCTTCCAGG	CAAGACCAAC	CACATCTGGT	5280
	CTCTGCCTTC	GGTGGCCAC	ACACCTAAGC	GTCTATCGTC	TTGCCATAGC	ATCATGATGC	5340
	AACACATCTA	CTGTAGTAGC	TACGACGTTA	TGTTTGGGTA	ATGTGGGGAT	GAAGTGCATG	5400
55	AGGCTCTGAT	TAAGGATGTG	GGGAAGTGGG	CTGCGGTCAC	TGTCGGCCTT	GCAAGGCCAC	5460
	CTGGAGGCCT	GTCTGTAGC	CAGTGGTGGG	GGAGCAAGGC	TTGAGGAAGG	GCCAGCCACA	5520
	TGCCATCTTC	CCTGCGATCA	GGCAAAAAAG	TGGAATTAAT	AAGTCAAACC	TTTATATGCA	5580
	TGTGTTATGT	CCATTTTGCA	GGATGAAC	AGTTTAAAG	AATTTTCTT	TCTCTTCAAG	5640
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60	TCTTTCTGAT	GATGGAGATG	ATCATTAGGT	ACTTTTGTTC	CAACCTTTAT	TCCTGTAAAT	5760
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	TCTCCATTGT	CTAAATCAGG	AAAACAGGAA	AACACAGCTT	TCTAGCAGCT	GCAAAATGGT	5940
65	TTAATGCCCC	CTACATATTT	CCATCACCTT	GAACAATAGC	TTTAGCTTGG	GAATCTGAGA	6000
	TATGATCCCCA	GAAAACATCT	GTCTCTACTT	CGGCTGCAAA	ACCCATGGTT	TAAATCTATA	6060
	TGGTTTGTGC	ATTTTCTCAA	CTAAAATAG	AGATGATAAT	CCGAATTTCT	CATATATTCA	6120
	CTAATCAAAG	ACACTATTTT	CATACTAGAT	TCCTGAGACA	AATACTCACT	GAAGGGCTTG	6180
	TTTAAAAATA	AAATTGTGTT	TGGTCTGTTT	TTGTAGATAA	TGCCCTTCTA	TTTTAGGTAG	6240
70	AAGCTCTGGA	ATCCCTTTAT	TGTGCTGTTG	CTCTTATCTG	CAAGGTGGCA	AGCAGTTCTT	6300
	TTCAGCAGAT	TTTGCCCACT	ATTCCTCTGA	GCTGAAGTTC	TTTGCATAGA	TTTGGCTTAA	6360
	GCTTGAATTA	GATCCCTGCA	AAGGCTTGCT	CTGTGATGTC	AGATGTAATT	GTAATGTGCA	6420
	GTAATCACTT	CATGAATGCT	AAATGAGAAT	GTAAGTATTT	TTAAATGTGT	GTATTTCAAA	6480
	TTTGTTTGAC	TAATTCTGGA	ATTACAAGAT	TTCTATGCAG	GATTTACCTT	CATCCTGTGC	6540
	ATGTTTCCCA	AACTGTGAGG	AGGGAAGGCT	CAGAGATCGA	GCTTCTCCTC	TGAGTTCTAA	6600
75	CAAAATGGTG	CTTTGAGGGT	CAGCCTTAGT	GAAGGTGCAG	CTTTGTGTC	CTTTGAGCTT	6660
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Seq ID No: 131 Protein sequence:
Protein Accession #: NP_036204.1

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      EDTPYSNWHK ELRNSCISKR CVSLLLDLSSQ PLLPNRLPKW SEGPCGSPGS PGSNIEGFVC    180
      KFSFKGMCRP LALGGPGQVT YTFPFQTTSS SLEAVPFASA ANVACGEGDK DETQSHYFLC    240
      KEKAPDVFWDW GSSGPLCVSP KYGCNFNNGG CHQDCFEFGD GSFLCGCRPG FRLLDLVTVC    300
      ASRNPCCSSP CRGGATCVLG PHGKNYTCRC PQGYQLDSSQ LDCVDVDEQC DSPCAQECVN    360
      TPGGFRCECW VGYEPGPGE GACQDVDECA LGRSPCAQGC TNTDGSFHCS CEEGYVLAGE    420
      DGTQCQDVDE CVGPGGPLCD SLCFNTQGSF HCGCLPGWVL APNGVSCMTG PVSIGPPSPG    480
      PDEEDKGEKE GSTVPRAATA SPTRGPEGTP KATPTTSRPS LSSDAPITSA PLKMLAPSGS    540
      SGVWREPSIH HATAASGPQE PAGGDSSVAT QNNDGTGGQK LLLFYILGTV VAILLLALA    600
      LGLLVYRKRR AKREEKKEKK PQNAADSYSW VPERAESRAM ENQYSPTPGT DC

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Seq ID NO: 132 DNA sequence

Nucleic Acid Accession #: NM_000963.1

Coding sequence: 135-1949 (underlined sequences correspond to start and stop codons)

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      ATACAGCAAA TCCTTGCTGT TCCCACCCAT GTCAAAACCG AGGTGTATGT ATGAGTGTGG    240
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      GTAAAAATCTA TATCAGCAAA AGGGTCTACC TTTAAATATA GCAATAACAA AGAAGAAAA    2880
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5 ACTGCAGGCC TGGTACTCAG ATTTTGCTAT GAGGTTAATG AAGTACCAAG CTGTGCTTGA 3000
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 TGTCTGTTTA TTTTGTACT ATTTA

Seq ID No: 133 Protein sequence:
 Protein Accession #: NP_000954.1

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 NMMFAFFAQH FTHQFFKTDH KRGPFTNGL GHGVDLNHIY GETLARQRL RLFKDGKMKY 240
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Seq ID NO: 134 DNA sequence
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 Coding sequence: 35-664 (underlined sequences correspond to start and stop codons)

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Seq ID No: 135 Protein sequence
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EVESEFARKNY GVTFFPIFHKI KILGSEGEPA FRFLVDSKK EPRWNFWKYL VNPEGQVVKF 180
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Seq ID NO: 136 DNA sequence

Nucleic Acid Accession #: NM_003003.1

15 Coding sequence: 304-2451 (underlined sequences correspond to start and stop codons)

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Seq ID No: 137 Protein sequence
 Protein Accession #: NP_002994.1

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 SLTWKQHQV DYILETWTPP QVLQDYIYAG WHHDKDGRF LYVLRQLGMD TKGLVRALGE 360
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 LGRDYSMVES PLICKEGESV QGSHVTRWPG FYILQWKFS MPACAASSLP RVDDVLASLQ 660
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Protein Accession #: NP_004172.1

1 11 21 31 41 51
MLNKVLSRLG VAGQWRFVDV LGLEEESLGS VPAPACALLL LFPLTAQHEN FRKKQIEELK 60
GQEVSPKVYF MKQTIGNSCG TIGLIHAVAN NQDKLGFEDG SVLKQFLSET EKMSPEDRAK 120
CFEKNEAIQA AHDAVAQEGQ CRVDDKVNPH FILFNNVDGH LYELDGRMPF PVNHHGASSED 180
TLKDAAKVC REPTEREQGE VRFSVALCK AA

Seq ID NO: 140 DNA sequence
Nucleic Acid Accession #: NM_000201.1
Coding sequence: 58-1656 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
GCGCCCCAGT CGACGCTGAG CTCCTCTGCT ACTCAGAGTT GCAACCTCAG CCTCGCTATG 60
GCTCCCAGCA GCCCCCGGCC CGCGCTGCCC GCACTCCTGG TCCTGCTCGG GGCTCTGTTC 120
CCAGGACCTG CCAATGCCCA GACATCTGTG TCCCCCTCAA AAGTCATCCT GCCCCGGGGA 180
GGCTCCGTGC TGGTGACATG CAGCACCTCC TGTGACCAGC CCAAGTTGTT GGCATAGAG 240
ACCCCGTTGC CTAAAAGGA GTTGCTCTCTG CCTGGGAACA ACCGGAAGGT GTATGAACTG 300
AGCAATGTGC AAGAAGATAG CCAACCAATG TGCTATTCAA ACTGCCCTGA TGGGCAGTCA 360
ACAGCTAAAA CCTTCCTCAC CGTGTACTGG ACTCCAGAAC GGGTGGAACT GGCACCCCTC 420
CCCTCTTGCC AGCCAGTGGG CAAGAACCTT ACCCTACGCT GCCAGGTGGA GGGTGGGGCA 480
CCCCGGGCCA ACCTCACCCT GGTGCTGCTC CGTGGGGAGA AGGAGCTGAA ACGGGAGCCA 540
GCTGTGGGGG AGCCCGCTGA GGTACAGACC ACGGTGCTGG TGAGGAGAGA TCACCATGGA 600
GCCAATTTCT CGTGCCGCAC TGAAGTGGAC CTGCGGCCCC AAGGGCTGGA GCTGTTTGAG 660
AACACCTCGG CCCCCACCA GCTCCAGACC TTTGTCTGCT CAGCGACTCC CCCACAACCTT 720
GTCAGCCCCC GGGTCTCTAGA GGTGGACACG CAGGGGACCG TGGTCTGTTC CCTGGACGGG 780
CTGTTCCAG TCTCGGAGGC CCAGGTCCAC CTGGCACTGG GGGACCAGAG GTTGAACCCC 840
ACAGTCACCT ATGGCAACGA CTCCTTCTCG GCCAAGCCCT CAGTCAGTGT GACCGCAGAG 900
GACGAGGGCA CCCAGCGGCT GACGTGTGCA GTAATACTGG GGAACCAGAG CCAGGAGACA 960
CTGCAGACAG TGACCATCTA CAGCTTTCGG CGGCCCAACG TGATTCTGAC GAAGCCAGAG 1020
GTCTCAGAAG GGACCGAGGT GACAGTGAAG TGTGAGGCCC ACCCTAGAGC CAAGGTGACG 1080
CTGAATGGGG TTCCAGCCCC GCCACTGGGC CCGAGGGCCC AGCTCCTGCT GAAGGCCACC 1140
CCAGAGGACA ACGGGCGCAG CTTCTCTGCT TCTGCAACCC TGGAGGTGGC CGGCCAGCTT 1200
ATACACAAGA ACCAGACCCG GGAGCTTCGT GTCTGTATG GCCCCGACT GGACGAGAGG 1260
GATTGTCCGG GAAACTGGAC GTGGCCAGAA AATCCCAGC AGACTCCAAT GTGCCAGGCT 1320
TGGGGGAACC CATTGCCCGA GCTCAAGTGT CTAAAGGATG GCACTTTCCC ACTGCCCATC 1380
GGGGAATCAG TGACTGTAC TCGAGATCTT GAGGGCACCT ACCTCTGTCT GGCCAGGAGC 1440
ACTCAAGGGG AGGTACCCCG CGAGGTGACC GTGAATGTGC TCTCCCCCG GTATGAGATT 1500
GTCATCATCA CTGTGGTAGC AGCCGAGTC ATAATGGGCA CTGCAGGCCT CAGCAGTAC 1560
CTCTATAACC GCCAGCGGAA GATCAAGAAA TACAGACTAC AACAGGCCCC AAAAGGGACC 1620
CCCATGAAC CGAACACACA AGCCACGCCT CCTTGAACCT ATCCCGGGAC AGGGCCTCTT 1680
CCTCGGCCTT CCCATATTGG TGGCAGTGGT GCCACACTGA ACAGAGTGGA AGACATATGC 1740
CATGCAGCTA CACCTACCCG CCCTGGGACG CCGGAGGACA GGGCATTGTC CTCAGTCAGA 1800
TACAACAGCA TTTGGGGGCA TGGTACCTGC ACACCTAAAA CACTAGGCCA CGCATCTGAT 1860
CTGTAGTCAC ATGACTAAGC CAAGAGGAAG GAGCAAGACT CAAGACATGA TTGATGGATG 1920
TTAAAGTCTA GCCTGATGAG AGGGGAAGTG GTGGGGGAGA CATAGCCCCA CCATGAGGAC 1980
ATACAACCTG GAAATACTGA AACTTGCTGC CTATTGGGTA TGCTGAGGCC CACAGACTTA 2040
CAGAAGAAGT GGCCCTCCAT AGACATGTGT AGCATCAAAA CACAAAGGCC CACACTTCCT 2100
GACGGATGCC AGCTTGGGCA CTGCTGTCTA CTGACCCCAA CCCTTGATGA TATGTATTTA 2160
TTCATTGTGT ATTTTACCAG CTATTTATTG AGTGTCTTTT ATGTAGGCTA AATGAACATA 2220
GGTCTCTGGC CTCACGGAGC TCCCAGTCCA TGTACATTG AAGGTCACCA GGTACAGTTG 2280
TACAGGTTGT ACACCTGAGG AGAGTGCCTG GCAAAAAGAT CAAATGGGGC TGGGACTTCT 2340
CATTGGCCAA CCTGCCCTTC CCCAGAAGGA GTGATTTTTC TATCGGCACA AAAGCACTAT 2400
ATGGACTGGT AATGGTTTAC AGGTTTCAAG ATTACCCAGT GAGGCCTTAT TCCTCCCTTC 2460
CCCCCAAAC TGACACCTTT GTTAGCCACC TCCCCACCCA CATACATTTC TGCCAGTGT 2520
CACAAATGACA CTCAGCGGTC ATGTCTGGAC ATGAGTGGCC AGGGAATATG CCCAAGCTAT 2580
GCCTGTCTCT CTTGTCTCTGT TGCATTTC A CTGGGAGCTT GCACTATTGC AGCTCCAGTT 2640
TCCTGCAGTG ATCAGGGTCC TGCAAGCAGT GGGGAAGGGG GCCAAGGTAT TGGAGGACTC 2700
CCTCCAGCT TTGGAAGGGT CATCCGCGTG TGTGTGTGTG TGTATGTGTA GACAAGCTCT 2760
CGCTCTGTCA CCCAGGCTGG AGTGCAGTGG TGCAATCATG GTTCACTGCA GTCTTGACCT 2820
TTTGGGCTCA AGTGATCCCT CCACCTCAGC CTCCTGAGTA GCTGGGACCA TAGGCTCACA 2880
ACACCACACC TGGCAAATTT GATTTTTCCT TTTTTCCTCA GAGACGGGGT CTCGCAACAT 2940
TGCCAGACT TCCTTGTGT TAGTTAATAA AGCTTCTCA ACTGCC

Seq ID No: 141 Protein sequence:
Protein Accession #: NP_000192.1

	1	11	21	31	41	51	
5	MLQFVRAGAR	AWLRPTGSQG	LSSLAEEAAR	ATENPEQVAS	EGLPEPVLRK	VELPVPTHRR	60
	PVQAWVESLR	GFEQERVGLA	DLHPDVFATA	PRLDILHQVA	MWQKNFKRIS	YAKTKTRAEV	120
	RGGGKPLAA	ERHWAGPAWQ	HPLSALARRR	CCPWPFGPTS	YYMLPMKVR	ALGLKVALTV	180
	KLAQDDLHIM	DSLELPTGDP	QYLTELAHYR	RWGDSVLLVD	LTHEEMPQSI	VEATSRLKTF	240
	NLIPAVGLNV	HSMLKHQTLV	LTLPTVAFLE	DKLLWQDSRY	RPLYPFSLPY	SDFPRPLPHA	300
	TQGPAAATPYH	C					

Seq ID NO: 142 DNA sequence

Nucleic Acid Accession #: NM_000270.1

Coding sequence: 110-979 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
	AACCTGTGCGA	ACCAGACCCG	GCAGCCTTGC	TCAGTTCAGC	ATAGCGGAGC	GGATCCGATC	60
	GGATCCGAGC	ACACCGGAGC	AGGCTCATCG	AGAAGGCGTC	TGCGAGACCA	<u>TGGAGA</u> ACGG	120
20	ATACACCTAT	GAAGATTATA	AGAACACTGC	AGAATGGCTT	CTGTCTCATA	CTAAGCACCG	180
	ACCTCAAGTT	GCAATAATCT	GTGGTCTCTG	ATTAGGAGGT	CTGACTGATA	AATTAACCTCA	240
	GGCCAGATC	TTTGACTACA	GTGAAATCCC	CAACTTTCCT	CGAAGTACAG	TGCCAGGTCA	300
	TGCTGGCCGA	CTGGTGTGTT	GGTTCCCTGAA	TGGCAGGGCC	TGTGTGATGA	TGCAGGGCAG	360
	GTTCCACATG	TATGAAGGGT	ACCCACTCTG	GAAGGTGACA	TTCCCACTGA	GGGTTTTCCTCA	420
25	CCTTCTGGGT	GTGGACACCC	TGGTAGTCAC	CAATGCAGCA	GGAGGGCTGA	ACCCCAAGTT	480
	TGAGGTTGGA	GATATCATGC	TGATCCGTGA	CCATATCAAC	CTACCTGGTT	TCAGTGGTCA	540
	GAACCTCTC	AGAGGGGCCA	ATGATGAAAG	GTTTGGAGAT	CGTTTCCCTG	CCATGTCTGA	600
	TGCCTACGAC	CGGACTATGA	GGCAGAGGGC	TCTCAGTACC	TGGAACAAA	TGGGGGAGCA	660
	ACGTGAGCTA	CAGGAAGGCA	CCTATGTGAT	GGTGGCAGGC	CCCAGCTTTG	AGACTGTGGC	720
30	AGAATGTCGT	GTGCTGCAGA	AGCTGGGAGC	AGACGCTGTT	GGCATGAGTA	CAGTACCAGA	780
	AGTTATCGTT	GCACGGCACT	GTGGACTTCG	AGTCTTTGGC	TTCTCACTCA	TCACTAACAA	840
	GGTCATCATG	GATTATGAAA	GCCTGGAGAA	GGCCAACCAT	GAAGAAGTCT	TAGCAGCTGG	900
	CAACACAGCT	GCACAGAAAT	TGGAACAGTT	TGTCTCCATT	CTTATGGCCA	GCATTCCACT	960
	CCCTGACAAA	<u>GCCAGTTGAC</u>	CTGCCTTGGA	GTCTCTGGC	ATCTCCACA	CAAGACCCAA	1020
35	GTAGCTGCTA	CCTTCTTTGG	CCCCTTGCTG	GAGTCATGTG	CCTCTGTCCT	TAGGTTGTAG	1080
	CAGAAAGGAA	AAGATTCTCTG	TCCTTCACCT	TTCCCACTTT	CTTCTACCAG	ACCCTTCTGG	1140
	TGCCAGATCC	TCTTCTCAA	GCTGGGATTA	CAGGTGTGAG	CATAGTGAGA	CCTTGGCGCT	1200
	ACAAAATAAA	GCTGTTCTCA	TTCTGTCTCT	TTCTTACACA	AGAGCTGGAG	CCCGTGCCCT	1260
	ACCACACATC	TGTGGAGATG	CCCAGGATTT	GACTCGGGCC	TTAGAACTTT	GCATAGCAGC	1320
40	TGCTACTAGC	TCTTTGAGAT	AATACATTCC	GAGGGGCTCA	GTTCTGCCTT	ATCTAAATCA	1380
	CCAGAGACCA	AACAAGGACT	AATCCAATAC	CTCTTGGA			

Seq ID No: 143 Protein sequence:

Protein Accession #: NP_000261.1

	1	11	21	31	41	51	
	MENGYTYEDY	KNTAEWLLSH	TKHRPQVAII	CGSGLGGLTD	KLTQAQIFDY	SEIPNFPRST	60
50	VPGHAGRLVF	GFLNGRACVM	MQGRFHMVEG	YPLWKVTFPV	RVFHLGVDV	LVTNNAAGGL	120
	NPKEFVGDM	LIRDHINLPG	FSGQNPLRGP	NDERFGDRFP	AMSDAYDRTM	QRALSTWKQ	180
	MGEQRELQEG	TYVMVAGPSF	ETVAECRVLQ	KLGADEVGMS	TVPEVIVARH	CGLRVFGFSL	240
	ITNKVIMDYE	SLEKANHEEV	LAAGKQAAQK	LEQFVSILMA	SIPLPDKAS		

Seq ID NO: 144 DNA sequence

Nucleic Acid Accession #: NM_015577.1

Coding sequence: 112-3054 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
	GAAGCGGCGG	GCGGGGTGGA	GCAGCCAGCT	GGGTCCGGGG	AGCGCCGCGG	CCGCCTCGAT	60
	GGGTGTTTGA	AAAGTCTCCT	CTAGAGCTTT	GGAAGGCTGA	ATGCACTAAA	<u>CATGAAGAGC</u>	120
	TTGAAAGCGA	AGTTCAAGAA	GAGTGACACC	AATGAGTGGA	ACAAGAATGA	TGACCGGCTA	180
65	CTGCAGGCGG	TGGAGAATGG	AGATGCGGAG	AAGGTGGCCT	CACTGCTCGG	CAAGAAGGGG	240
	GCCAGTGCCA	CCAAACACGA	CAGTGAGGGC	AAGACCGCTT	TCCATCTTGC	TGCTGCAAAA	300
	GGACACGTGG	AATGCCCTCAG	GGTCATGATT	ACACATGGTG	TGGATGTGAC	AGCCCAAGAT	360
	ACTACCGGAC	ACAGCGCCTT	ACATCTCGCA	GCCAAGAACA	GCCACCATGA	ATGCATCAGG	420
	AGGCTGCTTC	AGTCTAAATG	CCCAGCCGAA	AGTGTGACAA	GCTCTGGGAA	AACAGCTTTA	480
70	CATTATGCAG	CGGCTCAGGG	CTGCCTTCAA	GCTGTGCAGA	TTCTCTGCGA	ACACAAGAGC	540
	CCCATAAACC	TCAAAGATTT	GGATGGGAAT	ATACCGCTGC	TTCTTGCTGT	ACAAAATGGT	600
	CACAGTGAGA	TCTGTCACTT	TCTCTTGAT	CATGGAGCAG	ATGTCAATTC	CAGGAACAAA	660
	AGTGGAAGAA	CTGCTCTCAT	GCTGGCCTGT	GAGATTGGCA	GCTCTAACGC	TGTGGAAGCC	720
	TTAATTAAAA	AGGTGTCAGA	CCTAAACCTT	GTAAGATTCTC	TTGGATACAA	TGCCTTACAT	780
75	TATTCCAAAT	TGTCAGAAA	CAAAGCCTTC	TATTATCAAA	AATCTCTCAG		840
	GATGCTGATT	TAAAGACCCC	AACAAAACCA	AAGCAGCATG	ACCAAGTCTC	TAAAATAAGC	900

TCAGAAAGAA GTGGAATCC AAAAACACGC AAAGCTCCAC CACCTCCTAT CAGTCCTACC 960
 CAGTTGAGTG ATGTCTCTTC CCCAAGATCA ATAACCTCGA CTCCACTATC GGGAAAGGAA 1020
 TCGGTATTTT TTGCTGAACC ACCCTTCAAG GCTGAGATCA GTTCTATACG AGAAAACAAA 1080
 5 GACAGACTAA GTGACAGTAC TACAGGTGCT GATAGCTTAT TGGATATAAG TTCTGAAGCT 1140
 GACCAACAAG ATCTTCTCTC TCTATTGCAA GCAAAAAGTTG CTTCCCTTAC CTTACACAAT 1200
 AAGGAGTTAC AAGATAAATT ACAGGCCAAA TCACCCAAGG AGGCGGAAGC AGACCTAAGC 1260
 TTTGACTCAT ACCATTCCAC CCAAACTGAC TTGGGGCCAT CCCTGGGAAA ACCTGGTGAA 1320
 ACCTCTCCCC CAGACTCCAA ATCATCTCCA TCTGTCTTAA TACATTCTTT AGGTAAATCC 1380
 10 ACTACTGACA ATGATGTCAG AATTTCAGCA CTGCAAGAGA TTTTGCAAGA TCTACAGAAG 1440
 AGATTAGAGA GCTCTGAAGC AGAGAGAAAA CAGCTACAGG TCGAACTCCA ATCCCGAAGG 1500
 GCAGAACTGG TATGCTTAAA CAACACTGAG ATTTTCAGAGA ACAGCTCTGA CCTCAGCCAG 1560
 AAACCTTAAAG AAACCTCAGAG CAAATACGAG GAGGCTATGA AAGAAAGTCT TAGTGTGCAG 1620
 AAGCAGATGA AACTCGGTCT TGTCTCACCT GAAAGCATGG ATAATTATTC ACATTTCCAC 1680
 GAGCTGAGGG TCACGGAAGA GGAATAAAT GTGCTAAAGC AGGATCTGCA GAATGCATTA 1740
 15 GAAGAAAGTG AAAGAAATAA AGAGAAAGTG AGAGAGTTAG AGGAAAACT GGTAGAGAGG 1800
 GAGAAAGGTA CAGTGATTAA GCCACCTGTG GAAGAGTACG AGGAAATGAA AAGTTTCATAT 1860
 TGCTCTGTTA TTGAGAATAT GAATAAGGAG AAAGCATTTT TGTTTGAGAA ATACCAAGAA 1920
 GCCCAAGAAG AAATCATGAA ATTTAAAGAC AACTAAAAA GTCAGATGAC ACAGGAAGCC 1980
 20 AGTGTAGAG CTGAGGACAT GAAAGAAGCC ATGAATAGGA TGATAGATGA ATCAATAAA 2040
 CAGGTGAGCG AGCTGTCACA GCTGTACAAA GAAGCCCAGG CTGAGCTGGA GGATTACAGG 2100
 AAGAGGAAAT CTCTAGAGGA TGTACACAGT GAATATATCC ATAAAGCAGA GCATGAGAAA 2160
 CTGATGCAAT TGACAAACGT GTCCAGGGCT AAAGCAGAAG ATGCACTGTC TGAATGAAG 2220
 TCTCAGTATT CAAAAGTGT GAATGAGTTG ACCCAGCTCA AACAACCTGGT GGATGCACAA 2280
 25 AAAGAGAACT CTGTCTCTAT CACAGAACAT TTGCAAGTGA TAACCACGCT GCGGACTGCA 2340
 GCAAAAGAGA TGAAGAAAA AATAAGCAAT CTTAAGGAAC ACCTTGCAAG CAAGGAAGTG 2400
 GAAGTAGCAA AGCTGGAGAA ACAACTCTTA GAAGAGAAAG CTGCTATGAC TGATGCAATG 2460
 GTACCTCGGT CTCTCTATGA AAAACTCCAG TCATCCTTAG AGAGTGAAGT GAGTGTGTTG 2520
 GCATCGAAAT TAAAGGAATC TGTGAAAGAG AAAGAGAAGG TCCATTGAGA GGTGTTCCAG 2580
 30 ATTAGAAGTG AGGTCTCACA GGTGAAAAGA GAAAAGGAAA ATATTGAGAC TCTCTTGAAA 2640
 TCCAAGAGC AAGAAGTAAA TGAACCTCTG CAAAAATTCC AGCAAGCTCA GGAAGAACTT 2700
 GCAGAAATGA AAGATACGCG TGAGAGCTCT TCAAACTGG AGGAAGATAA AGATAAAAAG 2760
 ATAAATGAGA TGTGCAAGGA AGTCACCAAA TTGAAGGAGG CCTTGAACAG CCTCTCCAG 2820
 CTCTCTACT CAACAAGCTC ATCCAAAAGG CAGAGTCAGC AGCTGGAGGC GCTGCAGCAG 2880
 35 CAAGTCAAAAC AGCTCCAGAA CCAGCTGGCG GAATGCAAGA AACAACACCA GGAGGTCATA 2940
 TCAGTTTACA GAATGCATCT TCTGTATGCT GTGCGGGGCC AGATGGATGA AGATGTCAG 3000
 AAAGTACTGA AGCAAACTCT TACCATGTGT AAAAACCAGT CTCAAAAGAA GTAAAGTGGA 3060
 TTCCTTGCCA GGACACTGCC CCTTGTCTATC TGTCTTTGTG TTAGATCCAG AGTTGTGCGC 3120
 AGCCGCTGCC ATTGTTCTCA TTCGTGTAT GCACTGTGGC CTAGCGTAGC TTCTTCCCTT 3180
 40 TCCAAAGGTT TCTGAGGACT TCTCCAGGA GAAGACTGCC CGCCTCAGAA CTGCTTAGAG 3240
 ACTTCAAACC AGCAGAGGTG AAGTCCCTG TCATCCCTTC AGATTCCAGA GCTGGGATCA 3300
 GCCATGCCCC GAGGTCTGGT CCTGATGCTG GCAGGGGGGC CCCCTCCTCC ATCCCTGACT 3360
 GGCTGAGTGG CTTTATCACC ACCGAGTGAT GTGCTGAGGC CTCTGCGAGT GAATGCTCCT 3420
 TCCATTCCCTG TACTCGGGCA GTGCCATTCA GCACAGGAGA GCTCTTTTGT CCTTGGCTT 3480
 45 TCAATTCCAA AACATGATTT AATTTCTAAC TAAATTAGTA TGGCACTAGT TATGAAGTAT 3540
 CTGCTTAAAA CCCTTCATCA TGATATCCTG TGGATTAAAA AACTCTAATT CCATGTTTTC 3600
 TTCCCATCTG CCTTATATAT CTCATCACC TGCTTATCAA TATTGAGTTT GATGAGCACT 3660
 ATTAATAAAA ATATGAAACT TAAAAACAAA AGCAAGTTGT CCTTAAAGT TCTTTTTTFA 3720
 AGTAAATTGT TGACATACTG CAAATTTTCT ATGCAAACTT GCCTCCTGCT GTTATCTGTG 3780
 50 AAGCTCAGGA AATCCAAACA TTTGTGTTTC AACAAGGGAC AGTAAACTGT GTGTTTACAG 3840
 CCAAAAGAAA TGCTCATAG TTCTTAACCT CAACCTTTGT AGAAGTATTT TTTTCTCTGT 3900
 AATATTTTTA TTGGCTCATA AAGATGTTTT CATATCTGAA CTCCTAAATA AGTGAAATTA 3960
 CAGTAGATTA TATTAACAAA ATACTTTTTA GGTAGCCATG CTTGAGACTT TTTAAAAATA 4020
 TAACCTTTTT CTTAAAGTTT TCAGCTATAG CAAAAGGTAG TTATGTATGC CAGACCTAAT 4080
 55 ATGAGCTGCC ACCAACACCC CTAGAACTTT CAGCCATGGT GTCTTCAGAA TTGTAGCGCA 4140
 TTTCTGAATC TAGCAAAATCC TCCTTTTACC CGTTGAATGT TTGAATGCC CTGACTCTAC 4200
 CAGCGCCCAT AAATGATCTC TAGAAGGACT GTTAGTACCA ATCTGTTTTT CAACCTTGAA 4260
 GCTAAAAACC CTGATATGGT AATATTATGG TGCAATAGCAG AGGTCTCGGA AAAAAAATAT 4320
 TTCTGTTCAC TTTACTTTCA GGTAAAAAAT GTTTCTAACA CGCTTGCAAC TTCCCTTATG 4380
 60 GCATTAATCT TGTGAGGGGA GAGAGACAGA ATCCTGGACT CTCCAAAGTA TTTAATGAA 4440
 AGTAGGGCCT GCTCTGACAG GGCCCATGTC CCACAAGGCT GCTTGGCCTC AGTGGGTGCT 4500
 TGGCTGTGCT GGATGATATG TTGATCTGTA TTGGATAAGG ACCAATGACA GCAAAGCAAA 4560
 AATGGCTTTA AAGCTTGGTG TTACTTTTCT TAAGTTGTTT AATTATAGTT AAGCAATTC 4620
 AAAAAATGCTC CAAAGAAATG TGAAGGACC TTTTGTGACA GCACTTCAGA AAATACACAA 4680
 65 CAGCCCCCTC TGCCCCGCA CAGAAATGCT GCAGAGTATA TAAAACTTGA GACATTTTGT 4740
 TAGGATGCCT GACGAGGTGT AGCCTTTTAT CTTGTTCCG GATGCATATT TATTACGAGT 4800
 ACTCTGGTTA AATATTGAAA AGTTATATGC TGTAGTTTTT AGTATTTTGT CTTTGTAAAT 4860
 TACAGAAATT ATTGGAGAAA ATAACTTGT TTCATTTTGC AAAAAAAAAA AAAAAAAAAA 4920
 AAAAA

Seq ID No: 145 Protein sequence:
 Protein Accession #: NP_056392.1

1 11 21 31 41 51
 MKSLKAKFRK SDTNEWNKND DRLLQAVENG DAEEKVASLLG KKGASATKHD SEGKTAFHLA 60

	AAKGHVECLR	VMITHGVDVT	AQDTTGHSA	HLAAKNSHHE	CIRRLQSKC	PAESVDSSGK	120
	TALHYAAQ	CLQAVQILCE	HKSPINLKDL	DGNIPLLAV	QNGHSEICHF	LLDHGADVNS	180
	RNKSRTALM	LACEIGSSNA	VEALIKKGAD	LNLVDSLGYN	ALHYSKLSN	AGIQSLLLSK	240
	ISQDADLKTP	TKPKQHDQVS	KISSERSGTP	KTRKAPPPPI	SPTQLSDVSS	PRSTSTPLS	300
5	GKESVFFAEP	PFKAEISSIR	ENKDRLSST	TGADSLDIS	SEADQDLS	LLQAKVASLT	360
	LHNKELQDKL	QAKSPKEAEA	DLSDFSYHST	QTDLGPSLGG	PGETSPDDSK	SSPSVLIHSL	420
	GKSTTDNDVR	IQQLQEILQD	LQKRLESSEA	ERKQLQVELQ	SRRAELVCLN	NTEISENSSD	480
	LSQKLKETQS	KYEBAMKEVL	SVQKQMKLGL	VSPEMDNYS	HFHELVRTEE	EINVLKQDLQ	540
	NALEESERNK	EKVRELEEK	VEREKGTIVK	PPVEEYEMK	SSYCSVIENM	NKEKAFLFEK	600
10	YQEAQEEIMK	LKDTLKSQMT	QEASDEAEDM	KEAMNRMIDE	LNKQVSELSQ	LYKEAQAELE	660
	DYRKRKSLD	VTAEYIHKAE	HEKLMQLTNV	SRAKAEDALS	EMKSQYSKVL	NELTQLKQLV	720
	DAQKENSIVI	TEHLQVITTL	RTAAKEMEEL	ISNLKEHLAS	KEVEVAKLEK	QLLEKAAMT	780
	DAMVPRSSYE	KLQSSLESEV	SVLASKLKE	VKEKEKVHSE	VVQIRSEVSQ	VKREKENIQT	840
	LLKSKEQEVN	ELLQKFQQAQ	EELAEMKRYA	ESSSKLEEDK	DKKINEMSKE	VTKLKEALNS	900
15	LSQLSYSTSS	SKRQSQLEA	LQQQVQQLQ	QLAECKKQHQ	EVISVYRMHL	LYAVQQQMD	960
	DVQKVLKQIL	TMCKNQSQKK					

Seq ID NO: 146 DNA sequence

Nucleic Acid Accession #: NM_000459.1

Coding sequence: 149-3523 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
25	CTTCTGTGCT	GTTCTTCTT	GCCTCTAAT	TGTAACAAG	ACGTACTAGG	ACGATGCTAA	60
	TGGAAAGTCA	CAAACCGCTT	GGTTTTTGAA	AGGATCCTTG	GGACCTCATG	CACATTGTG	120
	GAAACTGGAT	GGAGAGATT	GGGGAAGCAT	GGACTCTTGA	GCCAGCTTAG	TTCTCTGTGG	180
	AGTCAGCTTG	CTCCTTTCTG	GAACGTGGA	AGGTGCCATG	GACTTGATCT	TGATCAATTC	240
	CCTACCTCTT	GTATCTGATG	CTGAAACATC	TCTCACCTGC	ATTGCTCTG	GGTGGCGCCC	300
30	CCATGAGCCC	ATCACCATAG	GAAGGACTT	TGAAGCCTTA	ATGAACCAGC	ACCAGGATCC	360
	GCTGGAAGTT	ACTCAAGATG	TGACCAGAGA	ATGGGCTAAA	AAAGTTGTTT	GGAAGAGAGA	420
	AAAGGCTAGT	AAGATCAATG	GTGCTTATTT	CTGTGAAGGG	CGAGTTCGAG	GAGAGGCAAT	480
	CAGGATACGA	ACCATGAAGA	TGCGTCAACA	AGCTTCCTTC	CTACCAGCTA	CTTTAACTAT	540
	GACTGTGGAC	AAGGGAGATA	ACGTGAACAT	ATCTTTCAAA	AAGGTATTGA	TTAAAGAAGA	600
35	AGATGCAGTG	ATTTACAAAA	ATGGTTCCTT	CATCCATTCA	GTGCCCCGGC	ATGAAGTACC	660
	TGATATTCTA	GAAGTACACC	TGCTTCATGC	TCAGCCCCAG	GATGCTGGAG	TGTACTCGGC	720
	CAGGTATATA	GGAGGAAACC	TCTTCACCTC	GGCCTTCACC	AGGCTGATAG	TCCGGAGATG	780
	TGAAGCCCAG	AAGTGGGGAC	CTGAATGCAA	CCATCTCTGT	ACTGCTTGTA	TGAACAATGG	840
	TGTCTGCCAT	GAAGATACTG	GAGAATGCAT	TTGCCCTCCT	GGGTTTATGG	GAAGGACGTG	900
40	TGAGAAGGCT	TGTGAAGTGC	ACACGTTTGG	CAGAACTTGT	AAAGAAAGGT	GCAGTGGACA	960
	AGAGGGATGC	AAGTCTTATG	TGTTCTGTCT	CCCTGACCCC	TATGGGTGTT	CCTGTGCCAC	1020
	AGGCTGGAAG	GGTCTGCAGT	GCAATGAAGC	ATGCCACCTT	GGTTTTTACG	GGCCAGATTG	1080
	TAAAGCTTAG	TGCAGCTGCA	ACAATGGGGA	GATGTGTGAT	CGCTTCCAAG	GATGTCTCTG	1140
	CTCTCCAGGA	TGGCAGGGGC	TCCAGTGTGA	GAGAGAAGGC	ATACCGAGGA	TGACCCCAAA	1200
45	GATAGTGGAT	TTGCCAGATC	ATATAGAAGT	AAACAGTGGT	AAATTTAATC	CCATTGTCAA	1260
	AGCTTCTGGC	TGGCCGCTAC	CTACTAATGA	AGAAATGACC	CTGGTGAAGC	CGGATGGGAC	1320
	AGTGCTCCAT	CCAAAAGACT	TAAACCATAC	GGATCATTTT	TCAGTAGCCA	TATTACCAT	1380
	CCACCGGATC	CTCCCCCTG	ACTCAGGAGT	TTGGGTCTGC	AGTGTGAACA	CAGTGGCTGG	1440
	GATGGTGGAA	AAGCCCTTCA	ACATTTCTGT	TAAAGTTCTT	CCAAAGCCCC	TGAATGCCCC	1500
50	AAACGTGATT	GACACTGGAC	ATAACTTTGC	TGTCATCAAC	ATCAGCTCTG	AGCCTTACTT	1560
	TGGGGATGGA	CCAATCAAA	CCAAGAAAGT	TCTATACAAA	CCCGTTAATC	ACTATGAGGC	1620
	TTGGCAACAT	ATTCAAGTGA	CAAATGAGAT	TGTTACACTC	AACTATTGG	AACCTCGGAC	1680
	AGAAATATGA	CTCTGTGTGC	AACCTGGTCC	TCGTGGAGAG	GGTGGGGAAG	GGCATCCTGG	1740
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	ACCAGCTGTG	CAGTTCAACT	CAGGGACTCT	GGCCCTAAAC	AGGAAGGTCA	AAAACAACCC	2580
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Seq ID No: 147 Protein sequence:

Protein Accession #: NP_000450.1

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 40 ARIKKDGLRM DAAIKRMKEY ASKDDHRDFA GELEVLCKLG HHPNIIINLLG ACEHRGYLYL 900
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Seq ID NO: 148 DNA sequence

Nucleic Acid Accession #: NM_000552.2

Coding sequence: 311-8752 (underlined sequences correspond to start and stop codons)

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Seq ID No: 149 Protein sequence:
Protein Accession #: NP_000543.1

55	1	11	21	31	41	51	
	MIPARFAGVL	LALALILPGT	LCAEGTRGRS	STARCSLFGS	DFVNTFDGSM	YSFAGYCSYL	60
	LAGGCQKRSE	SIIGDFQNGK	RVSLSVYLGE	FFDIHLFVNG	TVTQGDQVRS	MPYASKGLYL	120
60	ETEAGYYKLS	GEAYGFVARI	DGSGNFQVLL	SDRYFNKTCG	LCGNFNIPAE	DDFMTQEGTL	180
	TSDPYDFANS	WALSSGEQWC	ERASPPSSSC	NISSGEMQKG	LWEQCQLLKS	TSVFARCHPL	240
	VDPEFPVALC	EKTLCECAGG	LECACPALLE	YARTCAQEGM	VLYGWTDHSA	CSPVCPAGME	300
	YRQCVSPCAR	TCQSLHINEM	CQERCVDGCS	CPEGQLLDEG	LCVESTCEPC	VHSGKRYPPG	360
	TSLSRDCNTC	ICRNSQWICS	NEECPEGCLV	TGQSHFKSFD	NRYFTFSGIC	QYLLARDCQD	420
65	HSPSIVIVETV	QCADDDRAVC	TRSVTVRLPG	LHNSLVKLKH	GAGVAMDQD	IQPLLLKGD	480
	RIQHTVTASV	RLSYGEDLQM	DWDGRGRLLV	KLSPVYAGKT	CGLCGNYNGN	QDDDFLTPSG	540
	LAEPREVDPG	NAWKHLHGDCQ	DLQKHSDPDC	ALNPRMTRFS	EEACAVLTSP	TPEACHRAVS	600
	PLPYLRNCRY	DVCSGSDGRE	CLCGALASYA	AACAGRGVRV	AWREPGRCEL	NCPKGQVYLQ	660
	CGTPCNLTCT	SLSYPDDECN	EACLEGCFCP	PGLYMDERGD	CVPKACPCPY	YDGEIFQPED	720
70	IFSDHHTMCY	CEDGFMHCTM	SGVPGSLLPD	AVLSSPLSHR	SKRSLSCRPP	MVKLVCPADN	780
	LRAEGLECTK	TCQNYDLECM	SMGCVSGCLC	PPGMVRHENR	CVALERCPCF	HQKEYAPGE	840
	TVKIGCNTCV	CRDRKWNCTD	HVCDATCSTI	GMAHYLTFDG	LKYLFPGEQ	YVLVQDYCGS	900
	NPQTFRILVG	NKGCSPHSVK	CKKRVITLVE	GGEISLFDGE	VNVKRPMDKE	THFEVVESEGR	960
	YIILLGKAL	SVVWDRHLSI	SVVLKQTYQE	KVCGLCGNFD	GIQNNDLTSS	NLQVEEDPVD	1020
75	FGNSWKVSSQ	CADTRKVPD	SSPATCHNNI	MKQTMVDSSC	RILTSDFVQD	CNKLVDPPEPY	1080
	LDVCIYDTCS	CESIGDCACF	CDTIAAYAHV	CAQHGVVTTW	RTATLCPQSC	EERNLRENGY	1140
	ECEWRYNSCA	PACQVTCQHP	EPLACPVQCV	BGCHAHCPPG	KILDELLQTC	VDPEDCPVCE	1200

	VAGRRFASGK	KVTLNPSDPE	HCQICHCDVV	NLTCEACQEP	GGLVVPPTDA	PVSPTTLYVE	1260
	DISEPPLHDF	YCSRLLDLVF	LLDGSSRLSE	AEFEVLKAFV	VDMMERLRIS	QKWVRVAVVE	1320
	YHDGSHAYIG	LKDRKRPSLE	RRIASQVKYA	GSQVASTSEV	LKYTLFQIFS	KIDRPEASRI	1380
5	ALLLMAEQEP	QRMSRNFVRY	VQGLKKKKVI	VIPVGIGPHA	NLKQIRLIEK	QAPENKAFVL	1440
	SSVDELEQQR	DEIVSYLCDL	APEAPPPTLP	PHMAQVTVGP	GLLGVSTLGP	KRNSMVLDA	1500
	FVLEGSDKIG	EADFNRSKFE	MEEVIQRMVDV	GQDSIHVTVL	QYSYMTVEY	PFSEAQSKGD	1560
	ILQVRVREIRY	QGGNRTNTGL	ALRYLSDHSF	LVSQGDREQA	PNLVYMTGN	PASDEIKRLP	1620
	GDIQVVPIGV	GPANANVQELE	RIGWPNAPIL	IQDFETLPRE	APDLVLQRCC	SGEGLQIPTL	1680
10	SPAPDCSQPL	DVILLLDGSS	SFPASYFDEM	KSFAKAFISK	ANIGPRLTQV	SVLQVGSITT	1740
	IDVPWNVVPE	KAHLLSLVDV	MQREGGPSQI	GDALGFAVRY	LTSEMHGARP	GASKAVVILV	1800
	TDVSVDSVDA	AADAARSNRV	TVFPIGIGDR	YDAAQLRILA	GPAGDSNVVK	LQRIEDLPTM	1860
	VTLGNSFLHK	LCSGFVIRICM	DEGNEKRP	DVWTLPDQCH	TVTCQPDGQT	LLKSHRVNCD	1920
	RGLRPPCPNS	QSPVKVEETC	GCRWTCPCVC	TGSSSTRHIVT	FDGQNFKLITG	SCSYVLFQNK	1980
	EQDLEVLHNN	GACSPGARQ	CMKSIEVKHS	ALSVELHSDM	EVTVNGRLVS	VPYVGGNMEV	2040
15	NVYGAIMHEV	RFNHLGHIFT	FTPQNNFQ	QLSPKTFASK	TYGLCGICDE	NGANDFMLRD	2100
	GTVTTDWKTL	VQEWTVQRP	QTCQPILEEQ	CLVPDSSHQC	VLLPLPLFAEC	HKVLAPATFY	2160
	AICQDSDCHQ	EQWCVIASY	AHLCRTNGVC	VDWRTPDFCA	MSCPPSLVYN	HCEHGCPRHC	2220
	DGNVSSCGDH	PSEGCFCPPD	KVMLEGSCVP	EEACTQCIGE	DGVQHFLEA	WVPDHQPCQI	2280
	CTCLSGRKVN	CTTQPCPTAK	APTCGLCEVA	RLRQNAQDCC	PEYECVCDPV	SCDLPPVPHC	2340
20	ERGLQPTLTN	PGECRPNFTC	ACRKEECKRV	SPPSCPPHRL	PTLRKTQCCD	EYECACNCVN	2400
	STVSCPLGYL	ASTATNDCGC	TTTTCLPDKV	CVHRSTIYPV	GQFWEEGCDV	CTCTDMEDAV	2460
	MGLRVAQCSQ	KPCEDSCRSG	FTYVLHEGEC	CGRCLPSACE	VVTGSPRGDS	QSSWSKSVGSQ	2520
	WASPENPCLT	CEVRVKEEV	FIQQRNVSCP	QLEVPVPCPSG	FQLSCKTSAC	CPSCRCERME	2580
	ACMLNGTVIG	PGKTMIDVC	TTCRMVQVQ	VISGFKLECR	KTTCPNCPPLG	YKEENNTGEC	2640
25	CGRCLPTACT	IQLRGGQIMT	LKRDETLQDG	CDTHFCCKVNE	RGEYFWEKRV	TGCPPEDEHK	2700
	CLAEQGGKIMK	IPGTCCDTC	EPECNDITAR	LQYVKVGSCK	SEVEVDIHYC	QGKASKAMY	2760
	SIDINDVQDQ	CSCSPTRTE	PMQVALHCTN	GSVVYHEVLN	AMECKCSPRK	CSK	

Seq ID NO: 150 DNA sequence

Nucleic Acid Accession #: NM_001508.1

Coding sequence: 1-1362 (underlined sequences correspond to start and stop codons)

35	1	11	21	31	41	51	
	ATGGCTTCAC	CCAGCCTCCC	GGGAGTGAC	TGCTCCCAA	TCATTGATCA	CAGTCATGTC	60
	CCCGAGTTTG	AGGTGGCCAC	CTGGATCAAA	ATCACCCTTA	TTCTGGTGTA	CCTGATCATC	120
40	TTCTGTATGG	GCCTTCTGGG	GAACAGCGTC	ACCATTCCGG	TCACCCAGGT	GCTGCAGAAG	180
	AAAGGATACT	TGCAGAAGGA	GGTGACAGAC	CACATGGTGA	GTTTGGCTTG	CTCGGACATC	240
	TTGGTGTTCC	TCATCGGCAT	GCCCATGGAG	TTCTACAGCA	TCATCTGGAA	TCCCCTGACC	300
	ACGTCCAGCT	ACACCCTGTC	CTGCAAGCTG	CACACTTTCC	TCTTCGAGGC	CTGCAGCTAC	360
	GCTACGCTGC	TGCACGTGCT	GACGCTCAGC	TTTGAGCGCT	ACATCGCCAT	CTGTCACCCC	420
	TTCAGGTACA	AGGCTGTGTC	GGGACCTTGC	CAGGTGAAGC	TGCTGATTGG	CTTCGTCTGG	480
45	GTCACCTCCG	CCCTGGTGGC	ACTGCCCTTG	CTGTTTGCCA	TGGGTACTGA	GTACCCCTTG	540
	GTGAACGTGC	CCAGCCACCG	GGGTCTCACT	TGCAACCGCT	CCAGCACCCG	CCACCAGGAG	600
	CAGCCCGAGA	CCTCCAATAT	GTCCATCTGT	ACCAACCTCT	CCAGCCGCTG	GACCGTGTTC	660
	CAGTCCAGCA	TCTTCGGCGC	CTTCGTGGTC	TACCTCGTGG	TCCTGCTCTC	CGTAGCCTTC	720
	ATGTGCTGGA	ACATGATGCA	GGTGCTCATG	AAAAGCCAGA	AGGGCTCGCT	GGCCGGGGGC	780
50	ACGCGGCCCT	CGCAGCTGAG	GAAGTCCGAG	AGCGAAGAGA	GCAGGACCGC	CAGGAGGCAG	840
	ACCATCATCT	TCTGTAGGCT	GATTGTGTG	ACATTGGCCG	TATGCTGGAT	GCCCAACCAG	900
	ATTCGGAGGA	TCATGGCTGC	GGCCAAACCC	AAGCAGGACT	GGACGAGGTC	CTACTTCCGG	960
	CCGTACATGA	TCTCTCTCCC	CTTCTCGGAG	ACGTTTTTCT	ACCTCAGCTC	GGTCATCAAC	1020
	CCGCTCCTGT	ACACGGTGTG	CTCGCAGCAG	TTTCGGCGGG	TGTTCTGTGA	GGTGCTGTGC	1080
55	TGCCGCTGT	CGCTGCAGCA	CGCCAACCAC	GAGAAGCGCC	TGCGCGTACA	TGCGCACTCC	1140
	ACCACCGACA	GCGCCCGCTT	TGTGCAGCGC	CCGTTGCTCT	TCGCGTCCCG	GCGCCAGTCC	1200
	TCTGCAAGGA	GAACTGAGAA	GATTTTCTTA	AGCACTTTTC	AGAGCGAGGC	CGAGCCCAG	1260
	TCTAAGTCCC	AGTCATTGAG	TCTCGAGTCA	CTAGAGCCCA	ACTCAGGCGC	GAAACCAGCC	1320
60	AATTCTGCTG	CAGAGAATGG	TTTTCAGGAG	CATGAAGTTT	<u>GA</u>		

Seq ID No: 151 Protein sequence:

Protein Accession #: NP_001499.1

65	1	11	21	31	41	51	
	MASPSLPGSD	CSQIIDHSV	PEFEVATWIK	ITLILVYLII	FVMGLLGNV	TIRVTQVLQK	60
	KGYLQKEVTD	HMVSLACSDI	LVFLIGMPME	FYSIIWNPLT	TSSYTLSCKL	HTFLFEACSY	120
70	ATLLHVLTL	FERIYAICHP	FRYKAVSGPC	QVKLLIGFVW	VTSALVALPL	LPAMGTEYPL	180
	VNVPISHRLT	KNRSSTRHHE	QPETSNSIC	TNLSSRWTFV	QSSIFGAFV	YLVVLLSVAF	240
	MCCWNMQVLT	KSQKSLAGG	TRPPQLRKSE	SEESRTARRQ	TIIFLRLLIV	TLAVCWMPNQ	300
	IRIMAAAKP	KHDWTRSYFR	AYMILLPFSE	TFFYLSSVIN	PLLYTVSSQ	FRRVFVQVLC	360
	CRSLQHANH	EKRLRVHAHS	TTDSARFVQR	PILLFASRRQS	SARRTEKIFL	STFQSEAEFQ	420
75	SKSQSLSLES	LEPNSGAKPA	NSAAENGFOE	HEV			

Seq ID NO: 152 DNA sequence

Nucleic Acid Accession #: none found

Coding sequence: 3-65 (underlined sequences correspond to start and stop codons)

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5      1      11      21      31      41      51
      |      |      |      |      |      |
      TTATTATTTT GTGTAAACTA TATCTGCTT ATAGAGAGTC TCTGAGACTA AAATTGACAA 60
      CTTGAAAAGT ATTCCAAGGA ATATTATGAA AATAGGGCAA CATGGACTGT TTAAGATCTC 120
      CATGTAATTG AAATTCATGC AAGGAAACAA CTCATAGAAA AGATAAATAT GGATGCCCTT 180
10     CACATGTAT CAACCTCGTA ACTTTTGGTG CTTGCTGAAT CAGTCCATGA AAAGCTACAG 240
      CCCGCTCTTT GGGGAATGCTA CATACCCATT TCTGGTATTT AAAAAATATC TAGGAGGAGC 300
      TAAATGACAA AACACAGCAG TGTTTTGAGG GAGAAAGGAC CATCATTTAT AATGCTCTGT 360
      ACATACTACC AGAGCTGCTT GGAAAATTAA AGGCCACTTG TGGCTTTTTT CTACCAACTG 420
      ATACGTTTAA ATTTGCCCTA GGATTSAGCT AACAGCAAAA AAAAAAAAAA AAAAAAARA 480
15     GAGAGAAAGA AAGGAGKAAA CAGTGGTAAT AAAAAATCC ATCTGTCTTC TTGCTATGTT 540
      AATATTAATA AATCATAATA TGACAAGACC CTCACTGAAT AAGAGTATT TCAGTCATCA 600
      GAAGCCAGCT GTTGGTAGGC ATTAATGAGT TTAATAATTGT TCTCAATTGA AAAACATCA 660
      CACTATTTTG CCAAAACCAA AGTAATTATA ATACTGTGTC CTCTGTAAAT TTTTGTAGAA 720
      GTGGTTATAA AGGGCATATT TACATAAATT CTACTTTATT CCTCAACTTC TTTGATGAAT 780
20     GTAACCCAAT TTTACTTCTT TAAAAAGCT CAATTCAAGC TGGATTAGCC AGCTCAGCAT 840
      AATCAACTAG ACAGTGGTTT GTTAAATTA GCAGCATACT TCGTTCCCAT TCTAATTAAA 900
      GTCATGAGTT CTTGAATCCC AGAGAAATAA TGCTTAGGAA CTCTCTCAA TCTGCTTGGC 960
      TTGGCCTAGA GAAGTGCCCA TTTTATCAAC AGGRAAAAAA AAAATTTTCT CTACTACAAC 1020
      CCCGTGCGCT TCTGAAAAAC AGCAAGTTAT TTCTTTATAT AATTATCAIT TTATTATTTT 1080
25     ATGAAAAATT AATTTATTA TTAATAGCCT ATTATGTGTT CTCACTTGCT TCTCTAAGTA 1140
      ATATTTTGAG ATAAAATGTT GAATAAAACC ATGGATTATA GAGAAAAGTC AAAATATATG 1200
      TGTAAATATT AATTATTTTA TAAGTTTAT AATAAAGTAT TCCATTTCTT TATCTT

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30 Seq ID No: 153 Protein sequence:
Protein Accession #: none found

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35     1      11      21      31      41      51
      |      |      |      |      |      |
      IILCKLYSAY RESRLRLKLT

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Seq ID NO: 154 DNA sequence

Nucleic Acid Accession #: none found

40 Coding sequence: 1-36 (underlined sequences correspond to start and stop codons)

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45     1      11      21      31      41      51
      |      |      |      |      |      |
      CTGGATGATA TGGAAGAAAT GGATGGGTAA AGGTAAAAGG CTGATCACAG ATGGGTTTCCT 60
      CTCAAGGTTA AAATAGTTTA AGTGCCAGAA GAAAGGTTGG GCACCAGCGA ATTAAGAACC 120
      ATCTTTGAAT GGTCCCCTTG GTTAAATACT TAACTTTGT CATCAGTGTC TGCATTATATG 180
      AAATGAAGAG GAATTCACCT ATATGCTACG TGATCTTTTG TTTGTCATGA AAAGAGTTAC 240
      TGTGTGTAG TTCTCTGTTT CAGGGCTGCC TTTGCTCCAC AAAGCACTGA GAAGCAGTGG 300
50     CCCTGTACAA CCATACTGCC TCTCAACACT GTGTAATAGG CTAACACCGC CCAGCGAACC 360
      TTCCTGGGAG ATATAAATA CATAGGTTTA GGCTGGCAAA AAAAAAAAAA AAA

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Seq ID No: 155 Protein sequence:

Protein Accession #: none found

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55     1      11      21      31      41      51
      |      |      |      |      |      |
      LDDMEEMDGL R
60

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Seq ID NO: 156 DNA sequence

Nucleic Acid Accession #: NM_032961.1

65 Coding sequence: 827-3949 (underlined sequences correspond to start and stop codons)

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70     1      11      21      31      41      51
      |      |      |      |      |      |
      CAGGCTCAGA GGCTGAAGCA GGAGGAAGGA AGGACTGGAA GGAAAAAGAG ACAGGTTAGA 60
      GGGAAAGAGG CTTGGGAAGA AAACAGCAGA AAAGAAACTG CTCATTACAC TTACAGAGAG 120
      GCAAGTAACG GTGGAGATGA GGACAGAGGG AACCAAGACT CTGAAAGACA AAAAATACAA 180
      ATAGAGCGAA AGAGGAAAAA AATGTCAAGA AGAACATCCA TCCGGAGAAA TGAAGAGAAT 240
      GAAAGTTTAA AACTGCAGAG CCGTTCCTGT CTTTCCGGC ACAAATTTAT ATCGCTGATT 300
75     TTAAGCCCTT TTGCAATTGC CAGCCGTTGA CATTAAAGAG CATGTTTAAC GGTGCCAACA 360
      GCATCTCCTT TTCCTTCTCC TCTTCTCTT CTTCTTCTTC CTCCTCTCC TCCTCTTTT 420

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	CCTCCTCCTC	GTTCTCCTCC	CATCAGCAAG	AAGACAAACC	GAGGACAGTC	TTGAAATATC	480
	GAAATTTCTT	CTTTGGGATT	TGCCAGCGCC	AAGACTGTCT	GAATAAAGGA	CGCTGACTAT	540
	TGTATTATTG	TTATTTTATT	AATTAGTCAG	TGGAAAGATT	ACAGATGAGG	AAAGGGGACG	600
	CCTGTCACCC	TTCTGTGTCT	AAGATTTTAA	AAAAAATGAG	GCTGGATTGC	GGGAAGCTCT	660
5	AAAATGAAGC	AAAAGGAGTA	AGATTTTATA	AGACAGAAAG	CCACAGGAGC	CCCCACGTAG	720
	CGCACTTTTA	TTTGTATTTT	TTTCAGATTTC	TTTTGTGTTT	GTGGTGGTGG	GGGAGGTGAT	780
	TGGGTGGCTG	ACTGGCTGCG	GGAAGCTACT	TCCTTTCCTT	TTGGAGATGA	TTGTGCTATT	840
	ATTGTTTGCC	TTGCTCTGGA	TGGTGGAAAG	AGTCTTTTCC	CAGCTTCACT	ACACGGTACA	900
	GGAGGAGCAG	GAACATGGCA	CTTTCGTGGG	GAATATCGCT	GAAGATCTGG	GTCTGGACAT	960
10	TACAAAACCT	TCGGCTCGCG	GGTTTCAGAC	GGTGCCCAAC	TCAAGGACCC	CTTACTTAGA	1020
	CCTCAACCTG	GAGACAGGGG	TGCTGTACGT	GAACGAGAAA	ATAGACCGCG	AACAAATCTG	1080
	CAAACAGAGC	CCCTCCTGTG	TCCTGCACCT	GGAGGTCTTT	CTGGAGAACC	CCCTGGAGCT	1140
	GTTCCAGGTG	GAGATCGAGG	TGCTGGACAT	TAATGACAAC	CCCCCTCTT	TCCCGGAGCC	1200
	AGACCTGACG	GTGAAATCT	CTGAGAGCGC	CACGCCAGGC	ACTCGCTTCC	CCTTGGAGAG	1260
15	CGCATTCGAG	CCAGACGTGG	GCACCAACTC	CTTGCGCGAC	TACGAGATCA	CCCCCAACAG	1320
	CTACTTCTCC	CTGGACGTGC	AGACCCAGGG	GGATGGCAAC	CGATTCTGCT	AGCTGGTGGT	1380
	GGAGAAGCCA	CTGGACCGAG	AGCAGCAAGC	GGTGCACCGC	TACGTGCTGA	CCGCGGTGGA	1440
	CGGAGGAGGT	GGGGGAGGAG	TAGGAGAAGG	AGGGGGAGGT	GGCGGGGGAG	CAGGCCGTGC	1500
	CCCCCAGCAG	CAGCGCACCC	GCACGGCCCT	ACTCACCATC	CGAGTGCTGG	ACTCCAATGA	1560
20	CAATGTGCCC	CGTTTCGACC	AACCCGTCTA	CACGTGTGTC	CTACCAGAGA	ACTCTCCCCC	1620
	AGGCACTCTC	GTGATCCAGC	TCAACGCCAC	CGACCCGGAC	GAGGGCCAGA	ACGGTGAGGT	1680
	CGTGTACTCC	TTACAGCACC	ACATTTTCGCC	CCGGGCGCGG	GAGCTTTTCG	GACTCTCGCC	1740
	GGCACTGGC	AGACTGGAGG	TAAGCGGCGA	GTTGGACTAT	GAAGAGAGCC	CAGTGTACCA	1800
	AGTGACGTG	CAAGCCAAGG	ACCTGGGCCC	CAACGCCGTG	CCTGCGCACT	GCAAGGTGCT	1860
25	AGTGCGAGTA	CTGGATGCTA	ATGACAACGC	GCCAGAGATC	AGCTTCAGCA	CCGTGAAGGA	1920
	AGCGGTGAGT	GAGGGCGCGG	CGCCCGGCAG	TGTGGTGGCC	CTTTTCAGCG	TGACTGACCG	1980
	CGACTCAGAG	GAGATGGGGC	AGGTGCAGTC	CGAGCTACTG	GGAGACGTGC	CTTTCCGCCT	2040
	CAAGTCTTCC	TTTAAGAATT	ACTACACCAT	CGTTACCGAA	GCCCCCTTGG	ACCGAGAGGC	2100
	GGGGGACTCC	TACACCCTGA	CTGTAGTGGC	TCGGGACCGG	GGCGAGCCTG	CGCTCTCCAC	2160
30	CAGTAAGTCG	ATCCAGGTAC	AAGTGTCCGA	TGTGAACGAC	AACGCGCCGC	GTTTCAGCCA	2220
	GCCGGTCTAC	GACGTGTATG	TGACTGAAAA	CAACGTGCCT	GGCGCCTACA	TCTACGCGGT	2280
	GAGCGCCACC	GACCCGGATG	AGGGCGCCAA	CGCCAGCTT	GCCTACTCTA	TCCTCGAGTG	2340
	CCAGATCCAG	GGCATGAGCG	TCTTACCTTA	CGTTTCTATC	AACCTCTAGA	ACGGCTACTT	2400
	GTACGCCCTG	CGTCTCTTCG	ACTATGAGCA	GCTGAAGGAC	TTCAGTTTTT	AGGTGGAAGC	2460
35	CCGGGACGCT	GGCAGCCCCC	AGGCGCTGGC	TGGTAACGCC	ACTGTCAACA	TCCTCATAGT	2520
	GGATCAAAAT	GACAACGCCC	CTGCCATCGT	GGCGCCTCTA	CCAGGGCGCA	ACGGGACTCC	2580
	AGCGCGTGAG	GTCCTGCCCC	GCTCGGCGGA	GCCGGGTAC	CTGCTCAGCC	GCGTGGCCGC	2640
	CGTGGACGCG	GACGACGGCG	AGAACGCCCG	GCTCACTTAC	AGCATCGTGC	GTGGCAACGA	2700
	AATGAACCTC	TTTTCGATGG	ACTGGCGCAG	CGGGGAGCTG	CGCACAGCAC	GCCGAGTCCC	2760
40	GGCCAAGCGC	GACCCGAGC	GGCCTTATGA	GCTGGTGATC	GAGGTGCGCG	ACCATGGGCA	2820
	GCCGCCCTTT	TCCTCCACCG	CCACCCTGGT	GGTTCAGCTG	GTGGATGGCG	CCGTGGAGCC	2880
	CCAGGGCGGG	GGCGGGAGCG	GAGGCGGAGG	GTCAGGAGAG	CACCAGCGCC	CCAGTCGCTC	2940
	TGGCGGCGGG	GAAACCTCGC	TAGACCTCAC	CCTCATCCTC	ATCATCGCGT	TGGGCTCGGT	3000
45	GTCCTTCATC	TTCTCTGCTG	CCATGATCGT	GCTGGCCGTG	CGTTGCCAAA	AAGAGAAGAA	3060
	GCTCAACATC	TATACTTGTC	TGGCCAGCGA	TTGCTGCCTC	TGCTGCTGCT	GCTGCGGTGG	3120
	CGGAGGTTCT	ACCTGTCTGT	GCCGCCAAGC	CCGGGCGCGC	AAGAAGAAAC	TCAGCAAGTC	3180
	AGACATCATC	GCTGTGCGA	GCTCCAATGT	ACCCAGTAAC	CCGGCCGAGG	TGCCGATAGA	3240
	GGAGTCCGGG	GGCTTTGGCT	CCCACCACCA	CAACCAGAAT	TACTGCTATC	AGGTATGCCT	3300
	GACCCTGAG	TCCGCCAAGA	CCGACCTGAT	GTTTCTTAAG	CCCTGCAGCC	CTTCGCGGAG	3360
50	TACGGACACT	GAGCACAAAC	CTGCGGGGCG	CATCGTCACC	GGTTACACCG	ACCAGCAGCC	3420
	TGATATCATC	TCCAACGGAA	GCATTTTGTG	CAACGAGACT	AAACACCAGC	GAGCAGAGCT	3480
	CAGCTATCTA	GTTGACAGAC	CTCGCCGAGT	TAACAGTTCT	GCATTCAGG	AAGCCGACAT	3540
	AGTAAGCTCT	AAGGACAGTG	GTCATGGAGA	CAGTGAACAG	GGAGATAGTG	ATCATGATGC	3600
	CACCAACCTG	GCCCAGTCAG	CTGGTATGGA	TCTCTTCTCC	AATTGCACTG	AGGAATGTAA	3660
55	AGCTCTGGGC	CACCTCAGATC	GGTGTCTGGT	GCCTTCTTTT	GTCCCTTCTG	ATGGACGCCA	3720
	GGCTGCTGAT	TATCGCAGCA	ATCTGCATGT	TCCTGGCATG	GACTCTGTTC	CAGACACTGA	3780
	GGTGTTTGAA	ATCCAGAAAG	CCGAGCCTGG	GGCAGAGCGG	TCCTTTTCCA	CCTTTGGCAA	3840
	AGAGAAGGCC	CTTCACAGCA	CTCTGGAGAG	GAAGGAGCTG	GATGGACTGC	TGACTAATAC	3900
	GCGAGCGCCT	TACAAACCAC	CATATTTGAC	ACGGAAGAGG	ATATGCTAGT	CAATTCTACA	3960
60	GGACTTACCT	GAAGCAGCAT	GATTTGCACA	AAGTCGACCA	ACAAAAGCAT	CAACTTTTCA	4020
	ACTTCATTAT	CTTGGCCATC	CAGTTAGTCA	TGTGTAACCT	AGTATTAGAT	TTCGGATGGA	4080
	GTCATCATGG	CCAATTATAG	GACCTAATTG	CTCTCAGCAG	GCCTGAGAAA	TGAGTTGAAA	4140
	TGTGCGAAGC	TGTAGAAACT	TTAGAGGCCA	CAGATTTTGC	CTCCCCGATC	AGTGTGTGCC	4200
65	TGTTTACAGC	ACTATCTATC	TTTCTCTCTC	CAAATGTCAC	TGAGCCCTTT	AGATGTTTAT	4260
	ATTACCACAG	AGAAGCCAGT	CATAAAGATA	AAGGAAATTT	GTGCATTATA	AATGCAATAT	4320
	CACTGTTTTA	AACCTGACTG	TTTTATATTA	TTTTTGTGTG	ATCAAGTGT	CCGCAAGCTA	4380
	TTTCAACTTT	ACAAGAGAAA	TTGTGATTAT	GTTCTTTTCA	CCTGTGGGTT	ATAAAAAATG	4440
	TTGTATTCTG	AAGACCCACA	AAATATCAAA	GACATTTCTG	AGTTTATACA	CCGTGTTGCA	4500
70	AAGTGTTTAC	TGTACTATTT	CAAAGCTTCT	AAATAAATAT	AAAATATATA	TATTATATTA	4560
	TATAATTTTC	CTAAAATGTG	GTACAACCTA	GTTGGTTTTT	AAATGGATGC	ATACAGTCCA	4620
	CATACATCAA	TAAAATAAAA	GGTAATTCAG	GGTCCCAAAG	ACAAACTTAC	TAAGAAAAAA	4680
	TCATTAATAG	TTTTCTCCCA	ATTTCCATAT	CTTACTCAAC	CGTGTTTTTC	CTTGTTTAAA	4740
	AGAAAAATGAT	GCTCTAAGCT	ACAAAATTTT	GTCAAAAAC	CATATTGAAT	TTTCAATGCC	4800
75	AAAGATGTAG	CTAATTGATG	TATCAGACAG	AGCACTGACT	ATGTACTATC	AAACTATCTA	4860
	ACAATCTGCA	TAAGTCTGAT	TCTATTTCTA	TGACTTTGAA	TTTAGAATCA	CTTAAAGCTT	4920
	TTATAAAGAA	TCGATAAATT	CACCTGTATT	TGTTGTTAGA	AAAAAACTGG	GTGTCTGTAC	4980

ATTTTGTGGT GTAAATATG TAATTGAAGA TTTACTATTTT AAGAAGTCAT CAGTCATATC 5040
 ACTCACACAG AATTTTATTT TACATAGTTT TGTGACTTAA TTACACATGA ATATAAAATC 5100
 TATAATTCTA TATGAATATA TAGAGATATA GAAACATCTG AACTGGTAAA GAATAACTAT 5160
 AAAATATGAA AGCTCTAAAT TTTAAATATA TTTAGAGATA GAATCATGGT ACATTATTGT 5220
 TTCAGTATTC CATGTAAAAA TTTTATAGCT TAAATGTAGT CAGTGTGTTGA TTAATGAAAA 5280
 AATTCTTCAT GAGTCAGCCT TCAAAAGTTA AGCTTGCCCT TTTACTTTTAT GTCAACAATA 5340
 TTAATTATTA AATTTAGTAA GACGCAAAAA AAAAAAAAAA AAAA

Seq ID No: 157 Protein sequence
 Protein Accession #: NP_116586.1

1 11 21 31 41 51
 15 MIVLLLLFALL WMVEGVFSQL HYTVQEEQEH GTFVGNIAED LGLDITKLSA RGFQTPVNSR 60
 TPYLDLNLLET GVLYVNEKID REQICKQSPS CVLHLEVFL E NPLELFQVEI EVLDINDNPP 120
 SFPEPDLTVE ISESATPGTR FPLESAPDPD VGTNSLRDYE ITPNSYFSLD VQTQGDGNRF 180
 AELVLEKPLD REQQAVHRYV LTAVDGGGGG GVGEGGGGGG GAGLPPQQQR TGTALLTIRV 240
 20 LDSNDNVPAF DQPVYTVSLP ENSPPGTLVI QLNATDPDEG QNGEVVYSFS SHISPRAREL 300
 FGLSPRTGRL EVSGELDYEE SPVYQVYVQA KDLGPNVPA HCKVLVRVLD ANDNAPEISF 360
 STVKEAVSEG AAPGTVVALF SVTDRDSEEN GQVQCELLGD VPFRLKSSF K NYTIVTEAP 420
 LDREAGDSYT LTVVARDRGE PALSTSKSIQ VQVSDVNDNA PRFSQPVYDV YVTENNVPGA 480
 YIYAVSATDR DEGANALQAY SILECQIQGM SVFTYVSINS ENGYLYALRS FDYBQLKDFS 540
 25 FQVEARDAGS PQALAGNATV NILIVDQNDN APAIVAPLPG RGTGPAREVL PRSAEPGYLL 600
 TRVAAVDADD GENARLTYSI VRGNEMNLFR MDWRTGELRT ARRVPKRD P QRPYELVIEV 660
 RDHGQPPPLSS TATLVVQLVD GAVEPQGGGG SGGGGSGEHQ RPSRSGGGET SLDLTLILII 720
 ALGSVSFIFL LAMIVLAVRC QKEKKLNIYT CLASDCCLCC CCCGGGGSTC CGRQARARKK 780
 KLSKSDIMLV QSSNVPSPNA QVPIEESGGF GSHHHNQNYC YQVCLTPESA KTDLMFLKPC 840
 30 SPSRSTDTEH NPGCAIVTGY TDQOPDIISN GSILSNETKH QRAELSYLVD RPRRVNSSF 900
 QEADIVSSKD SGHGDSQQGD SDHDATNRAQ SAGMDLFSNC TEECKALGHS DRCWMPSPFV 960
 SDGRQAADYR SNLHVPGMDS VPDTEVFETP EAQPGAERSF STFGKEKALH STLERKELDG 1020
 LLTNTRAPYK PPYLTRKRIC

Seq ID NO: 158 DNA sequence

Nucleic Acid Accession #: NM_022159.1

Coding sequence: 70-1890 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 40 GTGAAATTTA AACTCCAGTC CTGTGGCGAA AATGCTAATT GCACTAACAC AGAAGGAAGT 60
 TATTATTGTA TGTGTGTACC TGGCTTCAGA TCCAGCAGTA ACCAAGACAG GTTTATCACT 120
 AATGATGGAA CCGTCTGTAT AGAAAAATGTG AATGCAAACT GCCATTTAGA TAATGTCTGT 180
 45 ATAGCTGCAA ATATTAATAA AACTTTAACA AAAATCAGAT CCATAAAAGA ACCTGTGGCT 240
 TTGCTACAAG AAGTCTATAG AAATTCTGTG ACAGATCTTT CACCAACAGA TATAATTACA 300
 TATATAGAAA TATTAGCTGA ATCATCTTCA TTTACTAGTT ACAAGAACAA CACTATCTCA 360
 GCCAAGGACA CCCTTTCTAA CTCAACTCTT ACTGAATTG TAAAAACCGT GAATAATTTT 420
 GTTCAAAGGG ATACATTTGT AGTTTGGGAC AAGTTATCTG TGAATCATAG GAGAACACAT 480
 50 CTTACAAAAC TCATGCACAC TGTTTGAACAA GCTACTTTAA GGATATCCCA GAGCTTCCAA 540
 AAGACCACAG AGTTTGATAC AAATTCAACG GATATAGCTC TCAAAGTTTT CTTTTTTGAT 600
 TCATATAACA TGAAACATAT TCATCCTCAT ATGAATATGG ATGGAGACTA CATAAATATA 660
 TTTCCAAAGA GAAAAGCTGC ATATGATTCA AATGGCAATG TTGCAGTTGC ATTTTATAT 720
 TATAAGAGTA TTGGTCTTTG GCTTTTCATCA TCTGACAACT TCTTATTGAA ACCTCAAAAT 780
 TATGATAATT CTGAAGAGGA GGGAAAGAGTC ATATCTTCAG TAATTTTCAGT CTCATGAGC 840
 55 TCAAACCCAC CCACATTATA TGAACCTGAA AAAATAACAT TTACATTAAG TCATCGAAAG 900
 GTCACAGATA GGTATAGGAG TCTATGTGCA TTTTGGAAAT ACTCACCTGA TACCATGAAT 960
 GGCAGCTGCT CTTCAAGAGG CTGTGAGCTG ACATACTCAA ATGAGACCCA CACCTCATGC 1020
 CGCTGTAATC ACCTGACACA TTTTGCAATT TTGATGTCCT CTGGTCTTTC CATTGGTATT 1080
 60 AAAGATTATA ATATTCTTAC AAGGATCACT CAACTAGGAA TAATTATTTT ACTGATTTGT 1140
 CTTGCCATAT GCATTTTTC CTTCTGGTTC TTCAGTGAAA TTCAAAGCAC CAGGACAACA 1200
 ATTCAAAAAA ATCTTTGCTG TAGCCTATTT CTTGCTGAAC TTGTTTTTCT TGTGGGATC 1260
 AATACAAATA CTAATAAGCT CTTCTGTTC ATCATTGCCG GACTGCTACA CTACTTCTTT 1320
 TTAGCTGCTT TTGCATGGAT GTGCATTGAA GGCATACATC TCTATCTCAT TGTGTGGGT 1380
 65 GTCATCTACA ACAAGGGATT TTTGCACAAG AATTTTATA TCTTTGGCTA TCTAAGCCCA 1440
 GCCGTGGTAG TTGGATTTTC GGCAGCACTA GGATACAGAT ATTATGGCAC AACCAGAGTA 1500
 TGTGGCTTA GCACCGAAAA CAACTTTATT TGGAGTTTTA TAGGACCAGC ATGCCATAATC 1560
 ATTCTTGTTA ATCTCTTGCG TTTTGGAGT ATCATATACA AAGTTTTTCG TCACACTGCA 1620
 GGGTTGAAAC CAGAAGTTAG TTGCTTTGAG AACATAAGGT CTTGTGCAAG AGGAGCCCTC 1680
 70 GCTCTTCTGT TCCTTCTCGG CACCACCTGG ATCTTTGGGG TTCTCCATGT TGTGCACGCA 1740
 TCAGTGGTTA CAGCTTACCT CTTCAAGATC AGCAATGCTT TCCAGGGGAT GTTCATTTT 1800
 TTATTCTGTT GTGTTTTATC TAGAAAGATT CAAGAAGAA ATTACAGATT GTTCAAAAA 1860
 GTCCCCTGTT GTTTTGGATG TTTAAGGTAA ACATAGAGAA TGGTGGATAA TTACAACCTGC 1920
 ACAAATAATA AAATTCCAAG CTGTGGATGA CCAATGTATA AAAATGACTC ATCAAAATTAT 1980
 75 CCAATTATTA ACTACTAGAC AAAAAGTATT TTAAATCAGT TTTTCTGTTT ATGCTATAGG 2040
 AACTGTAGAT ACTAAGGTAA AATTATGTAT CATATAGATA TACTATGTTT TTCTATGTGA 2100
 AATAGTTCTG TCAAAAATAG TATTGCAGAT ATTTGGAAAG TAATTGGTTT CTCAGGAGTG 2160

ATATCACTGC ACCCAAGGAA AGATTTTCTT TCTAACACGA GAAGTATATG AATGTCCTGA 2220
 AGGAAACAC TGGCTTGATA TTTCTGTGAC TCGTGTGACC TTGAAACTA GTCCCTACC 2280
 ACCTCGGTAA TGAGCTCCAT TACAGAAAGT GGAACATAAG AGAATGAAGG GGCAGAATAT 2340
 CAAACAGTGA AAAGGGAATG ATAAGATGTA TTTTGAATGA ACTGTTTTTT CTGTAGACTA 2400
 5 GCTGAGAAAT TGTTGCATA AAATAAGAA TTGAAGAAAC ACATTTTACC ATTTTGTGAA 2460
 TTGTTCTGAA CTAAATGTC CACTAAACA ACTTAGACTT CTGTTTGCTA AATCTGTTTC 2520
 TTTTCTAAT ATTCTAAA

Seq ID No: 159 Protein sequence:
 Protein Accession #: NP_071442.1

1 11 21 31 41 51
 | | | | | |
 15 MCVPGFRSSS NQDRFITNDG TVCIENVNAN CHLDNVCIAA NINKTLTKIR SIKEPVALLQ 60
 EVYRNSVTDL SPTDIITYIE ILAESSLLG YKNNTISAKD TLSNSTLTFE VKTVNNFVQR 120
 DTFVVDKLS VNHRRTHLTK LMHTVEQATL RISQSFQKTT EFDNSTDIA LKVFVFDSDYN 180
 MKHIHPHMNM DGDYINIFPK RKAAYDSNGN VAVAFLYYKS IGPLLSSSDN FLLKPQNYDN 240
 20 SEEERVISS VISVSMSSNP PLYELEKIT PTLSHRKVTD RYRSLCAFVN YSPDTMNGSW 300
 SSEGCELTYS NETHTSCRCN HLTHFAILMS SGPSIGIKDY NILTRITQLG IISLICLAI 360
 CIPTFWFFSE IQSTRITTHK NLCCSLFLAE LVFLVGINTN TNKLFCIIA GLLHYFFLAA 420
 FAWMCIEGHI LYLVIVGVIIY NKGFLHKNFY IFGYLSPAVV VGFSAAALGYR YYGTTKVCWL 480
 STENNFWSF IGPACLIILV NLLAFGVIIY KVRHTAGLK PEVSCFENIR SCARGALALL 540
 25 FLLGTTWIFG VLHVHVASV TAYLFTVSNA FQGMFIFLFL CVLSRKIQEE YYRLFKNVPC 600
 CFGCLR

Seq ID NO: 160 DNA sequence

Nucleic Acid Accession #: none found

Coding sequence: 1-216 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | | |
 35 TGCTGCTTA TGCGGTGGCT CGCTGCTCAG AACAGGATGG CAGAGATGAG CACCACCATC 60
 AAAAACTCAA GGACCACTGC TGTGGGTCCA GTCATCTGTT TCATGGAATT CACCAGTCTG 120
 GTATCTTCAA AATCCAGAAG GATGATGGCA GATGGCAGGA AGGAGGAAGA GGGTAATCTG 180
 GAAGAGTTTC CTGACCTACT CTGCTGCTGT GATTAAACAA CCACCAGGAA ATTTTGTATGA 240
 CACTGTTCTC CTGAGCTCCT CCCTTTCCTC GGGGAAGAAA AGCATTGAAA CTACAAAAAT 300
 40 AAAGTGTTAT TTGGCTGGAG TGAGGTCTCA TGTCTGCTTA TGCGGTGGCT CGCTGCTCAG 360
 AACAGGGAAC CATTTGAGAT ACTCATTACT CTTTGAAGGC TTACAGTGGA ATGAATTCAA 420
 ATACGACTTA TTTGAGGAAT TGAAGTTGAC TTTATGGAGC TGATAAGAAT CTTCTGGAG 480
 AAAAAAAGAC TGGTACTTCT GAATTAACCA AATCACAGT ATTCTGAAGA TGATTCTACA 540
 AAGCCTGCTG TTTCTACAAA GGCTGCTGAT GATTCTACA AAGCCTGCTG TAGTGTGCT 600
 45 GTGGCCTCTG CTTAAAAAAG TAGAAAACAC ATTGATGCAG CATGTTCCACC CCAACCTCCC 660
 TGCTTAAAGG CTCAGGGGACC ATCTTGAAG AGGAAGGCGC GTGAGATTGT AAGAGCCGAA 720
 TTAGGGGGAT GAGGTGTGGA GAATAAGGAC ACTTCATCTT GGATGCTCAC CTGCCAAATT 780
 GACTTCTGAT GAAAGCCAGC TCCAGAAATG TGCCTACAGT TACTACTTTC ACCTAAACCC 840
 TGCCCTTAGT CAAATCCTTC TCTTCTCTA AGCAATCAAC TTCAATTCCT TGTATAACCC 900
 50 ACAGTATAAA AGGGCTTTTA TACCATTCTA TCCTATTGCA TGTAAGCCTT GGGCTGCGGA 960
 GGTAACAGTG TGGGATTCCA CCATCTCATC TCCCTGCCAC CCAACATGCT CTGCTCTTCT 1020
 TTAAGCAATA TTAAATGTTT GTACTTCA

Seq ID No: 161 Protein sequence:

Protein Accession #: none found

1 11 21 31 41 51
 | | | | | |
 60 CLLMRWLAAQ NRMAEMSTTI KNSRTSAVGP VICFMEFTSL VSSKSRMMMA DGRKEEGNLL 60
 EEFPDLLCC D

Seq ID NO: 162 DNA sequence

Nucleic Acid Accession #: none found

Coding sequence: 1-159 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | | |
 70 GAGACCCTCC AGAGGCAGGG CCCAGGATTG AAGAGGGAAG CCCTGCTCCA CACGTGTTCA 60
 TCAGGAAGGA CCCACAGACT GCTGCTCCTG GAGGCCTCTC GGTTTATGGA TGTGTGTTTG 120
 TTCCATAAAC CCTCAGAGGG TCACCTGGAG ACCCGCTAAA ATGCAGGTTT TGGGGCCACA 180
 TCCTAGACCT TCTGACCGAC CCAGGGAGTG GGGCCAGGA AGCTGCATTT GACAGATATC 240
 CCCGTGTGAT CATCATGCAC ACAGGAGTGA GAGAACCACT GTTCTCCCG GGCAGAAGGG 300
 75 AAGCTCGTGT GCAGGACACC TCACACCTCC TTTCCCATTC CCCTGCCAGG CTCTCCCTGC 360
 TGACATTGTT TTTGCGGGAG AGCTGTGAAT TCTGAAGATT AGGTTGCTTC TCACCCCAAG 420

CTCCAGAAGT CCAGGCTGAG CCAAACCAAG CTTCAGTTG TGCCTGGACT TGGAGAACCA 480
GGAGGTGAGG GGACTGACTA CTTGAAGATC ACATGGAGGA GGAGTCTGAT CCAGGCCAG 540
GCACCAAGGA AAGGCCATGC AAGGACACAG GGAGAAGGGC AGCTGTCTGT AAGCCAGAAA 600
GAGCCTTCAC TAGAAACCAA ATCAGCCAGA ACCTTCATCT TGGACTTTCC AGCCTTCAGA 660
5 GATGTGAAAA AATAAATTC TGTGATTAA CCTAAAAA

Seq ID No: 163 Protein sequence:

Protein Accession #: none found

1 11 21 31 41 51
| | | | | |
15 ETLQRQGPGL KREALLHTCS SGRTHRLLLL BASRFMDVCL FHKPSEGHLE TR

Seq ID NO: 164 DNA sequence

Nucleic Acid Accession #: NM_020241.1

Coding sequence: 4-1557 (underlined sequences correspond to start and stop codons)

20 1 11 21 31 41 51
| | | | | |
GCCATGCAGA CCCC GCGAGC GTCCCTCCC CGCCCGGCC TCCTGCTTCT GCTGCTGCTA 60
CTGGGGGGCG CACACGGCCT CTTTCTGAG GAGCCGCGC CGCTTAGCGT GGCCCCCAGG 120
25 GACTACCTGA ACCACTATCC CGTGTGTGT GGCAGCGGC CCGGACGCCT GACCCCCGCA 180
GAAGGTGCTG ACACCTCAA CATCCAGCGA GTCTGCGGG TCAACAGGAC GCTGTTCAAT 240
GGGGACAGGG ACAACCTCTA CCGCGTAGAG TTGGAGCCCC CCACGTCCAC GGAGCTGCGG 300
TACCAGAGGA AGCTGACCTG GAGATCTAAC CCCAGCGACA TAAACGTGTG TCGGATGAAG 360
GGCAAACAGG AGGGCGAGTG TCGAACTTC GTAAAGGTGC TGCTCCTTCG GGACGAGTCC 420
ACGCTCTTTG TGTGCGGTTT CAACGCCTTC AACCCGGTGT GCGCCAACTA CAGCATAGAC 480
30 ACCCTGCAGC CCGTCGGAGA CAACATCAGC GGTATGGCCC GCTGCCCGTA CGACCCCAAG 540
CACGCCAATG TTGCCCTCTT CTCTGACGGG ATGCTCTTCA CAGCTACTGT TACCGACTTC 600
CTAGCCATTG ATGCTGTCTAT CTACCGCAGC CTCGGGGACA GGCCCAACCT GCGCACCGTG 660
AAACATGACT CCAAGTGGTT CAAAGAGCCT TACTTTGTCC ATGCGGTGGA GTGGGGCAGC 720
35 CATGTCTACT TCTTCTTCCG GGAGATTGCG ATGGAGTTTA ACTACCTGGA GAAGGTGGTG 780
GTGTCCCGCG TGGCCCGAGT GTGCAAGAAC GACGTGGGAG GCTCCCCCGG CGTGCTGGAG 840
AAGCAGTGGA CGTCTTCTCT GAAGGCGCGG CTCAACTGCT CTGTACCCGG AGACTCCCAT 900
TTCTACTTCA ACGTGTGCA GGCTGTACG GCGGTGGTCA GCCTCGGGGG CCGGCCCGTG 960
GTCCTGGCCG TTTTTCAC GCCCAGCAAC AGCATCCCTG GCTCGGCTGT CTGCGCCTTT 1020
40 GACCTGACAC AGGTGGCAGC TGTGTTTGAA GGCGGCTTCC GAGAGCAGAA GTCCCCCGAG 1080
TCCATCTGGA CGCCGGTGCG GGAGGATCAG GTGCCTCGAC CCCGGCCCCG GTGCTGCGCA 1140
GCCCCCGGGA TGCAGTACAA TGCTCCAGC GCCTTGCCGG ATGACATCCT CAACTTTGTC 1200
AAGACCACCC CTCTGATGGA CGAAGCGGTG CCCTCGCTGG GCCATGCGCC CTGGATCCTG 1260
CGGACCCTGA TGAGGCACCA GCTGACTCGA GTGGCTGTGG ACGTGGGAGC CGGCCCTTGG 1320
45 GGCAACCAGA CCGTTGTCTT CCTGGGTTCT GAGGCGGGGA CGGTCTCTAA GTTCCTCGTC 1380
CGGCCCAATG CCAGCACCTC AGGGACGTCT GGGCGTGTGT GTCAAGTGGG CCACGCGTGC 1440
AGGGTGTGTG TCCACGAGCG ACATCGTGG TGGCCCCAGC GGCTGGGCG TTGGCTGAGC 1500
CGACGCTGGG GCTTCCAGAA GGCCCCGGGG CCTCCGAGGT GCCGGTTAGG AGTTTGAACC 1560
CCCCCACTC TGCAGAGGGA AGCGGGGACA ATGCCGGGGT TTCAGGCAGG AGACACGAGG 1620
50 AGGGCCTGCC CGGAAGTCAC ATCGGCAGCA GCTGTCTAAA GGGCTTGGGG GCCTGGGGGG 1680
CGGCGAAGGT GGGTGGGGCC CCTCTGTAAA TACGGCCCCA GGGTGGTGAG AGAGTCCCAT 1740
GCCACCCGTC CCCTTGTGAC CTCCCCCTC TGACCTCCAG CTGACCATGC ATGCCACGTG 1800
G

Seq ID No: 165 Protein sequence:

Protein Accession #: NP_064626.1

1 11 21 31 41 51
| | | | | |
60 MQTPRASPPR PALLLLLLLLL GGAHGLFPEE PPPLSVAPRD YLNHYVPFVG SGPGRLTPAE 60
GADDLNIQRV LRVNRTLFIG DRDNLYRVEL EPPTSTELRY QRKLWRSNP SDINVCRMKG 120
KQEGECRNFF KVLLLRDEST LFVCGSNAFN PVCANYSIDT LQPVGDNISG MARCPYDPKH 180
ANVALFSDGM LFTATVDFDL AIDAVIYRSL GDRPTLRTVK HDKWFKEPY FVHAVEWGS 240
VYFFFREIAM EFNYLEKVVV SRVARVCKND VGGSPRVLEK QWTSFLKARL NCSVPGDSHF 300
YFNVLQAVTG VVSLGGRPVV LAVFSTPSNS IPGSAVCAFD LTQVAVFEG RFREQKSPES 360
65 IWTVPVEDQV PRPRPGCAA PGMQYNASSA LPDDILNFVK THPLMDEAVP SLGHAPWILR 420
TLMRHQLTRV AVDVGAGPVG NQTVVFLGSE AGTVLKFVLR PNASTSGTSG RVCQVGHACR 480
VCVHERRSWW PQRPRWLRSR RWGFQKARGP PRCRLGV

Seq ID NO: 166 DNA sequence

Nucleic Acid Accession #: NM_032108.1

Coding sequence: 39-2705 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
| | | | | |
75 TCCGAGGCGT CACCTCCTCC TGTCGCTGG CCTCGCCAT GCAGACCCCG CGAGCGTCCC 60
CTCCCCGCCC GGCCCTGCTG CTTCTGCTGC TGCTACTGGG GGGCGCCAC GGCCTCTTTC 120

CTGAGGACCC GCCGCCGCTT AGCGTGGCCC CCAGGGACTA CCTGAACCAC TATCCCGTGT 180
 TTGTGGGACG CGGGCCCGGA CGCCTGACCC CCGCAGAAGG TGCTGACGAC CTCAACATCC 240
 AGCGAGTCTGT GCGGGTCAAC AGGACGCTGT TCATTGGGGA CAGGGACAAC CTCTACCGCG 300
 TAGAGCTGGA GCGGGCCACG TCCACGGAGC TGGCGTACCA GAGGAAGCTG ACCTGGAGAT 360
 5 CTAACCCAG CGACATAAAC GTGTGTTCGA TGAAGGGCAA ACAGGAGGGC GAGTGTGCGA 420
 ACTTCGTAAG GGTGCTGCTC CTTCGGGACG AGTCCACGCT CTTGTGTGTC GGTTCACACG 480
 CCTTCAACCC GGTGTGCGCC AACTACAGCA TAGACACCTT GCAGCCCGTC GGAGACAACA 540
 TCAGCGGTAT GGGCCGCTGC CCGTACGACC CCAAGCACGC CAATGTTGCC CTCTTCTCTG 600
 ACGGGATGCT CTTACAGCTT ACTGTTACCG ACTTCCTAGC CATGATGCTG GTCATCTACC 660
 10 GCAGCCTCGG GGACAGGCCC ACCCTGCGCA CCGTGAAACA TGACTCCAAG TGGTTCAAAG 720
 AGCCTTACTT TGTCCATGCG GTGGAGTGGG GCAGCCATGT CTACTTCTTC TTCCGGGAGA 780
 TTGCGATGGA GTTTAACTAC CTGGAGAAGG TGGTGGTGTG CCGCGTGGCC CGAGTGTGCA 840
 AGAACGACGT GGGAGGCTTC CCGCGGTGTC TGGAGAAGCA GTGGACGTCC TTCCTGAAGG 900
 CGCGGCTCAA CTGCTCTGTA CCGGAGACT CCCATTTCTA CTTCAACGTG CTGCAGGCTG 960
 15 TCACGGGCGT GGTGAGCTC GGGGGCCGCG CCGTGGTCTT GGCCGTTTTT TCCACGCCCA 1020
 GCAACAGCAT CCCTGGCTCG GCTGTCTGCG CCTTTGACCT GACACAGGTG GCAGCTGTGT 1080
 TTGAAGGCGG CTTCGAGAG CAGAAGTCCC CCGAGTCCAT CTGGACGCCG GTGCCGAGG 1140
 ATCAGGTGCC TCGACCCCGG CCGGGGTGCT GCGCAGCCCC CGGATGTCAG TACAATGCCT 1200
 CCAGCGCCTT GCGGATGAC ATCTCAACT TTGTCAAGAC CCACCTCTG ATGGACGAGG 1260
 20 CGGTGCCCTC GCTGGGCAT GCGCCCTGGA TCCTGCGGAC CCTGATGAGG CACCAGCTGA 1320
 CTCGAGTGGC TGTGGACGTG GGAGCCGGCC CCTGGGGCAA CCAGACCGTT GTCTTCCTGG 1380
 GTTCTGAGGC GGGGACGCTC CTCAAGTTCC TCGTCCGGCC CAATGCCAGC ACCTCAGGGA 1440
 CGTCTGGGCT CAGTGTCTTC CTGGAGGAGT TTGAGACCTA CCGGCCGGA AGGTGTGGAC 1500
 GGGCCGCGCG TGGCGAGACA GGGCAGCGCG TGCTGAGCTT GGAGCTGGAC GCAGCTTCGG 1560
 25 GGGGCGTCTT GGCTGCCTTC CCGCGTGGC TGGTCCGAGT GCCTGTGGCT CGCTGCCAGC 1620
 AGTACTCGGG GTGTATGAAG AACTGTATCG GCAGTCAGGA CCCCTACTGC GGGTGGGCCC 1680
 CCGACGGCTC TGCATCTTTC CTCAGCCCGG GCACAGAGC GCCTTTGAG CAGGACGTGT 1740
 CCGGGGCCAG CACCTCAGGC TTAGGGGACT GCACAGGACT CCTGCGGGCC AGCCTCTCCG 1800
 AGGACCGCGC GGGGCTGTG TCGTGAAC TGCTGGTAAC GTCGTGCGTG GCGGCCCTTCG 1860
 30 GGGAGCTGGC CCGGCGCAAG GACAAGGAGG CCATCCTGGC GCACGGGGCG GCGAGGCGG 1920
 TGCTGAGCGT CAGCCGCTG GCGGAGCGCA GGGCGCAGGG TCCCGGGGGC CCGGGCGGAG 2040
 GCGGTGGCGG TGGCGCGGGG GTTCCCCCGG AGGCCCTGCT GCGGCCCTTG ATGCAGAACG 2100
 GCTGGGCCAA GGCCACGCTG CTGAGGGCG GCGCCACGCA CCTGGACTCG GGGCTGCTGC 2160
 35 CCACGCCCGA GCAGACGCGG CTGCGCGAGA AGCGCCTGCC CACTCCGCAC CCGCACCCCC 2220
 ACGCCTTGGG CCGCGCGGCC TGGGACCAAG GCCACCCCTT GCTCCCGGCC TCCGCTTCAT 2280
 CCTCCCTCCT GCTGCTGGCG CCGCGCGGG CCGCGGAGCA GCGCCCGCG CCTGGGGAGC 2340
 CGACCCCGCA GCGCCGCTC TATGCTGCCG GGCCCGGCCG GCCTCCAC GGCGACTTCC 2400
 40 CGCTCACCCC CCACGCCAGC CCGGACCGCC GCGGGGTGGT GTCCGCGCCC ACGGGCCCTT 2460
 TGGACCCAGC CTCAGCCGCC GATGGCCTCC CGCGGCCCTG GAGCCCGCCC CCGACGGGCA 2520
 GCCTGAGGAG GCACTTGGC CCGCACGCCG CTCGCGGCCG CACCCTGCGC CGCACCCACA 2580
 CGTTCAACAG CCGCGAGGCC CCGCCTGGGG ACCGCCACCG CGGCTGCCAC GCGCGCGCGG 2640
 GCACAGACTT GGGCCACCTC CTCCCTATG GGGGGGCGGA CAGGACTGCG CCCCCCGTGC 2700
 CCTAGGCCGG GGGCCCCCGG ATGCTTGGC AGTGCCAGCC ACGGGAACCA GGAGCGAGAG 2760
 45 ACGGTGCCAG AACGCCGGGG CCGGGGGCAA CTCCGAGTGG GTGCTCAAGT CCCCCCGCG 2820
 ACCCACCCGC GGAGTGGGGG GCGCCCTCCG CCACAAGGAA GCACAACCAG CTCGCCCTCC 2880
 CCTACCCGG GCGCGCAGGA CGCTGAGACG GTTGGGGGT GGGTGGCGG GAGGACTTTC 2940
 CTATGGATTG AGGTGAGC TTATGCGCT AGGTTTTGGT TTTTTTTGCA GTTTTGGTTT 3000
 50 CTTTTGCGGT TTTCTAACCA ATTGCACAAC TCCGTTCTCG GGGTGGCGGC AGGCAGGGGA 3060
 GGCCTGGAGC CCGGTGGGGA ATGGGGGGCC ACAGCTGCAG ACCTAAGCCC TCCCCACCC 3120
 CTGGAAGGT CCCTCCCCAA CCCAGGCCCC TGGCGTGTGT GGGTGTGCGT GCGTGTGCGT 3180
 GCGGTGTTTC TGTGCAAGGG GCGGGGGAGG TGGGCGTGTG TGTGCGTGCC AGCGAAGGCT 3240
 GCTGTGGGCG TGTGTGTCAG GTGGGCCACG CGTGCAGGGT GTGTGTCCAC GAGCGACGAT 3300
 55 CGTGGTGGCC CCAGCGGCCG GGGCGTGGC TGAGCCGACG CTGGGGCTTC CAGAAGGCC 3360
 GGGGTCTTCC GAGGTGCGCG TTAGGAGTTT GAACCCCCC CACTCTGCAG AGGGAAGCGG 3420
 GGACAATGCC GGGGTTTCAG GCAGGAGACA CGAGGAGGGC CTGCCCGGAA GTACATCGG 3480
 CAGCAGCTGT CTAAAGGGCT TGGGGGCTTG GGGGGCGGCG AAAG

60 Seq ID No: 167 Protein sequence:
 Protein Accession #: NP_115484.1

1 11 21 31 41 51
 65 MQTPRASPPR PALLLLLLLL GGAHLFPED PPPLSVAPRD YLNHPVVFVG SGPGRLTPAE 60
 GADDLNIQRV LRVNRTLFIG DRDNLYRVEL EPPTSTELRY QRKLWTRSNP SDINVCRMKG 120
 KOEGECRNFV KVLRLRDEST LFCVGSNAFN PFCANYSIDT LQPVGDNISG MARCPYDPKH 180
 ANVALFSDGM LFTATVTDFL AIDAVIYRSL GDRPTLRTVK HDSKWFKEPY FVHAEVWGS 240
 70 VYFFREIAM EFNYLEKVVV SRVARVCKND VGGSPRVLEK QWTSFLKARL NCSVPGDSHP 300
 YFNVLQAVTG VVSLGGRPVV LAVFSTPNS IPGSAVCAFD LTQVAAVFEG RFREQKSPES 360
 IWTVPEDQV PRPRPGCAA PGMQYNASSA LPDDILNFVK THPLMDEAVP SLGHAPWILR 420
 TLMRHQLTRV AVDVAGAPWG NQTVVFLGSE AGTVLKFLVR PNSTSGTSG LSVFLEEFET 480
 YRPDRCGRP GGETGQRLS LELDAASGGL LAAPRCVVR VPVARCQYS GCMKNCIGSQ 540
 DPYCVWAPDG SCIFLSPGR AAFQDVSGA STSGLGDCTG LLRASLSER AGLVSVNLLV 600
 75 TSSVAAFVVG AVVSGFVGV FVGLRERREL ARRKDEAIL AHGAGEAVLS VSLGERRAQ 660
 GPGRGCGGG GAGVGPPEAL LAPLMQNGWA KATLLQGGPH DLDSGLLPPT EQTLPQKRL 720

PTPHPHPHAL GPRAWDHGHP LLPASASSSL LLLAPARAPE QPPAPGEPTP DGRLYAARPG 780
RASHGDFPLT PHASPDORRV VSAPTGPLDP ASAADGLPRP WSPPTGSLR RPLGPHAPPA 840
ATLRRTHFTN SGEARPGDRH RGCHARPGTD LAHLLPYGGA DRTAPPVP

5

Seq ID NO: 168 DNA sequence

Nucleic Acid Accession #: AW205664

Coding sequence: 1-135 (underlined sequences correspond to start and stop codons)

10

1	11	21	31	41	51	
CGGCACGAGG	AGAACAGGGG	CCTCTGCCTC	AGTTTGCCCG	GGAGCCAGCC	AGGGCCCATC	60
CTAATTGGA	GCACAGTCTT	CCCGGTGCCT	AGACATGCCA	AGGCCCTCC	CACGTGGTAC	120
ACCTCTCCG	TTTAGTACCT	GACCCTGT	TTCAAAACGC	AGGTGTTTCT	GGTTTAGAAA	180
CTTGAAGGC	GGAATGTGTT	TTCGTGCTT	CTAGGAAGGG	TCTGCTGAGG	ACCAGACCAC	240
GTAAGCCTGA	GTGGATCCTG	ACTCAGCTGC	AGCCCTTACC	TGCCTCGTGC	TGATGATCTA	300
TGCATGGCGT	TATGTAGATC	ACGTGCGGCA	GAGACAGCCA	CTGTCCTGTG	TGCGGGTTTT	360
TAAACAGCT	GCCCTGGATG	AAACGGAATA	AACCAGTGAT	GCTAAAAAAA	AAAAAAAAAA	

20

Seq ID No: 169 Protein sequence

Protein Accession #: AW205664

25

1	11	21	31	41	51
RHEENRGLCL	SLPGSQPGPI	LIWSTVFPVP	RHAKAPPTWY	TLVS	

30

Seq ID NO: 170 DNA sequence

Nucleic Acid Accession #: AB033100

Coding sequence: 32-2623 (underlined sequences correspond to start and stop codons)

35

1	11	21	31	41	51	
AGGTCTGGGG	TCCTGAGGCT	GCTGGCAGAC	<u>TATGGGTACA</u>	ACGGCCAGCA	CAGCCCAGCA	60
GACGGTCTCG	GCAGGCACCC	CATTGAGGG	CCTACAGGGC	AGTGGCAGCA	TGGACAGTCG	120
GCACTCCGTC	AGCATCCACT	CCTTCCAGAG	CAC TAGCTTG	CATAACAGCA	AGGCCAAGTC	180
CATCATCCCC	AACAAGGTGG	CCCTGTTGT	GATCACGTAC	AACTGCAAGG	AGGAGTTCCA	240
GATCCATGAT	GAGCTGCTCA	AGGCTCATTA	CACGTTGGGC	CGGCTCTCGG	ACAACACCCC	300
TGAGCACTAC	CTGGTGCAAG	GAGCTCAGGC	CTTACCCAG	GGCCGCTACT	TCCTGGTGCG	360
GGATGTCACT	GAGAAGATGG	ATGTGCTGGG	CACCGTGGGA	AGCTGTGGGG	CCCCCAACTT	420
CCGGCAGGTG	CAGGGTGGGC	TCACTGTGTT	CGGCATGGGA	CAGCCCAGCC	TCTTAGGGTT	480
CAGGCGGGTC	CTCCAGAAAC	TCCAGAAGGA	CGGACATAGG	GAGTGTGTCA	TCTTCTGTGT	540
GCGGGAGGAA	MCTGTGCTTT	TCCTGCGTGC	AGATGAGGAC	TTTGTGTCTT	ACACACCTCG	600
AGACAAGCAG	AACCTTTCAT	AGAACCTCCA	GGGCCTTGGA	CCCGGGGTCC	GGGTGGAGAG	660
CCTGGAGCTG	GCCATCCGGA	AAGAGATCCA	CGACTTTGCC	CAGCTGAGCG	AGAACACATA	720
CCATGTGTAC	CATAACACCG	AGGACCTGTG	GGGGGAGCCC	CATGCTGTGG	CCATCCATGG	780
TGAGGACGAG	TGTCATGTGA	CGGAGGAGGT	GTACAAGCGG	CCCTCTTCC	TGCAGCCCAC	840
CTACAGGTAC	CACCGCCTGC	CCCTGCCGGA	GCAAGGGAGT	CCCTCTGGAG	CCCAGTTGGA	900
CGCCTTTGTC	AGTGTCTTCC	GGGAGACCCC	CAGCCTGCTG	CAGTCCGTCG	ATGCCACCGG	960
GCCTCCCCCA	GCCCTCGTCT	TCAGCTGCCA	GATGGGCGTG	GGCAGGACCA	ACCTGGGCAT	1020
GGTCTGGGGC	ACCCTCATCC	TGCTTACCCG	CAGTGGGACC	ACCTCCCAGC	CAGAGGCTGC	1080
CCCCACGCAG	GCCAAGCCCC	TGCCTATGGA	GCAGTTCCAG	GTGATCCAGA	GCTTTCTCCG	1140
CATGGTGCCC	CAGGGAAGGA	GGATGGTGGA	AGAGGTGGAC	AGAGCCATCA	CTGCCTGTGC	1200
CGAGTTGCAT	GACCTGAAAG	AAGTGGTCTT	GGAAAACCAG	AAGAAGTTAG	AAGGTATCCG	1260
ACCGGAGAGC	CCAGCCCAGG	GAAGCGGCAG	CCGACACAGC	GTCTGGCAGA	GGGCGCTGTG	1320
GAGCCTGGAG	CGATACTTCT	ACCTGATCCT	GTTTAACTAC	TACCTTCATG	AGCAGTACCC	1380
GCTGGCCTTT	GCCCTCAGTT	TCAGCCGCTG	GCTGTGTGCC	CACCCTGAGC	TGTACCGCCT	1440
GCCCGTGACG	CTGAGCTCAG	CAGGCCCTGT	GGCTCCGAGG	GACCTCATCG	CCAGGGGCTC	1500
CCTACGGGAG	GACGATCTGG	TCTCCCCGGA	CGCGCTCAGC	ACTGTCTAGG	AGATGGATGT	1560
GGCCAACTTC	CGGCGGGTGC	CCGCGATGCC	CATCTACGGC	ACGGCCCAGC	CCAGCGCCAA	1620
GGCCCTGGGG	AGCATCCTGG	CCTACCTGAC	GGACGCCAAG	AGGAGGCTGC	GGAAGGTTGT	1680
CTGGGTGAGC	CTTCGGGAGG	AGGCCGTGTT	GGAGTGTGAC	GGGCACACCT	ACAGCCTGCG	1740
GTGGCCTGGG	CCCCCTGTGG	CTCCTGACCA	GCTGGAGACC	CTGGAGGCC	AGCTGAAGGC	1800
CCATCTAAGC	GAGCCTCCCC	CAGGCAAGGA	GGCCCCCTGT	ACCTACAGGT	TCCAGACCTG	1860
CCTTACCATG	CAGGAGGTCT	TCAGCCAGCA	CCGAGGGGCC	TGTCTGGGCC	TCACCTACCA	1920
CCGCATCCCC	ATGCCGGACT	TCTGTGCCCC	CCGAGAGGAG	GACTTTGACC	AGCTGCTGGA	1980
GGCCCTGCGG	GCCGCCCTCT	CCAAGGACCC	AGGCACTGGC	TTCTGTGTCA	GCTGCCTCAG	2040
CGGCCAGGGC	CGTACCAACAA	CTGCGATGGT	GGTGGCTGTC	CTGGCCTTCT	GGCACATCCA	2100
AGGCTTCCCC	GAGGTGGGTG	AGGAGGAGCT	CGTGAGTGTG	CCTGATGCCA	AGTTCACTAA	2160
GGGTGAATTT	CAGGTAGTAA	TGAAGGTGGT	GACAGTGCTA	CCCGATGGGC	ACCGTGTGAA	2220
GAAGGAGGTG	GACGCAGCGC	TGGACACTGT	CAGCGAGACC	ATGACGCCCA	TGCACTACCA	2280
CCTGCGGGAG	ATCATCATCT	GCACCTACCG	CCAGGCGAAG	GCAGCGAAAG	AGGCGCAGGA	2340
AATGCGGAGG	CTGCAGCTGC	GGAGCCTGCA	GTACTTGGAG	CGCTATGTCT	GCCTGATTCT	2400

5 CTTCAACGCG TACCTCCACC TGGAGAAGGC CGACTCCTGG CAGAGGCCCT TCAGCACCTG 2460
 GATGCAGGAG GTGGCATCGA AGGCTGGCAT CTACGAGATC CTTAACGAGC TGGGCTTCCC 2520
 CGAGCTGGAG AGCGGGGAGG ACCAGCCCTT CTCCAGGCTG CGCTACCGGT GGCAGGAGCA 2580
 GAGCTGCAGC CTCGAGCCCT CTGCCCCCGA GGACTTGCTG TAGGGGGCCCT TACTCCCTGT 2640
 10 CCCCCACCC ACAGGGCCCC ACGCAGGCCCT GGGGTGTCTG AGGTGCTCTT GGCTGGGAGC 2700
 GGGCTGAGG GGTGCTGGCC TTGAAATGAT TCCCCACTT CCTGGAGAGA CTGAGCGGAG 2760
 TTGGGAGCCT TTTTAGAAAG AACTTTTAT AGGACAGGGA GACAGCACAG CCATCCCTTG 2820
 CAAACCACCA AGGTGTGTGG CTGACCTCCA GGGAGGAGCA CTCCTGGAG TGCTCACAA 2880
 GTGCACACTG CTGTGTGTAC CTTGCAGACA GGCCGGCGTT CAGCCTCCAA GGGGCTCACT 2940
 15 CCCCCAGTTG CCAAACACTG TGGATCTCTC TGTCCTCTTC TCCCCCTCTC CAGATTGGCC 3000
 TGGCAGCCCC TGGCAGAGAG CAGACCCGGC CACTGGTAGC TCCCCACTTC CTACTCCTG 3060
 CTGCTCTGCC ATTGCCGCTC CCCCTCTTGC TGCCCAAGCA CTGCCCTCGG GCGTCTGGCA 3120
 GCGTGAAGTG CCGTGGAGGG ACAGTGTCTT GGATAGATCT ATTATGTGAA AGGCAGCTTC 3180
 ACCCAGTTTT CTGGACTCTC ATGCCCCCAT CTCCGACCTG GGAGACTTCA GGAATGACAA 3240
 20 CCTACCCAGC CTGGTGGGGG TGGCAGGATG GTGGAGGTTT CTCAAGGAGC TGGAGACTTC 3300
 AGGGAGCCCC TCTCATGGGG AGGAAAGAGC TTCCAGGGGG CGAACGCAGC ACAGAGGAAG 3360
 AGGCCTGCTC CACTTGTCTG GGAACCTGGG CAGGAGGCAC AGAGGAAGCC AAGGCCTGGA 3420
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 CCTGCTGCAG CAGGAGCCCC AAGGAGTGCT AGCTGAGGGT GGTGCTGGG GTGGTCTCA 3540
 25 TGGACAGTGA GGTGTGCAAG GGTGCACTGA GGGTGGTGGG AGGGGATCAC CTGGGTTCAC 3600
 GGCCATCCTT GCTGAGCATC TTTGAGCCTG CCTTCCGGTG GGAGCAGAAA AGGCCAGACC 3660
 CTGCTGAGTT AGAGGCTGCT GGGATCCACT GTTTCACAC AGCGGGAAGG CTGCTGGGAA 3720
 CAGGTGGCAG AGAAGTGCCA TGTTTGCGTT GAGCCTTGCA GCTCTTCCAG CTGGGGACTG 3780
 GTGCTTGCTG AAACCCAGGA GCTGAACAGT GAGGAGGCTG TCCACCTTGC TTGGCTCACT 3840
 30 GGGACCAGSA AAGCCTGTCT TTGGTTAGGC TCGTGTACTT CTGCAGGAAA AAAAAAAG 3900
 GATGTGTCAT TGGTCAATG ATTTGAAAG GGGAGGAGGC CGAAGTTGTT CCCATTATC 3960
 CAGTATTGGA AATATTTGA CCCCCTTGGC TGAATCTTT TGCAAGACTA CTGTGTGTCT 4020
 GTTCACTACC TTTTCAGGTT TATTGTTTTT ATTTTTCAT GAATTAAGAC GTTTTAATTT 4080
 CTTTCAGAC AAGGTCTAGA TGCGGAGTCA GAGATGGGAC TGAATGGGGA GGGATCCTTT 4140
 35 GTGTTCTCAT GGTGGCTCT GACTTTCAGC TGTGTTGGGA CCACTGGCTG ATCACATCAC 4200
 CTCTCTGCCT CAGTTTCCCC ATCTGTAAAA TGGGAGAATA ATACTTGCCT ACCTACCTCA 4260
 CRGGGGTGTT GTGAGGATTC ATTTGTGATT TTTTTTTTTT TTTTGTACA GAGCTTTTAA 4320
 GCATTAAAAA CAGCTAAATG TG

35 Seq ID No: 171 Protein sequence:
 Protein Accession #: BAA86588.1

40 1 11 21 31 41 51
 | | | | | |
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 ITYNCKEEFQ IHDELLKAHY TLGRLSDNTP EHYLVQGAQA LPQGRYFLVR DVTEKMDVLG 120
 TVGSCGAPNF RQVQGGTLVF GMGQPSLLGF RRVLQKLQKD GHRECVIFCV REEVFLRAD 180
 EDFVSYTPRD KQNLHENLQG LGPGVRVESL ELAIRKEIHD FAQLSENTYH VYHNTEDLWG 240
 45 EPHAVAIHGE DDLHVTEEVY KRPLFLQPTY RYHRLPLPEQ GSPLEAQLDA FVSVLRETPS 300
 LLQLRDAHGP PPALVFSCQM GVGRTNLGMV LGTLILLHRS GTTSQPEAAP TQAKPLPMEQ 360
 FQVIQSFLRM VPQRRMVVEE VDRAITACAE LHDLEKEVLE NQKLEGIRP ESPAQSGSSR 420
 HSWVQRALWS LERYFYLLIF NYLHEQYPL AFALSFSRWL CAHPELYRLP VTLSSAGPVA 480
 PRDLIARGSL REDDLVSPDA LSTVREMDVA NFRRVPRMPI YGTAQPSAKA LGSILAYLTD 540
 50 AKRRLRKVVW VSLREEAVLE CDGHTYSLRW PGPPVAPDQL ETLEAQLKAH LSEPPPGKEG 600
 PLTYRFQTC LTMQEVFSQHR RACPLGLTYHR IPMPDFCAPR EEDFDQLLEA LRAALSKDPG 660
 TGFVFSCLSG GQRTTTAMVV AVLAFWHIQG FPEVGEEELV SVPDAKFRTKG EFQVVMKVQ 720
 LLPDGHVRVK EVDAAALDVS ETMTPMHYHL REIIICTYRQ AKAKEAQEM RRLQLRSLQY 780
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 55 RLRYRWQEQS CSLEFSAPED LL

Seq ID NO: 172 DNA sequence
 Nucleic Acid Accession #: AK021806.1
 Coding sequence: 1-645 (underlined sequences correspond to start and stop codons)

60 1 11 21 31 41 51
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 ACTGTGCTTT TCCTGCGTGC AGATGAGGAC TTTGTGTCCT ACACACCTCG AGACAAGCAG 60
 AACCTTCATG AGAACCTCCA GGGCCTTGGA CCCGGGGTCC GGGTGGAGAG CCTGGAGCTG 120
 65 GCCATCCGGA AAGAGATCCA CGACTTTGCC CAGCTGAGCG AGAACACATA CCATGTGTAC 180
 CATAACACCG AGGACCTGTG GGGGGAGCCC CATGCTGTGG CCATCCATGG TGAGGACGAC 240
 TTGATGTGA CGGAGGAGGT GTACAAGCGG CCCCTCTTCC TGCAGCCAC CTACAGGTAC 300
 CACGCGCTGC CCTTGCCCGA GCAAGGGAGT CCCCTGGAGG CCCAGTTGGA CGCCTTTGTC 360
 70 AGTGTCTCTC GGGAGACCCC CAGCCTGCTG CAGCTCCGTG ATGCCACCG GCCTCCCCCA 420
 GCCCTCGTCT TCAGCTGCCA GATGGGCGTG GGCAGGACCA ACCTGGGCAT GGTCTGGGC 480
 ACCCTCATCC TGCTTCAACG CAGTGGGACC ACCTCCAGC CAGAGGCTGC CCCACGCAG 540
 GCCAAGCCCC TGCCATGGA GCAGTTCCAG GTGATCCAGA GCTTTCTCCG CATGGTGCCC 600
 CAGGGAAGGA GGATGTGGA AGAGGTGGAT AGATCTATTA TGTGAAAGGC AGCTTCACCC 660
 75 AGTTTCTTGG ACTCTATG CCCCATCTCG GACCTGGGAG ACTTCAGGAA TGACAACCTA 720
 CCCAGCCTGG TGGGCTGGC AGGATGGTGG AGGTTTCTCA AGGAGCTGGA GACTTCAGGG 780
 AGCCCTCTC ATGGGGAGGA AAGAGCTTCC AGGGGGCGAA CGCAGCACAG AGGAAGAGGC 840

CTGCTCCACT TGTCTGGGAA CCTGGGCAGG AGGCACAGAG GAAGCCAAGG CCTGGAGCTG 900
 CAGGTCCCCC GGCATCTCTC TCTGTCCCCG CAGCCCAGGA TGGCCTGGTG CCCCCACCTG 960
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 CAGTGAGGTG TGCAAGGGTG CACTGAGGGT GGTGGGAGGG GATCACCTGG GTTCCAGGCC 1080
 5 ATCCTTGCTG AGCATCTTTG AGCCTGCCTT CCGGTGGGAG CAGAAAAGGC CAGACCCTGC 1140
 TGAGTTAGAG GCTGTGGGGA TCCACTGTTT CCACACAGCG GGAAGGCTGC TGGGAACAGG 1200
 TGGCAGAGAA GTGCCATGTT TGCCTTGAGC CTTGCAGCTC TTCCAGCTGG GGAAGGCTGC 1260
 TTGCTGAAAC CCAGGAGCTG AACAGTGAGG AGGCTGTCCA CCTGTGCTGG CTCACTGGGA 1320
 CCAGGAAAGC CTGTCTTGG TTAGGCTCGT GTACTTCTGC AGGAAAAAAA AAAAAGGATG 1380
 10 TGTCAATGGT CATGATATTT GAAAAGGGGA GGAGGCCGAA GTTGTTCCTA TTTATCCAGT 1440
 ATTGAAAAAT ATTTGACCCC CTGGGCTGAA TTCTTTTGCA GAACTACTGT GTGTCTGTTC 1500
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 15 CTGCTCAGT TTCCCATCT GTAAAATGGG AGAATAATAC TTGCTACCT ACCTCACGGG 1740
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 TAAAAACAGC TAAATGTG

20

Seq ID No: 173 Protein sequence:
 Protein Accession #: AK021806.1

25 1 11 21 31 41 51
 | | | | |
 TVLFLRADED FVSYTPRDKQ NLHENLQGLG PGVRVESLEL AIRKEIHDFD QLSENTYHVV 60
 HNTEDLWGEF HAVAIHGEDD LHVTEEVYKR PLFLQPTYRY HRLPLPEQGS PLEAQLDAFV 120
 30 SVLRETPSLL QLRDAHGPPP ALVFSCQMGV GRTNLGMVLG TLILLHRSRG TSQPEAAPTQ 180
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Seq ID NO: 174 DNA sequence

Nucleic Acid Accession #: NM_016580.2

35 Coding sequence: 1212-4766 (underlined sequences correspond to start and stop codons)

40 1 11 21 31 41 51
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 TCAGAGGTA GCCATAGGGT GTGACAAGTT GTGCAGATTA CAACACTCAC CCCTTGCAAT 180
 AACGTCACTG CCTGTGACTC GGGGCCAGGC CCAGGCCAAA GCGCTTCCTA CATCATTTCTG 240
 45 TTTAATCCTC ACAGTTTCTT GCTGAAAGGG CTACTATTCT TACTCCATC CCCACTCTAC 300
 AGATGAGGTA ATGGAGGCCC AGGAAAGTTA AGTGACTTGT CCCAGATGAC ACCGCTGGTA 360
 AGTTGCAAAG TCAGAAATTG AACTCAGGCA GTTACCTCT GATGGCTGCT CTGTTAATCA 420
 CAGCTGCTTT CCAGTGAGAC AAAAACGGGT GATCAGGGCA GAGTCAAGAC AGAGAGGTAA 480
 ACAAGATTGG GAAAAAGACA GGAATGAGAG GGGAAACAATG GGGGAAAAGA TAGGAACAAA 540
 GAGAGTTGGG GAAGGGGAGA GAAACAGGAA ACATGACTTG CCGGGAGGG GCATCAGTCC 600
 50 ACGTGCAAGC AGGTGGAGGC TCAAGTTTTC TGCTCACTTG GTGATGCAGA GGCTCCCTTT 660
 CCCTCAGCAG CCGCCTTGCT GCGTGGACAG CAGCTTCCA TCTGGCCTGT CCGCGAGGCC 720
 CCGGCCTCAT CCTCCTCAGC GGCAGGCCAC TTAGCTTCAC AGGAAATGCT CTTTCTCTAA 780
 TTGGCATTGA AACTCAGAGC CCTCCCTTTT CCGTAGGTG GGGTTTCCAT AGGAAAAAGC 840
 TGCTTCTCTG TTTCCCCAGC CTAGCAACTG TTTGGCAGTC AGAGTCCCAC ATCCTGCTCA 900
 55 ACTGGGTTCG GTCCCTCTTA GACCAGCTCT TGTCATCAT TTGCTGAAGT GGACCAACTA 960
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 CTTCCAATGA AGATGGCCTT GCCTTGGGGT CCGCTTGTT TCATAATCAT CTAATATAG 1080
 GACAAGGTTG TGCCGGCAGC TCTGGGGGAA GGAGCACGGG GCTGATCAAG CCATCCAGGA 1140
 AACACTGGAG GACTGTGCTA GCCTTGAAAG AACTCTAGTG GTTCTGAAT CTAGCCCACT 1200
 60 TGGCGGTAAG CATGATGCAA CTTCTGCAAC TTCTGCTGGG GCTTTTGGGG CCAGGTGGCT 1260
 ACTTATTTCT TTTAGGGGAT TGTCAAGAGG TGACCACTCT CACGGTGAAA TACCAAGTGT 1320
 CAGAGGAAGT GCCATCTGGT ACAGTGATCG GGAAGCTGTC CCAGGAACCTG GGCCGGGAGG 1380
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 65 TTCAGGTGGA CTCTGAGGAA GGCTTGCTCA GCACAGGCAG GCGGCTGGAT CGAGAGCAGC 1500
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 CTCTGATCCA TGTGAGATC CAAGTGCTGG ACATCAATGA CCACCAGCCA CGGTTTCCCA 1620
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 70 GTGAGCACTT TGCTTGGAT GTCAATGTGG GCCCTGATGA GACCAAACAT GCAGAACTCA 1800
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	AAGTTCTCAT	CAAGGTTCTG	GATGTCAATG	ACAACATCCC	AAGCATCCAC	GTCACATGGG	2280
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	TGGCAGATGA	CTTGGATTCA	GGACACAATG	GTTTGGTCCA	CTGCTGGCTG	AGCCAAGAGC	2400
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5	CACGTGGACG	AGAGCAGTGG	CCCAAATATA	CCCTCACTCT	GTTAGCCCAA	GACCAAGGAC	2520
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	TTCACCTCAT	TACCATCAAG	GCTCATGATG	CAGACTTGGG	CATTAATGGA	AAAGTCTCAT	2700
	ACCGCATCCA	GGACTCCCCA	GTTGCTCACT	TAGTAGCTAT	TGACTCCAAC	ACAGGAGAGG	2760
10	TCACTGCTCA	GAGGTCACTG	AACTATGAAG	AGATGGCCGG	CTTTGAGTTC	CAGGTGATCG	2820
	CAGAGGACAG	CGGGCAACCC	ATGCTTGCA	CCAGTGTCTC	TGTGTGGGTC	AGCCTCTTGG	2880
	ATGCCAATGA	TAATGCCCCA	GAGGTGGTCC	AGCCTGTGCT	CAGCGATGGA	AAAGCCAGCC	2940
	TCTCCGTGCT	TGTGAATGCC	TCCACAGGCC	ACCTGCTGGT	GCCCATCGAG	ACTCCCAATG	3000
	GCTTGGGCCC	AGCGGGCACT	GACACACCTC	CACTGGCCAC	TCACAGCTCC	CGGCCATTCC	3060
15	TTTTTGACAAC	CATTGTGGCA	AGAGATGCAG	ACTCGGGGGC	AAATGGAGAG	CCCTCTTACA	3120
	GCATCCGCAG	TGGAATGAAG	GCCCACCTCT	TCATCCTCAA	CCCTCATACG	GGGCAGCTGT	3180
	TCGTCAATGT	CACCAATGCC	AGCAGCCTCA	TTGGGAGTGA	GTGGGAGCTG	GAGATAGTAG	3240
	TAGAGGACCA	GGGAAGCCCC	CCCTTACAGA	CCCGAGCCCT	GTTGAGGGTC	ATGTTTGTCA	3300
	CCAGTGTGGA	CCACCTGAGG	GACTCAGCCC	GCAAGCCTGG	GGCCTTGAGC	ATGTCGATGC	3360
20	TGACGGTGAT	GTGCCTGGCT	GTAATGTTGG	GCATCTTCGG	GTTGATCCTG	GCTTTGTTCA	3420
	TGTCCATCTG	CCGGACAGAA	AAGAAGGACA	ACAGGGCCTA	CAACTGTCGG	GAGGCCGAGT	3480
	CCACCTACCG	CCAGCAGCCC	AAGAGGCCCC	AGAAAACAT	TCAGAAGGCA	GACATCCACC	3540
	TCGTGCTGCT	GCTCAGGGT	CAGGCAGGTG	AGCCTTGTTG	AGTCGGGCGC	TCCACAAAG	3600
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25	ACCTCACCCC	GACCCTGTAC	AGGACGCTGC	GTAATCAAGG	CAACCAGGGA	GCACCGGCGG	3720
	AGAGCCGAGA	GGTGCTGCAA	GACACGGTCA	ACCTCCTTTT	CAACCATCCC	AGGCAGAGGA	3780
	ATGCCTCCCG	GGAGAACCTG	AACCTTCCCG	AGCCCCAGCC	TGCCACAGGC	CAGCCACGTT	3840
	CCAGGCCTCT	GAAGGTTGCA	GGCAGCCCCA	CAGGGAGGCT	GGCTGGAGAC	CAGGCGAGTG	3900
	AGGAAGCCCC	ACAGAGGCCA	CCAGCCTCCT	CTGCAACCC	GAGACGGCAG	CGACATCTCA	3960
30	ATGGCAAAGT	GTCCCCTGAG	AAAGAATCAG	GGCCCCGTCA	GATCCTGCGG	AGCCTGGTCC	4020
	GGCTGTCTGT	GGCTGCCTTC	GCCGAGCGGA	ACCCCGTGGA	GGAGCTCACT	GTGGATTCTC	4080
	CTCCTGTTCA	GCAAAATCTC	CAGCTGCTGT	CCTTGCTGCA	TCAGGGCCAA	TTCCAGCCCC	4140
	AACCAAACCA	CCGAGGAAAT	AAGTACTTGG	CCAAGCCAGG	AGGCAGCAGG	AGTGCAATCC	4200
35	CAGACACAGA	TGGCCCCAAGT	GCAAGGGCTG	GAGGCCAGAG	AGACCCAGAA	CAGGAGGAAG	4260
	GGCCTTTTGA	TCCTGAAGAG	GACCTCTCTG	TGAAGCAACT	GCTAGAAGAA	GAGCTGTCAA	4320
	GTCTGCTGGA	CCCCAGCACA	GGTCTGGCCC	TGGACCGGCT	GAGCGCCCC	GACCCGGCCT	4380
	GGATGGCGAG	ACTCTCTTTT	CCCCTCACCA	CCAACCTACG	TGACAATGTG	ATCTCCCCCG	4440
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	AGCTGAGCCC	AACAGGCACG	AGGCTGGCCA	GCACCTTTGT	CTCGGAGATG	AGCTCACTGC	4560
40	TGGAGATGCT	GCTGGAACAG	CGCTCCAGCA	TGCCCGTGGA	GGCCGCCTCC	GAGGCGCTGC	4620
	GGCGGCTCTC	GCTCTGCGGG	AGGACCTCTA	GTTTAGACTT	GGCCACCACT	GCAGCCTCAG	4680
	GCATGAAAGT	GCAAGGGGAC	CCAGGTGGAA	AGACGGGGAC	TGAGGGCAAG	AGCAGAGGCA	4740
	GCAGCAGCAG	CAGCAGGTGC	CTGTGAACAT	ACCTCAGACG	CCTCTGGATC	CAAGAACCAG	4800
	GGGCGTGAGG	ATCTGTGGAG	AAGAGCTGGT	TTCTAAATATC	TTGTAACCTA	CTAGCTAGCG	4860
45	GCGGCTGAG	AACTTTAGGG	TGACTGATGC	TACCCCCACA	GAGGAGGCAA	GAGCCCCAGG	4920
	ACTAACAGCT	GACTGACCAA	AGCAGCCCC	TGTAAGCAGC	TCTGAGTCTT	TTGGAGGACA	4980
	GGGACGGTTT	GTGGCTGAGA	TAAGTGTTTC	CTGGCAAAAC	ATATGTGGAG	CACAAAGGGT	5040
	CAGTCTCTCT	GCAGAACAGA	TGCCACGGAG	AGGAAAGGGT	GGCCTTCTTG		5100
50	GGTAGCAGGA	GTCAGGGGGC	TGTACCCTGG	GGGTGCCAGG	AAATGCTCTC	TGACCTATCA	5160
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Seq ID No: 175 Protein sequence:
Protein Accession #: NP_057664.1

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	QAGAAFOVLQ	LPQALPIQVD	SEEGLLSTGR	RLDREQLCRQ	WDPCLVSFV	LATGDLALIH	120
60	VEIQVLDIND	HQPRFPKGEQ	ELEISESASL	RTRIPLDRAL	DPDTGPNTLH	TYTLSPSEHF	180
	ALDIVVGPDE	TKHAELIVVK	ELDREIHSFF	DLVLTAYDNG	NPPKSGTSLV	KVNVLDSDND	240
	SPAFAESSLA	LEIQEDAAPG	TLLIKLTATD	PDQGPNGEVE	FFLSKHMPPE	VLDTFSIDAK	300
	TGQVILRRPL	DYEKNPAYEV	DVQARDLGNP	PIPAHCKVLI	KVLDVNDNIP	SIHVTWASQP	360
	SLVSEALPKD	SFIALVMADD	LDSGHNLVH	CWLSQELGHF	RLKRTNGNTY	MLLTNATLDR	420
65	EQWPKYTLTL	LAQDQGLQPL	SAKKQLSIQI	SDINDNAPVF	EKSRYEVSTR	ENNLPSLHLI	480
	TIKAHDADLG	INGKVSRIQ	DSPVAHLVAI	DSNTGEVTAQ	RSLNVEEMAG	FEFQVIAEDS	540
	GQPMILASSVS	VWVSLLDAND	NAPEVVQPV	SDGKASLSVL	VNASTGHLLV	PIETPNGLGP	600
	AGTDPPLAT	HSSRPFLLT	IVARDADSGA	NGEPLYSTRS	GNEAHLFILN	PHTGQLFVNV	660
	TNASSLIGSE	WELEIVVEDQ	GSPPLQTRAL	LRVMFVTSVD	HLRDSARKPG	ALSMSMLTVI	720
70	CLAVLLGIFG	LILALFMSIC	RTEKKNDRAP	NCREAESTYR	QQPKRPQKHI	QKADIHLVPV	780
	LRGQAGEPCE	VGQSHKDVKD	EAMMEAGWDP	CLQAPFHLP	TLYRTLNRQG	NQGAPAESRE	840
	VLQDTVNLLF	NHPRQRNASR	ENLNLPEPQP	ATGQPRSRPL	KVAGSPTGRL	AGDQGSSEAP	900
	QRPPASSATL	RRQRHLNGKV	SPEKESGPRQ	ILRSLVRLSV	AAFAERNPVE	ELTVDSPPVQ	960
	QISQLLSLLH	QQQFQPKPNH	RGNKYLAKEG	GSRSAPDPTD	GPSARAGGQT	DPEQEEGFLD	1020
75	PEEDLSVKQL	LEELSSLLD	PSTGLALDRL	SAPDPANMAR	LSLPLTTNYR	DNVISPDAAA	1080
	TEEPRTFQTF	GKAEAPELSP	TGTRLASTFV	SEMSSLLEML	LEQRSSMPVE	AASEALRRLS	1140

VCGRTLSDL ATSAASGMKV QGDPGGKTGT EGKSRGSSSS SRCL

Seq ID NO: 176 DNA sequence

Nucleic Acid Accession #: AL109712.1

Coding sequence: 2-128 (underlined sequences correspond to start and stop codons)

```
10 1 11 21 31 41 51
| | | | |
GAGTCTCTTT GGGCCAGCCG GGCTGCTGCA GACAGACAGG AAGCACGCCT GACGCTCCTC 60
TACCCTCGGG CAGCACAGCG GGGCTGGGAC TCACTCTAGC TTGCCCCAGCA ACTTGCTTTC 120
CTGTGTGAAC TCTGGCAGGC TGCCCTCTCT GTGCAAAGCT GCCACTGGGG CCTGCTCAGG 180
GTGGCCTGGA ACTTGGAGGT GGGCAGTCAG GGCCTAGGAT GGGCCTGTGT CACCAGGGCA 240
TGTGCCCTTG GGCCAGTTAC TTCTCTCAG AGCCTTGGGC TCCTCTCTG AGGATGGGGC 300
15 TTGTTGGTGT GAAATGAGGT GAGCATGTTG AGTTGGGGAG CAGCAGGACA CGCACCTGCA 360
GGCAGCCGCC CTGGCCACGC TCCCTCCCTA CCTCCGAGT CCTGGGACAG ACACAGTAGA 420
GCACAGCGGG CCAGCCTGCT CTCTTCTCTG TCTACTTTT GCAGAAGAGT CAACAGATAC 480
AACAGGCCCA GGGAGGTGCC CCTGGGGGCC CCAGTCCCCA TCACTCCAAG GGGCAGTCCT 540
GCAAGTGACA AGGTGGGGCC AATCCCTGTG GAACAGGTCT CTGAGGACCA CAGAGTGGGG 600
20 CCCCAGGGAA AGCTGGGAGC CGAGCTAGAG GCAGGCAGCA AGTAAGGGCA AAGCTGTGCC 660
CCTGCCCGGA AGACCTTCCT GCGCCAGAA CCGACCCCTC CGCAGATAGC CCTCCCTGGG 720
CAGCAGCCCC CCAGCTTCCA AGGCCCCGTC CTCACCAGAC GCCATGCTCT CACGGAATTG 780
TTTGCTGCTC TGTACCTTGC AGATCTGCCC CAGAGGAGCA GGTGAAAAGC CGCGCCTGCC 840
25 GAGGTGCTGT GGCCTGTGAG TTTTGGGAG AGGAGTGGGG GGAAGAGTTT CTCACCTTTA 900
AGATTCTCCA AATCCAAGAT GAAGTCATGC TGTGCTTTGG AATGGTAGAT GCTCATTTAT 960
GTAAAATCAT AATAAATGTT ACACAACTG TTAACAAAAA AAAAAAATA AAAAAA
```

Seq ID No: 177 Protein sequence:

Protein Accession #: AL109712.1

```
30 1 11 21 31 41 51
| | | | |
VSLGQPGCCR QTGSTPDAPL PSGSTAGLGL TLACPATCFP V
```

Seq ID NO: 178 DNA sequence

Nucleic Acid Accession #: none found

Coding sequence: 3-107 (underlined sequences correspond to start and stop codons)

```
40 1 11 21 31 41 51
| | | | |
AATGGAGCAC TCCAAAGAAC GATTTGACCA ATAGCATTTC TTCTCTGGGG GTTGTATTTC 60
AAAGCATGCA ACTCTCCAGG GAACCAGAAC TAAATTGCTT AAAATGAAGT CATTCCTCAG 120
45 ATTAACCTCC TCAGATAAAG TGTACGCGGT CTGCAGAAAC GAAGAAGACA AAATGAGAT 180
TATCACTCAT AATTCTCTTA CTTACTATGT CAGTGAAACA ATGAGTTTGC ATTTTTCGAA 240
TCCTAGAACA TTCTTCATTA GCCCTGGGTC ATGACCTCTT CCAGTTAATT CTCTTTCACA 300
CCTTTAGGAA AGATTTAAGA TGAACCTTCA ATAGGATATT AACATACTC ATAGCCAATA 360
CCACAGCTGC CTTTCAAATT AATGAGGTTA ATTGTTCTCC AGCAAACATG AGTTTGTCTT 420
50 TGGCATTTTA AATGCTTCCC ATTGATCTGA CATTTTGCTG TTTCAAGTTT TAAAGGCTC 480
AAATCAAAGA CTATTGATAA CTGAGCAAAG AGCGAAGATC CAGAAATACG AAAACATTGT 540
CTTTTTTTTT CCATGAAAAA CAATCATAGC CTTTGAATT CAATCGAAGT TTCTACATTA 600
GCCATCTAAG ACTATTTTAA TTATTTCTGT TCTCAGTCAA GCTAATTCAG GTGAATGAAC 660
AGTATTGACT TTTAAATCT TTTTAAATT TTTTAAATC TTTAGTTTAT TAAGTTTGTA 720
55 GAAAAGCTCT GGGGCCATGA CCACCTACGT AAATGTTTCA GTTTAAAAAC AAAAGATTCA 780
GGCCTCTAAT TTGAGCCAAA TCCAGGTGAT CTGTGTTGAA ATTTTGTATG AATTTGAAAA 840
GATGAAAGTG GAACTTTTAA CATTCATGTT CCCCAAATT TCACTGGGA AGGGATGCTA 900
ATTGCCTACT TAAGATATAA GTTCAAGAT AACATTTTCA TAGAAAAATC AGAAAACTGC 960
TTGACACAGC AGTGACATAG TTAGATGTGG CTCAGATGCC TTCCAAACCT GAGGGTCCCC 1020
60 AAAGATTCTT TACCAGTTG TTTTAACTA TGAATCTTAA TCTGTTCAT TCCCCTGCCA 1080
AAACAAATTT AAAAG
```

Seq ID No: 179 Protein sequence:

Protein Accession #: none found

```
65 1 11 21 31 41 51
| | | | |
WSTPKNDLTN SISSLGVVFQ SMQLSREPEL NCLK
```

Seq ID NO: 180 DNA sequence

Nucleic Acid Accession #: none found

Coding sequence: 2-176 (underlined sequences correspond to start and stop codons)

```
75 1 11 21 31 41 51
| | | | |
```

CCGGGTGGGG CCTCGGGATG CAGGCGCCGG TGCCCCGGCC CCTGGGCCTG CTGGACCCCG 60
 CAGAAGGGGT TTCGAGGAGG AAGAAGACGT CGCTCTGGTT TGTGGGGTCT CTGCTGCTGG 120
 TGTCCGTCCT CATAGTCACC GTCGGGCTGG CTGCATCAGC AGGACGGAGA ATGTGACCGT 180
 TGGGGGCTAC TACCCAGGGA TCATTCTCGG CTTTGGATCT TTCTTAGGAA TTATTGGCAT 240
 CAACTTGGTG GAGAATAGAA GGCAAATGCT GGTGGCAGCG ATCGTGTTTA TCAGTTTGG 300
 CGTGGTGGCC GCCTTCTGCT GCGCCATCGT GGACGGCGTA TTGCAGCAC AGCACATTGA 360
 ACCGAGGCC CACACACAGG TGAGCAGGAG CACTGAGATT CATGTGGGT TTGCTCAGCT 480
 CGATGTCTAC CAGACAGAGG GTTTTCCCTG CACATAGGCG TGGTCTGAAT ATTTGGATTC 540
 AACCCCGCCG ACCCCACGCG GTTTTCCCTG CACATAGGCG TGGTCTGAAT ATTTGGATTC 540
 TAATAGTTCC TGGGGGTAC CCCTGCAGCT GGTGAACCGT TGATGCCCC TGTGTAAGGG 600
 ACCTTGACAT TTCGATGTGC TGTATTTTAC TCTGGAGTCA GAGTTCTGGA CTTGCTTCAT 660
 TAAATCACAA CAGTCTCAGA AAACAACCGC ACCACCCCGC AATCCCACCA AAGGGGCGCG 720
 CCGTCCCTAA GAGTTATCCC

Seq ID No: 181 Protein sequence:
 Protein Accession #: none found

1 11 21 31 41 51
 | | | | |
 RVGPRDAGAG ARAPGPAGPR RRAFEEEDV ALVCGVSAAG VRPHSHRRAG CISRTENV

Seq ID NO: 182 DNA sequence
 Nucleic Acid Accession #: AK001579.1
 Coding sequence: 1150-2637 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 TTTTCTCTGC TTTTCGCTAC CCGGTCACCT CTCATTTCTC TCCCCTATTC CTGTGTCTCTT 60
 CCCCCATCCC CCTTTCTCCT GTCTCTCCCC TGCTCTTACA GTGGTTCTCC CCGCTGAGCT 120
 GCCACCAGCT GCTGGGCCCC GGGCTGCTGC GGTGGGCGG CCTATGGCTG CCGTCCCCCT 180
 CCCATACAGC CCGGGCCCTT GGTCTCTGGC TGTGAGGTT TGGCCTCCTT CGTGGTGACC 240
 ACCTCTCTCT GTGCTCAGCG CCGGGCCAG GCCCCCAGC CCCTGAGGAC ATGGTGCATC 300
 TCGCGGCGCT ACAGGAGATC AGTGTGGTT CTGCAGTGA CACCCAGAT AAGAAAGAGC 360
 ATTTGGTCTT GGTGGAGACA GGAAGGACCC TGTATCTGCA AGGAGAGGGC CCGCTGGACT 420
 TCACGGCATG GAACGCAGCC ATTGGGGCG CCGCTGGTGG GGGCGGCACA GGGCTGCAGG 480
 AGCAGCAGAT GAGCCGGGT GACATCCCA TCATCGTGA TGCTGCATC AGTTTGTGTA 540
 CCCAGCATGG GCTCCGGCTG GAAGGTGTAT ACCGAAAGG GGGCGCTCGT GCCCGCAGCC 600
 TGAGACTCCT GGTCTGAGTC CGTCGGGATG CCGGTTCGGT GAAGCTCCGA CCAGGGGAGC 660
 ACTTTGTGGA GGATGTCACT GACACACTCA AACGCTTCTT TCGTGAGCTC GATGACCTG 720
 TGACCTCTGC ACGGTTGCTG CCTCGCTGGA GGGAGGCTGC TGGTATTCTT AAGATCCCTG 780
 AGAGCCAAGG CCCAACCAAG ATCTCTGCCT TCCCCACCA GAATCCATGG TTTGGCAGCC 840
 CTCGCCCCCA TCACTTCCCA CCCTGGGGGA TCATCCAGAG ACTTGGCTCA GGGGGAGGTG 900
 GGAAGGGGGC AGAGACACAT CCATCCTGCA TTTGTGCCTA AAAATCCCTC CCTCTGTACC 960
 AGCTGCCACT CTTTCTTCCC GGGTCTCTCC CAACCTCTCT CCATTCATC CCCAGAGCTG 1020
 CCCCAGAAGA ATCAGCGCCT GGAGAAATAT AAAGATGTGA TTGGCTGCCT GCCGCGGGTC 1080
 AACCGCCGCA CACTGGCCAC CCTCATTGGG CATCTCTATC GGGTGCAGAA ATGTGCGGCT 1140
 CTAAACCAGA TGTGCACGCG GAACCTGGCT CTGCTGTTTG CACCCAGCGT GTTCCAGACG 1200
 GATGGGCGAG GGGAGCACGA GGTGCGAGTG CTGCAAGAGC TCATTGATGG CTACATCTCT 1260
 GTCTTTGATA TCGATTCTGA CCAGGTAGCT CAGATTGACT TGGAGGTCAG TCTTATCACC 1320
 ACCTGGAAGG ACGTTCAGCT GTCTCAGGCT GGAGACCTCA TCATGGAAGT TTATATAGAG 1380
 CAGCAGCTCC CAGACAACTG TGTACCCCTG AAGGTGTCCC CAACCTGAC TGCTGAGGAG 1440
 CTGACTAACC AGGTACTGGA GATGCGGGGG ACAGCAGCTG GGATGGACTT GTGGGTGACT 1500
 TTTGAGATTG CCGAGCTAGG GGAGCTGGAG CCGCCACTGC ATCCCAAGGA AAAGGTCTTA 1560
 GAGCAGGCTT TACAATGGTG CCAGCTCCCA GAGCCCTGCT CAGCTTCCCT GCTCTTGAAA 1620
 AAAGTCCCCC TGGCCCAAGC TGGTGCCTC TTCACAGGTA TCCGACGTGA GAGCCACGG 1680
 GTGGGGCTGT TGGGTGTGCG TGAGGAGCCA CCTCGCTTGC TGGGAAGCCG CTTCCAGGAG 1740
 AGGTCTTTTC TGCTGCGTGG CCGCTGCCTG CTGCTGCTCA AGGAGAAGAA AAGCTCTAAA 1800
 CCAGAACGGG AGTGGCCTTT GGAAGGTGCC AAGGTCTACC TGGGAATCCG CAAGAAGTTA 1860
 AAGCCCCCAA CACCGTGGGG CTTACATTG ATACTAGAGA AGATGCACCT CTAATTGTCC 1920
 TGCATGACG AGGATGAAAT GTGGGATTGG ACCACCAGCA TCCTTAAAGC CCAGCACGAT 1980
 GACCAGCAGC CAGTGGTCTT ACGACGCCAT TCCTCTCTG ACCTTGCCCG TCAGAAGTTT 2040
 GGCATATGCT CTTTGTCTGCC TATCCGTGGG GATGACAGTG GAGCCACCCT CCTCTCTGCC 2100
 AATCAGACCC TCGCGGCGAT ACACAACCGG AGGACCTGT CCATGTTCTT TCCAATGAAG 2160
 TCATCCCAAG GGTCTGTGGA GGAGCAAGAG GAGCTGGAGG AGCTGTGTGA CGAGGAGCCA 2220
 GTGTATGAGG AAGTAGGGGG CTTCCCTGAG TTGATCCAGG ACATTCTAC CTCCTCTCTC 2280
 ACCACCGGG AGTGGACAGT GAAGCCAGAG AACCCCTCA CCAGCCAGAA GTCATTGGAT 2340
 CAACCTTTTC TCTCCAAGTC AAGCACCTTT GGCCAGGAGG AGAGGCCACC TGAGCCCCCT 2400
 CCAGGCCCCC CTTCAAAGAG CAGTCCCCAG GCACGGGGGT CCCTAGAGGA ACAGCTGCTC 2460
 CAGGAGCTCA GCAGCTCAT CCTGAGGAAA GGAGAGACCA CTGCAGGCCT GGGAAGTCTT 2520
 TCCCAGCCAT CCAGCCCCCA ATCCCCCAGC CCCACTGGCC TTCCAACACA GACACCTGGC 2580
 TTCCCCACCC AACCCCATG CACTTCCAGT CCACCCTCCA GCCAGCCCCT CACATGACCC 2640
 TAGGACCAGC AGTCTGAGAG GGTAGGTACC AGAAGACCCA GAAACTCTTA TCGTGGCACT 2700
 GTTGCACTGT CCTCTGCCCT GGCTGGAAG ACTCCAGAAT CCAGTGTGGT GCTGTGGAAG 2760
 GAGCACTGGA CTAAGGCTT CAGTGGCTGC GTGTCCAGG ACAGGTATG GCCCCTCTCT 2820
 GGGCCAGGCC CATTTATCTA TACCATGAGG TAACTGAAGT AAGGAGAGCA GTGAATGTCA 2880

AACTGTGTTT CTTAGAGCCA TAAGCCCCAC ATATTATCCC TGAACAAGGG CAGCTCCTGC 2940
 TTTATATATT TGATACGTAG GGGTTCCATG AGAGATTTTG GGTTTTAAAG GAATGGTTTT 3000
 ACTGCATTAA AGAAAAAATA TGCTTTGGAA ACCAGAGGCC TGGGTGATGT TAAAGTCTAT 3060
 CCTGTCCCAC TTCCTACATT CTGGGACTAC CGTGAAGCCT GGAGTAGGGA GAGCGAGTTT 3120
 GGGAGCTGGG ACTCGGGGAG TCAAAAATAG ATGAGTAATT GTCAATAAAC CTGGGAACC

Seq ID No: 183 Protein sequence:
 Protein Accession #: AK001579.1

1 11 21 31 41 51
 MSLTHSNASF VSSMTLPLHG CCLAGGRLLV FLRLSLRAKQ PGSPLSPTRI HGLAALRPIT 60
 SHPGSSSRDL AQGEVGRGQR HIHPAFVPKN PSLCTSCHSF FPGPPQPSI PSPPLPQKNQ 120
 15 HEVRVLQELI DGYISVFDID SDQVAQIDLE VSLITTWKDV QLSQAGDLIM EVYIEQQLPD 180
 NCVTILKVSPT LTAEELTNQV LEMRGTAAGM DLWVTFEIRE HGELEPLHP KEKVLQEQALQ 240
 WCQLPEPCSA SLLLLKKVPLA QAGCLFTGIR RESPRVGLLR CREEPRLLG SRFQERFFLL 300
 RGRCLLLKE KKSSKPEREW PLEGAKVYLG IRKCLKPPTP WGFTLILEKM HLYLSCTDED 420
 20 EMWDWTTTSL KAQHDDQQPV VLRRHSSDDL ARQKFGTMPL LPIRGDDSGA TLLSANQTLR 480
 RLHNRRTLISM FFPKMSSQGS VEEQEELERP VYEEPVYEEV GAFPELIQDT STSFSTTREW 540
 TVKPENPLTS QKSLDQPFLL KSSTLGQEEER PPEPPPGPPS KSSPQARGSL EEQLLQELSS 600
 LILRKGETTA GLGSPSQPS PPSPTGLP TQTPGFPTQP PCTSSPPSSQ PLT

Seq ID NO: 184 DNA sequence
 Nucleic Acid Accession #: none found
 Coding sequence: 1-81 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 GTAGAGTTAG TGTCATGTG CTTAGAATAT ACCAAATTCA TAAACATTTT CTCTAAAAAA 60
 GTATTAAAGCT TAAAAAGTTA ATTCAGTTTA AGGAATATAA ACCAAATTAT TTTATATTTG 120
 35 AATCTCAACA TAAGAAGTCA AAATGTAATG CTGCCAGATA ACAATATCAA AGGTATTTTT 180
 CTTTCTCTAT AATTTTCATCA GTATGTCCTC TCCCTTTTCT CCTATTTGTC AAATTTTAGC 240
 AACCTTAAC CTGCTAATTA TAAGCTAGGC AAGTAATCTT GGACAAGTTA TTTGACCTCT 300
 CACTGCACCA GCTTTGTTAT CTGTAAATG ATGATAATAC CAACACCTTC TTCTGGGGT 360
 ACTGAAGATG AGAGAATATG ATATGTGTAA AGTGCCTTCC ACAATACCCA GAACATAGCA 420
 AACATGTAAT GAATGTAGTA ATAGTAATTA TTTTATTTTC TTTTGATTCA GTTGGGACTA 480
 40 TGTTCAGCTG TAACAGAATA CCCAAATATA CAGTTTAAAG CAAATTAAGG TTTTGTGTG 540
 AAGTTTGTG ACGAATTCAG ACAATCCAGG GCTTTTATAG ATGCACCAGG ATCAGCAGGT 600
 ACAAAGGCAT CTTTCCTGAT TTCTGCCAGT CTCAATGCAT GGGTTGCAAT CCAGAGTCCA 660
 GGATGGCAGT TCCAGCCCTG GTTACGCCCA TATTAGCACA CAGAAAGAAA GAGAAAGGGA 720
 TGTGCCTCTT CACTTTAATC ATAGCTCCCA CTAGATGCAC CCACTACTTC TGCTGATACT 780
 45 CCATTAGCTA ATGCTTGCTT ACATGGTCAC ACTTAGTTTC CAGAGAGACA TGTCTGGACA 840
 GTCATGTGCT CAATTAATAT CCAAGTGTC AATTACTGAG AAAAAAGAA ACTAGCACCT 900
 TTGCTTGGTT GCATTCTTCT TAGCATAAGC CACATTCTTT TTATGAAGTT GTCCTCAGTT 960
 ACTTGATGCT CTCAGTTGTC CTTTCATTTA GAAATGCTCC TTGGACATCC TGAATCTGAC 1020
 50 TTCTTTTGTG ATCAGCACCA TCACTACCAC TGCCCTCTTC AAAGCCACCA CGTTCTGTCC 1080
 CAGGATGGTT GCAACAACCA CCATAGGGAC TTTTGTGCTC TACTTCCACA CAATAGCCAG 1140
 AGTAAGCTTT TGAAAATGTA GGTCAGATCA TGCTCTCTC TTCTCTTCAA AACCCTCCGA 1200
 TGGCTTTTCA TATTACTCAA AAGAAAACCT AAAACTTTGC TGTGAGATCT ATGTGACCCG 1260
 GCTTATTCTT CCTCTTACTT TATCTCTGTA TTGCTCTTCC TCACTCTACT CCAGCCATCC 1320
 55 CACCTCCTTG CTGCTTGTC TATACTCTTA AAAGAAGTTC AGTCTTCCCT TATGATATTT 1380
 GCACTTAAAA TAGAAAAAAA AAAAAAAAAG AGCTCAGAGA GGCTGAGTTG TCCAAGGTCA 1440
 TGCAGGTTAG AAGTCATGGA GCTGGGATCT AAATCCATGT CAGTCTGACT ATGAGTCTG 1500
 CACCGTTCTA TTCAACCCCA TTGCCTAGAG GTGCTTGATT GCTCAATAAT AGATTCCATG 1560
 GACACAGTCA GCTCTTCTG AGAAAAGGCA GCTCAGCATT TCCATGAGAT CCGCACATCC 1620
 TTTTGCAGAA GAAAC

Seq ID No: 185 Protein sequence:
 Protein Accession #: none found

1 11 21 31 41 51
 VELVSMCLEY TKFINIFSKK VLSLKS

Seq ID NO: 186 DNA sequence
 Nucleic Acid Accession #: NM_002203.2
 Coding sequence: 43-3588 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 CTGCAAACCC AGCGCAACTA CGGTCCCCCG GTCAGACCCA GGATGGGGCC AGAACGGACA 60
 GGGGCCGCGC CGCTGCCGCT GCTGCTGGTG TTAGCGCTCA GTCAAGGCAT TTTAAATTGT 120

	TGTTTGGCCT	ACAATGTGG	TCTCCAGAA	GCAAAAATAT	TTTCCGGTCC	TTCAAGTGAA	180
	CAGTTTGGGT	ATGCAGTGCA	GCAGTTTATA	AATCCAAAAG	GCAACTGGTT	ACTGGTTGGT	240
	TCACCCTGGA	GTGGCTTTCC	TGAGAACCAG	ATGGGAGATG	TGTATAAATG	TCCTGTTGAC	300
5	CTATCCACTG	CCACATGTGA	AAAACATAAT	TTGCAAACTT	CAACAAGCAT	TCCAATGTGT	360
	ACTGAGATGA	AAACCAACAT	GAGCCTCGGC	TTGATCCTCA	CCAGGAACAT	GGGAAGTGGA	420
	GGTTTTCTCA	CATGTGGTCC	TCTGTGGGCA	CAGCAATGTG	GGAATCAGTA	TTACACAACG	480
	GGTGTGTGTT	CTGACATCAG	TCCTGATTTT	CAGCTCTCAG	CCAGCTTCTC	ACCTGCAACT	540
	CAGCCCTGCC	CTTCCCTCAT	AGATGTTGTG	GTTGTGTGTG	ATGAATCAAA	TAGTATTTAT	600
	CCTTGGGATG	CAGTAAAGAA	TTTTTTGGAA	AAATTTGTAC	AAGGCCTTGA	TATAGGCCCC	660
10	ACAAAGACAC	AGGTGGGGTT	AATTCAGTAT	GCCAATAATC	CAAGAGTTGT	GTTTAACTTG	720
	AACACATATA	AAACCAAGA	AGAAATGATT	GTAGCAACAT	CCCAGACATC	CCAATATGGT	780
	GGGGACCTCA	CAACACATT	CGGAGCAATT	CAATATGCAA	GAAAATATGC	CTATTAGCA	840
	GCTTCTGGTG	GGCGACGAAG	TGCTACGAAA	GTAATGGTAG	TTGTAAGTGA	CGGTGAATCA	900
	CATGATGGTT	CAATGTTGAA	AGCTGTGATT	GATCAATGCA	ACCATGACAA	TATACTGAGG	960
15	TTTGGCATAG	CAGTTCTTGG	GTACTTAAAC	AGAAACGCCC	TTGATACTAA	AAATTTAATA	1020
	AAAGAAATAA	AAGCGATCGC	TAGTATTCCA	ACAGAAAGAT	ACTTTTTCAT	TGTGTCTGAT	1080
	GAAGCAGCTC	TACTAGAAAA	GGCTGGGACA	TTAGGAGAAC	AAATTTTCAG	CATTGAAGGT	1140
	ACTGTTCAAG	GAGGAGACAA	CTTTCAGATG	GAAATGTCAC	AAGTGGGATT	CAGTGCAGAT	1200
	TACTCTTCTC	AAAATGATAT	TCTGATGCTG	GGTGCAAGTG	GAGCTTTTGG	CTGGAGTGGG	1260
20	ACCATTTGCC	AGAAGACATC	TCATGGCCAT	TTGATCTTTC	CTAAACAAGC	CTTTGACCAA	1320
	ATTCTGCAGG	ACAGAAATCA	CAGTTTCATAT	TTAGGTTACT	CTGTGGCTGC	AATTTCTACT	1380
	GGAGAAAGCA	CTCACTTTGT	TGCTGGTGCT	CCTCGGGCAA	ATTATACCGG	CCAGATAGTG	1440
	CTATATAGTG	TGAATGAGAA	TGGCAATATC	ACGGTTATTTC	AGGCTCACCG	AGGTGACCAG	1500
	ATTGGCTCCT	ATTTTGGTAG	TGTGCTGTGT	TCAGTTGATG	TGGATAAAGA	CACCATTACA	1560
25	GACGTGCTCT	TGGTAGGTGC	ACCAATGTAC	ATGAGTGACC	TAAAGAAAGA	GGAAGGAAGA	1620
	GTCTACCTGT	TTACTATCAA	AAAGGGCATT	TTGGGTGAGC	ACCAATTTCT	TGAAGGCCCC	1680
	GAGGGCATTG	AAAACACTCG	ATTTGGTTCA	GCAATTCAG	CTCTTTTCTG	CATCAACATG	1740
	GATGGCTTTA	ATGATGTGAT	TGTTGGTTCA	CCACTAGAAA	ATCAGAAATC	TGGAGCTGTA	1800
	TACATTTACA	ATGGTCATCA	GGGCACTATC	CGCACAAAGT	ATTCACAGAA	AATCTTGGGA	1860
30	TCCGATGGAG	CCTTTAGGAG	CCATCTCCAG	TACTTTGGGA	GGTCTTGGGA	TGGCTATGGA	1920
	GATTTAAATG	GGGATTCAT	CACCGATGTG	TCTATTGGTG	CCTTTGGACA	AGTGGTTCAA	1980
	CTCTGGTCAC	AAAGTATTGC	TGATGTAGCT	ATAGAAGCTT	CATTCACACC	AGAAAAATC	2040
	ACTTTGGTCA	ACAAGAATGC	TCAGATAATT	CTCAAACCTC	GCTTCAGTGC	AAAGTTTCAA	2100
	CCTACTAAGC	AAAACAATCA	AGTGGCCATT	GTATATAACA	TCACACTTGA	TGCAGATGGA	2160
35	TTTTCATCCA	GAGTAACCTC	CAGGGGGTTA	TTTAAAGAAA	ACAATGAAAG	GTGCCTGCAG	2220
	AAGAAATATG	TAGTAAATCA	AGCACAGAGT	TGCCCCGAGC	ACATCATTTA	TATACAGGAG	2280
	CCCTCTGATG	TTGTCAACTC	TTTGGATTGG	CGTGTGGACA	TCAGTCTGGA	AAACCTTGGC	2340
	ACTAGCCCTG	CCCTTGAAGC	CTATTCTGAG	ACTGCCAAGG	TCTTCAGTAT	TCCTTTCCAC	2400
	AAAGACTGTG	GTGAGGATGG	ACTTTGCATT	TCTGATCTAG	TCCTAGATGT	CCGACAAATA	2460
40	CCAGCTGCTC	AAGAACAAC	CTTTATTGTC	AGCAACCAAA	ACAAAAGGTT	AACATTTTCA	2520
	GTAACACTGA	AAAATAAAG	GGAAAGTGCA	TACAACACTG	GAATTGTTGT	TGATTTTTC	2580
	GAAAACCTGT	TTTTTGCATC	ATTCTCCCTA	CCGGTTGATG	GGACAGAAAT	AACATGCCAG	2640
	GTGGCTGCAT	CTCAGAAGTC	TGTTGCCTGC	GATGTAGGCT	ACCCTGCTTT	AAAGAGAGAA	2700
	CAACAGGTGA	CTTTTACTAT	TAACCTTGAC	TTCAATCTTC	AAAACCTTCA	GAATCAGGCG	2760
45	TCTCTCAGTT	TCCAAGCCTT	AAGTGAAAGC	CAAGAAGAAA	ACAAGGCTGA	TAATTTGGTC	2820
	AACCTCAAAA	TTCTCTCTCT	GTATGATGCT	GAAATTCATC	TAACAAGATC	TACCAACATA	2880
	AATTTTATG	AAATCTCTCT	GGATGGGAAT	GTTCTCTCAA	TCGTGCACAG	TTTGAAGAT	2940
	GTTGGTCCAA	AATTCATCTT	CTCCCTGAAG	GTAACAACAG	GAAGTGTTC	AGTAAGCATG	3000
	GCAACTGTAA	TCATCCACAT	CCCTCAGTAT	ACCAAAGAAA	AGAACCCACT	GATGTACCTA	3060
50	ACTGGGGTGC	AAACAGACAA	GGCTGGTGAC	ATCAGTTGTA	ATGCAGATAT	CAATCCACTG	3120
	AAAATAGGAC	AAACATCTTC	TCTGTATCT	TTCAAAAAGT	AAAATTTTCAG	GCACACCAAA	3180
	GAATTGAAC	GCAGAAGTGC	TTCCTGTAGT	AATGTTACCT	GCTGGTTGAA	AGACGTTTCA	3240
	ATGAAAGGAG	AATACCTTGT	TAATGTGACT	ACCAGAAATT	GGACGGGAC	TTTCGCATCA	3300
	TCAACGTTCC	AGACAGTACA	GCTAACGGCA	CTGCAGAAA	TCAACACCTA	TAACCTTGAG	3360
55	ATATATGTGA	TTGAAGATAA	CACGTGTTAC	ATCCCCCTGA	TGATAATGAA	ACCTGATGAG	3420
	AAAGCCGAAG	TACCAACAGG	AGTTATAATA	GGAAGTATAA	TTGTGGAAT	CCTTTTGCTG	3480
	TTAGCTCTGG	TTGCAATTTT	ATGGAAGCTC	GGCTTCTTCA	AAAGAAAATA	TGAAAAGATG	3540
	ACCAAAAAATC	CAGATGAGAT	TGATGAGACC	ACAGAGCTCA	GTAGCTGAAC	CAGCAGACCT	3600
	ACCTGCAGTG	GGAACCGGCA	GCATCCCAGC	CAGGGTTTGC	TGTTTGCCTG	CATGGATTTT	3660
60	TTTTTAAATC	CCATATTTT	TTTATCATGT	CGTAGGTAAA	CTAACCTGGT	ATTTTAAAGAG	3720
	AAAACCTGCAG	GTGAGTTTGG	ATGAAGAAAT	TGTGGGGGGT	GGGGGAGGTG	CGGGGGGCAG	3780
	GTAGGGAAAT	AATAGGGAAA	ATACCTATTT	TATATGATGG	GGGAAAAAAA	GTAATCTTTA	3840
	AACTGGCTGG	CCCAGAGTTT	ACATTCTAAT	TTGCATTGTG	TCAGAAACAT	GAAATGCTTC	3900
	CAAGCATGAC	AATTTTAA	GAAAAATATG	ATACTCTCAG	ATTTTAAAGG	GGAAAACTGT	3960
65	TCCTTTTAAA	ATATTGTCT	TTAAACAGCA	ACTACAGAAG	TGGAAAGTGT	TGATATGTAA	4020
	GTACTTCCAC	TTGTGTATAT	TTTAATGAAT	ATTGATGTTA	ACAAGAGGGG	AAAACAAAAC	4080
	ACAGGTTTTT	TCAATTTTAT	CTGCTCATCC	AAAGTTGCCA	CAGATGATAC	TTCCAAGTGA	4140
	TAATTTTAT	TATAAACTAG	GTAATAATTG	TTGTTGGTTC	CTTTTATACC	ACGGCTGCCC	4200
	CTTCCACACC	CCATCTTGCT	CTAATGATCA	AAACATGCTT	GAATAACTGA	GCTTAGAGTA	4260
70	TACCTCTTAT	ATGTCATTTT	AAGTTAGGAG	AGGGGGCGAT	ATAGAGACTA	AGGCACAAAA	4320
	TTTTGTTTTAA	AACTCAGAAAT	ATAACATTTA	TGTAAATATC	CATCTGCTAG	AAGCCCATCC	4380
	TGTGCCAGAG	GAAGGAAAAAG	GAGGAAATTT	CCTTTCTCTT	TTAGGAGGCA	CAACAGTTCT	4440
	CTTCTAGGAT	TTGTTTGGCT	GACTGGCAGT	AACCTAGTGA	ATTTTGAAGA	GATGAGTAAT	4500
	TTCTTTGGCA	AGCTTCTCTC	TCCCTTACTG	AACCACTCTC	CCACCTCCTG	GTGGTACCAT	4560
75	TATTTATGAA	GCCCTCTACA	GCCTGACTTT	CTCTCCAGCG	GTCCAAAGTT	ATCCCTCTCT	4620
	TTACCCCTCA	TCCAAAGTTC	CCACTCCTTC	AGGACAGCTG	CTGTGCATTA	GATATTAGGG	4680

5 GGGAAAGTCA TCTGTTTAAT TTACACACTT GCATGAATTA CTGTATATAA ACTCCTTAAC 4740
 TTCAGGGAGC TATTTTCATT TAGTGCTAAA CAAGTAAGAA AAATAAGCTA GAGTGAATTT 4800
 CTAATGTTG GAATGTTATG GGTGTAAGAC AATGTAAAGT AAAACACTCT CAGGATTTCA 4860
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 GTTCAAAGG TAGATCCTGA GATGATTGG TCAGATTGGG ATAAGGCCCA GCAATCTGCA 5040
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 10 CTTAGATTAA AATTCACAGA CACTACATAT CTAAAGCTTT GACAAGTCCT TGACCTCTAT 5220
 AAACCTTCAGA GTCCTCATT TAAATGCGGA AGACTGAGCT GGAGTTCAGC AGTGATGCTT 5280
 TTTAGTTTAA AAAGTCTATG ATCTGATCTG GACTTCCTAT AATACAAATA CACAATCCTC 5340
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Seq ID NO: 187 Protein sequence
 Protein Accession #: NP_002194.1

1 11 21 31 41 51
 20 MGPRTGAAP LPLLLVLALS QGILNCCLAY NVGLPEAKIF SGPSSSEQFGY AVQQFINPKG 60
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 RNMGTGGFLT CGPLWAQCGC NOYTTGVCS DISPDFQLSA SFPSPATQPCP SLIDVVVVCD 180
 ESNSIYPWDA VKNFLEKFVQ GLDIGPTKTQ VGLIQYANNP RVVFNLTNYK TKEEMIVATS 240
 QTSQYGGDLT NTFGAIQYAR KYAYSAASGG RRSATKVMVV VTDGESHDGS MLKAVIDQCN 300
 25 HDNILRFGIA VLGYLNRNAL DTKNLIKEIK AIASIPTRY FFNVSDEAAL LEKAGTLGEQ 360
 IFSIEGTVOG GDNFQMEMSQ VGFSADYSSQ NDILMLGAVG AFGWSGTIVQ KTSHGHLIFP 420
 KQAFDQILQD RNHSSYLGYV VAAISTGEST HFVAGAPRAN YTGQIVLYSV NENGNITVIQ 480
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 QFLEGPEGIE NTRFGSAIAA LSDINMDGFN DIVVGSPLN QNSGAVYIYN GHQGTIRTKY 600
 30 SQKILGSDGA FRSHLQYFGR SLDGYGDLNG DSITDVSIGA FGQVQLWSQ SIADVAIEAS 660
 FTPEKITLVN KNAQIILKLC FSAKFRPTKQ NNQVAIVYNI TLDADGFSSR VTSRGLFKEN 720
 NERCLQKNMV VNQAQSCPEH IYIQEPSDV VNSLDLRVDI SLENPGTSPA LEAYSETAKV 780
 FSIPFHKDCG EDGLCISDLV LDVRQIPAAQ EQPFIVSNQN KRLTFSVTLK NKRESAYNTG 840
 IVVDFSENLF FASFSLPVDG TEVTCQVAAS QKSVACDVGY PALKREQQVT PTINFDNLQ 900
 35 NLQNQASLSF QALSSESQEN KADNLVNLKI PLLYDAEIH LTRSTNINFYE ISSDGNVPSI 960
 VHSFEDVGPK FIFSLKVTG SVPVSMATVI IHIPQYTKK NPLMYLTGVQ TDKAGDISCN 1020
 ADINPLKIGQ TSSSVSFKE NFRHTKELNC RTASCSNVTC WLKDVHMKGE YFVNVTTRI 1080
 NGTFASSTFQ TVQLTAAAEI NTYNPEIYVI EDNTVTIPLM IMKPDEKAEV PTGVIIGSII 1140
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Seq ID NO: 188 DNA sequence
 Nucleic Acid Accession #: NM_002210.1
 Coding sequence: 42-3188 (underlined sequences correspond to start and stop codons)

45 1 11 21 31 41 51
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 TCGTGGGAGC TCCCAAAGCA AACACCACCC AGCCTGGGAT TGTGGAAGGA GGCAGGTCC 300
 TCAAAATGTA CTGCTTTCT ACCCGCCGGT GCCAGCAAT TGAATTTGAT GCAACAGGCA 360
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 CTGTGAGGTC GAAACAGGAT AAAATTTTGG CCTGTGCCCC ATTGTACCAT TGGAGAAGTC 480
 55 AGATGAAACA GGAGCGAGAG CCTGTTGGAA CATGCTTTCT TCAAGATGGA ACAAAGACTG 540
 TTGAGTATGC TCCATGTAGA TCACAAGATA TTGATGCTGA TGGACAGGGA TTTGTCAAG 600
 GAGGATTCAG CATTGATTTT ACTAAAGCTG ACAGAGTACT TCTTGGTGGT CCTGGTAGCT 660
 TTATTGGCA AGGTCAGCTT ATTTCCGATC AAGTGGCAGA AATCGTATCT AAATACGACC 720
 CCAATGTTTA CAGCATCAAG TATAATAACC AATTAGCAAC TCGGACTGCA CAAGCTATTT 780
 60 TTGATGACAG CTATTTGGGT TATTCTGTGG CTGTCGGAGA TTTCAATGGT GATGGCATAG 840
 ATGACTTTGT TTCAGGAGTT CCAAGAGCAG CAAGGACTTT GGAATGGTT TATATTTATG 900
 ATGGGAAGAA CATGTCCTCC TTATACAATT TACTGGCGA GCAGATGGCT GCATATTTCC 960
 GATTTTCTGT AGCTGCCACT GACATTAATG GAGATGATTA TGCAGATGTG TTTATTGGAG 1020
 CACCTCTCTT CATGGATCGT GGCTCTGATG GCAAACCTCA AGAGGTGGGG CAGGTCTCAG 1080
 65 TGTCTCTACA GAGAGCTTCA GGAGACTTCC AGACGACAAA GCTGAATGGA TTTGAGGTCT 1140
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 70 ATGGATATCC AGACTTAATT GTAGGAGCTT TTGGTGTAGA TCGAGCTATC TTATACAGGG 1440
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 75 TTCTTTTGGG TAAACTCAAG CAAAAGGGAG CAATTCGACG AGCACTGTTT CTCTACAGCA 1680
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TTCTTAACCA GTTCACGCCT GCTAACATTA GTCGACAGGC TCACATTCTA CTGACTGTG 1920
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 CAGCGCCCAT GCCTGTGCC TGTGGGTGA TCATTTAGC AGTTCAGCA GGATTGTTGC 3060
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 TTATAGATTT AAACCTTCTT CATGAGGAGT AAAAATCCAA GGCTTTACTG CTGATAGTGC 3300
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 TGGAGTATAG ATTTTATTA GTAGCTTGAA AGAGCTTAAT CATATGCAGT AAGTATTTTT 4980
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 ATCATGATTA AATATCAAAA AATTGCCCTA TGAAAACCTT AAATCTCTAA AACATTTGAA 5460
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 TTGGTAAGAA ATATTGATAC TGATATTGAT TTTTATATAG GTATTATTT CAGAATTGAT 5640
 ATTTTGAGAA AAATACATGT GAGTCATTT TTCTGTTTCT CTTTCTCTT AACGATTATC 5700
 ACTGTAATTC TGAATCT

Seq ID NO: 189 Protein sequence:
 Protein Accession #: NP_002201.1

70
 75

1 11 21 31 41 51
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 SSRMFLLVGA PKANTTQPGI VEGGQVLKCD WSSTRRCQPI EFDATGNRDY AKDDPLEFKS 120
 HQWFGASVRS KQDKILACAP LYHWRTMKQ EREPVGTCFL QDGTKTVEYA PCRSQDIDAD 180
 GQGFCQGGFS IDFTKADRVL LGGPGSFYQW QQLISDQVAE IVSKYDPNVY SIKYNNQLAT 240
 RTAQAIFFDS YLGYSVAVGD FNGDGIDDFV SGVPRAARTL GMVYIYDGKN MSSLYNFTGE 300

QMAAYFGFSV AATDINGDDY ADVFIGAPLF MDRGSDGKLQ EVGQVSVSLQ RASGDFQTTK 360
 LNGFEVFARF GSAIAPLGDL DQDGFNDIAI AAPYGGEDKK GIVYIFNGRS TGLNAVPSQI 420
 LEGQWAARSM PPSFGYSMKG ATDIDKNGYP DLIVGAFGVD RAILYRARPV ITVNAGLEVY 480
 PSILNQDNKT CSLPGTALKV SCFNVRFLCK ADGKGVLPK LNFQVELLLD KLKQKGAIRR 540
 5 ALFLYSRSPS HSKNMTISRG GLMQCEELIA YLRDESEFRD KLTPTITFME YRLDYRTAAD 600
 TTGLQPILNQ FTPANISRQA HILLDCGEDN VCKPKLEVS DSDQKKIYIG DDNPLTLIVK 660
 AQNQEGEYAE AELIVSIPLQ ADFIGVVRNN EALARLSCAF KTENQTRQVV CDLGNPMKAG 720
 TQLLAGLRFS VHQQSEMDTS VKFDLQIQSS NLFDKVSPVV SHKVDLAVLA AVEIRGVSSP 780
 10 DHIFLPIPNW EHKENPETEE DVGPPVQHIY ELRNNGPSSP SKAMHLQWP YKYNNTLLY 840
 ILHYDIDGPM NCTSDMEINP LRIKISSLTQ TEKNQTVAGQ GERDHLITKR DLALSEGDIH 900
 TLGCGVAQCL KIVCQVGRLD RGKSAILYVK SLLWTETFMN KENQNHSSYL KSSASFNVIE 960
 FPKYKNLPIED ITNSTLVTN VTWGIQAPM PVPVWVILA VLAGLLLLAV LVFVMYRMGF 1020
 FKRVRFPQEE QEREQLQPHE NGEENSET

Seq ID NO: 190 DNA sequence

Nucleic Acid Accession #: NM_004864

Coding sequence: 26-952 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
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 GGCCGAGGCG AGCCGCGCAA GTTTCCTGGG ACCCTCAGAG TTGCACTCCG AAGACTCCAG 180
 25 ATTCGAGAG TTGCGGAAAC GCTACGAGGA CTGTCTAACC AGGCTGCGGG CCAACCAGAG 240
 CTGGGAAGAT TCGAACACCG ACCTCGTCCC GGCCCTGCA GTCCGGATAC TCACGCCAGA 300
 AGTGC GGCTG GATCCGCGC GCCACCTGCA CTGCGTATC TCTCGGGCGC CCCTTCCGA 360
 GGGGCTCCCC GAGGCTCCCC GCCTTACCG GGCTCTGTTC CGGCTGTCCC CGACGGCGTC 420
 AAGGTCGTGG GACGTGACAC GACCGCTGCC GCGTCAGCTC AGCCTTGCAA GACCCCAAGC 480
 30 GCCCGCGCTG CACCTGCGAC TGTGCGCGCC GCCGTCGCG TCGGACCAAC TGCTGGCAGA 540
 ATCTTCGTCC GCACGGCCCC AGCTGGAGTT GCACTTGCGG CCGCAAGCCG CCAGGGGGCG 600
 CCGCAGAGCG CGTGC GCGCA ACGGGGACGA CTGTCCGCTC GGGCCCGGGC GTTGCTGCCG 660
 TCTGCACACG GTCCGCGCGT CGCTGGAAGA CCTGGGCTGG GCCGATTGGG TGCTGTCCGC 720
 ACGGGAGGTG CAAGTGACCA TGTGCATCGG CGCGTGCCCG AGCCAGTTCC GGGCGGCAAA 780
 CATGCACGCG CAGATCAAGA CGAGCTGCA CCGCTGAAG CCCGACACGG AGCCAGCGCC 840
 35 CTGCTGCGTG CCCGCCAGCT ACAATCCCAT GGTGCTCATT CAAAAGACCG ACACCGGGGT 900
 GTCGCTCCAG ACCTATGATG ACTTGTAGC CAAAGACTGC CACTGCATAT GAGCAGTCCT 960
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 40 TTATTTATTA TTAATTTATT GGGGTGACCT TCTTGGGGAC TCGGGGGCTG GTCTGATGGA 1140
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 AAAA

Seq ID NO: 191 Protein sequence

Protein Accession #: NP_004855

1 11 21 31 41 51
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 50 HRALFRLSPT ASRSWDVTRP LRRQLSLARP QAPALHLRLS PPPSQSDQLL AESSSARPOL 180
 ELHLRPQAAR GRRRARARNG DDCPLPGRC CRLHTVRASL EDLGWADWVL SPREVQVTMC 240
 IACPSQFRA ANMHAQIKTS LHRLKPDTEP APCCVPASYN PMVLIQKTDG GVSQTYDDL 300
 LAKDCHCI

Seq ID NO: 192 DNA sequence

Nucleic Acid Accession #: XM_061731.1

Coding sequence: 1-567 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
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 GTAAAAGAAC CTTTCTCTCT GATTGGACTT GACACACAGA AGGATCTCAG TAAAGATTG 180
 65 CTGTTGTGTA TGTCCACAGA CACTGGCAAG GACAGGTTTA CCAACATACT GCTGTACAC 240
 TCCCTCCAA TGTGCACCAA ATCAGTAA AATGGGGATA ATGACTCCCC TGCCTTCACA 300
 TGGGGTGGCA AAGACACCA GAGCAATACT GATCTTCTTA TCAGAGACCC TGGGGGCAAG 360
 AGTCTTTTAC TACCAAACA TTCCCAAG CTTGTCCTG AGCATCAGTG TGACCAGAGA 420
 GAGGTCTTCC AGCCACTTTC AGAGCCAGGT GTAGAAGCAG AGATGGAAGT GTTCGTGAT 480
 70 GCTGGATGGT GGATTATCA GAGCTGTCAG GTTCCTTCT CAACCCTTGC AAGAAAGAAG 540
 ATGTTTATT CTAAAGAAAC TGAGTGA

Seq ID NO: 193 Protein sequence

Protein Accession #: XP_061731.1

1 11 21 31 41 51

MRKGNEGENT EGRILAQLAQ RKFLKEDGIT LHISLCLSLIA VKEPFSLIGL DTQKDLKDL 60
 LLLMSTDTGK DRFTNILLSH SPPMCTKSRK NGDNDSPAFT WGGKDTRSNT DLPIRDGGK 120
 SLSLTKHSHK PVPEHQCDQR EVFQPLSEPG VEAEMEVPAD AGWWIYQSCQ VPSSTLARKK 180
 MVYSKETE

Seq ID NO: 194 DNA sequence

Nucleic Acid Accession #: NM_005415.2

Coding sequence: 371-2410 (underlined sequences correspond to start and stop codons)

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	CGCCTCGATC	TCCTCGTCTC	CCGCTCCGCC	CTCCCTTTTC	CCTGGATGAA	CTGCGTCTCT	120
	TTCTCTTCTC	CGCCATGGAA	TTCTGTCTCG	TGCTTTTAGC	CCTCCTGAGC	CAAAGAAACC	180
15	CCAGACAACA	GATGCCATA	CGCAGCGTAT	AGCAGTAACT	CCCCAGCTCG	GTTTCTGTGC	240
	CGTAGTTTAC	AGTATTTAAT	TTTATATAAT	ATATATTATT	TATTATAGCA	TTTTTGATAC	300
	CTCATATTCT	GTTTACACAT	CTTGAAAGGC	GCTCAGTAGT	TCTCTTACTA	AACAACCACT	360
	ACTCCAGAGA	<u>ATGGCAACGC</u>	TGATTACCAG	TACTACAGCT	GCTACCGCCG	CTTCTGGTCC	420
	TTTGGTGGAC	TACCTATGGA	TGCTCATCCT	GGGCTTCATT	ATTGCATTTG	TCTTGGCATT	480
20	CTCCGTGGGA	GCCAATGATG	TAGCAAATTC	TTTTGGTACA	GCTGTGGGCT	CAGGTGTAGT	540
	GACCCTGAAG	CAAGCCTGCA	TCCTAGCTAG	CATCTTTGAA	ACAGTGGGCT	CTGTCTTACT	600
	GGGGGCCAAA	GTGAGCGAAA	CCATCCGGA	GGGCTTGATT	GACGTGGAGA	TGTACAACCTC	660
	GACTCAAGGG	CTACTGATGG	CCGGCTCAGT	CAGTGCATAG	TTTGGTTCTG	CTGTGTGGCA	720
	ACTCGTGGCT	TCGTTTTTGA	AGCTCCCTAT	TTCTGGAACC	CATTGTATTG	TTGGTGCAAC	780
25	TATTGGTTTC	TCCCTCGTGG	CAAAGGGGCA	GGAGGGTGTG	AAGTGGTCTG	AACTGATAAA	840
	AATTGTGATG	TCTTGGTTTC	TGTCCCACT	GCTTTCTGGA	ATTATGTCTG	GAATTTTATT	900
	CTTCTCGGTT	CGTGCAATCA	TCCTCCATAA	GGCAGATCCA	GTTCCTAATG	GTTTGCAGAGC	960
	TTTGCCAGTT	TTCTATGCCT	GCACAGTTGG	AATAAACCTC	TTTTCCATCA	TGTATACTGG	1020
	AGCACCGTTG	CTGGGCTTTG	ACAAACTTCC	TCTGTGGGGT	ACCATCCTCA	TCTCGGTGGG	1080
30	ATGTGCAGTT	TTCTGTGCCC	TTATCGTCTG	GTTCTTTGTA	TGTCCAGGA	TGAAGAGAAA	1140
	AATTGAACGA	GAAATAAAGT	GTAGTCCTTC	TGAAAGCCCC	TTAATGGAAA	AAAAGAATAG	1200
	CTTGAAGGAA	GACCATTGAG	AAACAAAGTT	GTCTGTTGGT	GATATTGAAA	ACAAGCATCC	1260
	TGTTTCTGAG	GTAGGGCTCG	CCACTGTGCC	CCTCCAGGCT	GTGGTGGAGG	AGAGAACAGT	1320
35	CTCATTCAAA	CTTGAGAGAT	TGGAGGAAGC	TCCAGAGAGA	GAGAGGCTTC	CCAGCGTGGA	1380
	CTTGAAAGAG	GAAACCAGCA	TAGATAGCAC	CGTGAATGGT	GCAGTGCAGT	TGCCTAATGG	1440
	GAACCTTGTC	GAGTTTCAGT	AAGCCGTCAG	CAACCAAATA	AACTCCAGTG	GCCACTCCCA	1500
	GTATCACACC	GTGCATAAGG	ATTCCGGCCT	GTACAAAGAG	CTACTCCATA	AATTACATCT	1560
	TGCCAAGGTC	GGAGATTGCA	TGGGAGACTC	CGGTGACAAA	CCCTTAAGGC	GCAATAATAG	1620
	CTATACTTTC	TATACCATGG	CAATATGTGG	CATGCCTCTG	GATTCAATCC	GTGCCAAAGA	1680
40	AGGTGAACAG	AAGGGCGAAG	AAATGGAGAA	GCTGACATGG	CCTAATGCAG	ACTCCAAGAA	1740
	GCGAATTGCA	ATGGACAGTT	ACACCAAGTA	CTGCAATGCT	GTGTCTGACC	TTCACTCAGC	1800
	ATCTGAGATA	GACATGAGTG	TCAAGGCAGC	GATGGGTCTA	GGTGACAGAA	AAGGAAGTAA	1860
	TGGCTCTCTA	GAAGAATGGT	ATGACCAGGA	TAAGCCTGAA	GTCTCTCTCC	TCTTCCAGTT	1920
	CCTGCAGATC	CTTACAGCCT	GCTTTGGGTC	ATTGCGCCAT	GGTGGCAATG	ACGTAAGCAA	1980
45	TGCCATTGGG	CCTCTGGTTG	CTTTATATTT	GGTTTATGAC	ACAGGAGATG	TTTCTTCAA	2040
	AGTGGCAACA	CCAATATGGC	TTCTACTCTA	TGGTGGTGTG	GGTATCTGTG	TTGGTCTGTG	2100
	GGTTTGGGGA	AGAAGAGTTA	TCCAGACCAT	GGGGAAGGAT	CTGACACCGA	TCACACCCTC	2160
	TAGTGGCTTC	AGTATTGAAC	TGGCATCTGC	CCTCACTGTG	GTGATTGCAT	CAAATATTGG	2220
50	CCTTCCCATC	AGTACAACAC	ATTGTAAGT	GGGCTCTGTT	GTGTCTGTTG	GCTGGCTCCG	2280
	GTCCAAGAAG	GCTGTTGACT	GGCGTCTCTT	TCGTAACATT	TTTATGGCCT	GGTTTGTCTC	2340
	AGTCCCATTT	TCGGAGTTA	TCAGTGCTGC	CATCATGGCA	ATCTTCAGAT	ATGTCATCCT	2400
	CAGAATGTGA	AGCTGTTTGA	GATTAATAAT	TGTGTCAATG	TTTGGGACCA	TCTTAGGTAT	2460
	TCCTGCTCCC	CTGAAGAATG	ATTACAGTGT	TAACAGAAGA	CTGACAAGAG	TCTTTTATT	2520
	TGGGAGCAGA	GGAGGGAAGT	GTTACTTGTG	CTATAACTGC	TTTTGTGCTA	AATATGAATT	2580
55	GTCTCAAAAT	TAGCTGTGTA	AAATAGCCCG	GGTTCCACTG	GCTCCTGCTG	AGGTCCCCTT	2640
	TCCTTCTGGG	CTGTGAATTC	CTGTACATAT	TTCTCTACTT	TTTGTATCAG	GCTTCAATTC	2700
	CATTATGTTT	TAATGTTGTC	TCTGAAGATG	ACTTGTGATT	TTTTTTTCTT	TTTTTTAAAC	2760
	CATGAAGAGC	CGTTTGACAG	AGCATGCTCT	GC GTTGTTGG	TTTCACCAGC	TTCTGCCCTC	2820
	ACATGCACAG	GGATTTAACA	ACAAAATAT	AACTACAAT	TCCCTTGTA	TCTCTTATAT	2880
60	AAGTAGAGTC	CTTGGTACTC	TGCCCTCCTG	TCAGTAGTGG	CAGGATCTAT	TGGCATATTC	2940
	GGGAGCTTCT	TAGAGGGATG	AGGTCTCTTG	AACACAGTGA	AAATTTAAAT	TAGTAACTTT	3000
	TTTGCAAGCA	GTTTATTGAC	TGTTATTGCT	AAGAAGAAGT	AAGAAAGAAA	AAGCCTGTTG	3060
	GCAATCTTGG	TTATTTCTTT	AAGATTCTCT	GCAGTGTGGG	ATGGATGAAT	GAAGTGGAAT	3120
65	GTGAACCTTG	GGCAAGTTAA	ATGGGACAGC	CTTCCATGTT	CATTGTGCTA	CCTCTTAACT	3180
	GAATAAAAAA	GCCTACAGTT	TTTAGAAAAA	ACCCGAATTC			

Seq ID NO: 195 Protein sequence:

Protein Accession #: NP_005406.2

70	1	11	21	31	41	51	
	MATLITSTTA	ATAASGPLVD	YLWMLILGFI	IAFVLAFSVG	ANDVANSFGT	AVSGGVVTLK	60
	QACILASIFE	TVGSVLLGAK	VSETIRKGLI	DVEMYNSTQG	LLMAGSVSAM	FGSAVWQLVA	120
	SFLKLPISGT	HCIVGATIGF	SLVAKGQEGV	KWSELIKIVM	SWFVSPLLSG	IMSGILFFLV	180
75	RAFILHKADP	VPNGLRALPV	FYACTVGINL	FSIMYTGAPL	LGFDKLPLWG	TILISVGCAY	240
	PCALIVWFFV	CPRMKRKIER	EIKCSPSESP	LMEKKNSLKE	DHEETKLSVG	DIENKHPVSE	300

VGPATVPLQA VVBERTVSFK LGDLEEAPER ERLPSVDLKE ETSIDSTVNG AVQLPNGNLV 360
 QFSQAVSNQI NSSGHSQYHT VHKDSGLYKE LLHKLHLAKV GDCMGDSGDK PLRRNNSYTS 420
 YTMAICGMPL DSFRAGEGEQ KGEEMEKLTV PNADSKKRIR MDSYTSYCNA VSDLHSASEI 480
 DMSVKAAMGL GDRKGSNGSL EEWYDQDKPE VSLLFQFLQI LTACFGSFAH GGNDVSNAG 540
 5 PLVALYLVYD TGDVSSKVAT PIWLLLYGGV GICVGLWVWG RRVIQTMGKD LTPITPSSGF 600
 SIELASALTV VIASNIGLPI STTHCKVGSV VSVGWLRSKK AVDWRLFRNI FMAWFVTVPI 660
 SGVISAAIMA IFRYVILRM

Seq ID NO: 196 DNA sequence

Nucleic Acid Accession #: NM_000020.1

Coding sequence: 283-1794 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 15 AGGAAACGGT TTATTAGGAG GGAGTGGTGG AGCTGGGCCA GGCAGGAAGA CGCTGGAATA 60
 AGAAACATTT TTGCTCCAGC CCCCATCCCA GTCCCGGGAG GCTGCCGCGC CAGCTGCGCC 120
 GAGCGAGCCC CTCCCCGGCT CCAGCCCGGT CCGGGGCCGC GCCGGACCCC AGCCCGCCGT 180
 CCAGCGCTGG CGGTGCAACT GCGGCCGCGC GGTGGAGGGG AGGTGGCCCC GGTCCGCCGA 240
 20 AGGCTAGCGC CCCGCCACCC GCAGAGCGGG CCCAGAGGGA CCATGACCT GGGCTCCCCC 300
 AGGAAAGGCC TCTGATGCT GCTGATGGCC TTGGTGACCC AGGGAGACCC TGTGAAGCCG 360
 TCTCGGGGCC CGCTGGTGAC CTGCACGTGT GAGAGCCCAC ATTGCAAGGG GCCTACCTGC 420
 CGGGGGGCCT GGTGCACAGT AGTGCTGGTG CGGGAGGAGG GGAGGCACCC CCAGGAACAT 480
 CGGGGCTGCG GGAACCTGCA CAGGGAGCTC TGCCAGGGGC GCCCACCAGA GTTCGTCAAC 540
 25 CACTACTGCT GCGACAGCCA CCTCTGCAAC CACAACGTGT CCCTGGTGCT GGAGGCCACC 600
 CAACCTCCTT CGGAGCAGCC GGAACAGAT GGCCAGCTGG CCCTGATCCT GGGCCCCGTG 660
 CTGGCCTTGC TGGCCCTGGT GGCCCTGGGT GTCTTGGGCC TGTGGCATGT CCGACGGAGG 720
 CAGGAGAAGC AGCGTGGCCT GCACAGCGAG CTGGGAGAGT CCAGTCTCAT CCTGAAAGCA 780
 TCTGAGCAGG GCGACACGAT GTTGGGGGAC CTCTTGGACA GTGACTGCAC CACAGGGAGT 840
 30 GGCTCAGGGC TCCCTTCTCT GGTGCAGAGG ACAGTGGCAC GGCAGGTTGC CTTGGTGGAG 900
 TGTGTGGGAA AAGGCCGCTA TGGCGAAGTG TGGCGGGGCT TGTGGCACGG TGAGAGTGTG 960
 GCCGTCAAGA TCTTCTCTCT GAGGGATGAA CAGTCTTGGT TCCGGGAGAC TGAGATCTAT 1020
 AACACAGTAT TGCTCAGACA CGACAACATC CTAGGCTTCA TCGCCTCAGA CATGACCTCC 1080
 CGCAACTCGA GCACGCAGCT GTGGCTCATC ACGCACTACC ACGAGCACGG CTCCTCTTAC 1140
 35 GACTTTCTGC AGAGACAGAC GCTGGAGCCC CATCTGGCTC TGAGGCTAGC TGTGTCCGCG 1200
 GCATGCGGCC TGGCGCACCT GCACGTGGAG ATCTTCGGTA CACAGGGCAA ACCAGCCATT 1260
 GCCCACCAGC ACTTCAAGAG CCGCAATGTG CTGGTCAAGA GCAACCTGCA GTGTTGCATC 1320
 GCCGACCTGG GCCTGGCTGT GATGCACTCA CAGGGCAGCG ATTACCTGGA CATCGGCAAC 1380
 AACCCGAGAG TGGGCACCAA CCGGTACATG GCACCCGAGG TGCTGGACGA GCAGATCCGC 1440
 40 ACGGACTGCT TTGAGTCCTA CAGTGGAGT GACATCTGGG CCTTTGGCCT GGTGCTGTGG 1500
 GAGATTGCCC GCCGGACCAT CGTGAATGGC ATCGTGGAGG ACTATAGACC ACCCTTCTAT 1560
 GATGTGGTGC CCAATGACCC CAGCTTTGAG GACATGAAGA AGGTGGTGTG TGTGGATCAG 1620
 CAGACCCCA CCATCCCTAA CCGGCTGGCT GCAGACCCGG TCCTCTCAGG CCTAGCTCAG 1680
 ATGATCGGGG AGTGCTGGTA CCCAAACCCC TCTGCCCCGAC TCACCCGCT CCGGATCAAG 1740
 45 AAGACACTAC AAAAAATTAG CAACAGTCCA GAGAAGCCTA AAGTGATTCA ATAGCCAGG 1800
 AGCACCTGAT TCCTTTCTGC CTGCAGGGGG CTGGGGGGGT GGGGGGCAGT GGATGGTGCC 1860
 CTATCTGGGT AGAGGTAGTG TGAGTGTGGT GTGTGCTGGG GATGGGCAGC TGCGCCTGCC 1920
 TGCTCGGCCC CCAGCCACC CAGCCAAAAA TACAGCTGGG CTGAAACCTG

Seq ID NO: 197 Protein sequence:

Protein Accession #: NP_000011.1

1 11 21 31 41 51
 55 MTLGSPRKGL LMLLMALVTQ GDPVKPSRGP LVTCTCESPH CKGPTCRGAW CTVVLVREEG 60
 RHPQEHRCG NLHRELRCGR PTEFVNHYCC DSHLCMHNVS LVLEATQPPS EQPGTDGQLA 120
 LILGPVLALL ALVALGVGL WHVRRRQEKQ RGLHSELGES SLILKASEQG DTMLGDLDS 180
 DCTTSGSGSL PFLVQRTVAR QVALVECVK GRYGEVWRGL WHGESVAVKI FSSRDEQSWF 240
 RETEIYNTVL LRHDNILGFI ASDMTSRNSS TQLWLITHYH EHGSLYDFLQ RQTLEPHLAL 300
 60 RLAVSAACGL AHLHVEIFGT QGKPAIAHRD FKSRLVLVKS NLQCCIADLG LAVMHSQGS 360
 YLDIGNNPRV GTKRYMAPEV LDEQIRTDCE ESYKWTDIWA FGLVLWEIAR RTIVNGIVED 420
 YRPPFYDVVP NDPSFEDMKK VVCVDQQTPT IPNRLAADPV LSGLAQMMRE CWYPNPSARL 480
 TALRIKKTLO KISNSPEKPK VIQ

Seq ID NO: 198 DNA sequence

Nucleic Acid Accession #: NM_003199.1

Coding sequence: 200-2203 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 70 CGGGGGGATC TTGGCTGTGT GTCTGCGGAT CTGTAGTGGC GGCGGCGGCG GCGGCGGCGG 60
 GGAGGCAGCA GGCGCGGGAG CGGGCGCAGG AGCAGGCGGC GGCGGTGGCG GCGGCGGTTA 120
 GACATGAACG CCGCCTCGGC GCCGGCGGTG CACGGAGAGC CCCTTCTCGC GCGGCGGCGG 180
 TTTGTGTGAT TTTGCTAAAA TGCATCACCA ACAGCGAATG GCTGCCTTAG GGACGGACAA 240
 75 AGAGCTGAGT GATTACTGGG ATTTCACTGC GATGTTTCA CTCTCTGTA GCAGTGGGAA 300
 AAATGGACCA ACTTCTTTGG CAAGTGGACA TTTTACTGGC TCAAATGTAG AAGACAGAAG 360
 TAGCTCAGGG TCCTGGGGGA ATGGAGGACA TCCAAGCCCC TCCAGGAACCT ATGGAGATGG 420

	GACTCCCTAT	GACCACATGA	CCAGCAGGGA	CCTTGGGTCA	CATGACAATC	TCTCTCCACC	480
	TTTGTGCAAT	TCCAGAATAC	AAAGTAAAC	AGAAAGGGGC	TCATACTCAT	CTTATGGGAG	540
	AGAATCAAAC	TTACAGGGTT	GCCACCAGCA	GAGTCTCCTT	GGAGGTGACA	TGGATATGGG	600
	CAACCCAGGA	ACCTTTTCGC	CCACCAAACC	TGGTTCCCAG	TACTATCAGT	ATTCTAGCAA	660
5	TAATCCCCGA	AGGAGGCCTC	TTACAGTAG	TGCCATGGAG	GTACAGACAA	AGAAAGTTCG	720
	AAAAGTTTCT	CCAGGTTCGC	CATCTTCAGT	CTATGTCTCA	TCAGCAAGCA	CTGCCGACTA	780
	CAATAGGGAC	TCGCCAGGCT	ATCCTTCCTC	CAAACCAGCA	ACCAGCACTT	TCCTTAGCTC	840
	CTTCTTCATG	CAAGATGGCC	ATCACAGCAG	TGACCCCTGG	AGCTCCTCCA	GTGGGATGAA	900
10	TCAGCCTGGC	TATGCAGGAA	TGTTGGGCAA	CTCTTCTCAT	ATTCCACAGT	CCAGCAGCTA	960
	CTGTAGCCTG	CATCCACATG	AACGTTTGAG	CTATCCATCA	CACCTCTCAG	CAGACATCAA	1020
	TTCCAGTCTT	CCTCCGATGT	CCACTTTCCA	TCGTAGTGGT	ACAAACCATT	ACAGCACCTC	1080
	TTCTGTACG	CCTCCTGCCA	ACGGGACAGA	CAGTATAATG	GCAAATAGAG	GAAGCGGGGC	1140
	AGCCGGCAGC	TCCCAGACTG	GAGATGCTCT	GGGGAAAGCA	CTTGCTTCGA	TCTATTCTCC	1200
	AGATCACACT	AACAACAGCT	TTTCATCAAA	CCCTTCAACT	CCTGTTGGCT	CTCCTCCATC	1260
15	TCTCTCAGCA	GGCACAGCTG	TTTGGTCTAG	AAATGGAGGA	CAGGCCTCAT	CGTCTCCTAA	1320
	TTATGAAGGA	CCCTTAGACT	CTTTGCAAG	CCGAATTGAA	GATCGTTTAG	AAAGACTGGA	1380
	TGATGCTATT	CATGTTCTCC	GGAAACATGC	AGTGGGCCCA	TCCACAGCTA	TGCCTGCTGG	1440
	TCATGGGGAC	ATGCATGGAA	TCATTGGACC	TTCTCATAAT	GGAGCCATGG	GTGGTCTGGG	1500
	CTCAGGGTAT	GGAAACGGCC	TTCTTTCAG	CAACAGACAT	TCACTCATGG	TGGGGACCCA	1560
20	TCGTGAAGAT	GGCGTGGCCC	TGAGAGGCAG	CCATTCTCTT	CTGCCAAACC	AGGTTCCGGT	1620
	TCCACAGCTT	CCTGTCCAGT	CTGCGACTTC	CCCTGACCTG	AACCCACCCC	AGGACCTTTA	1680
	CAGAGGCATG	CCACCAGGAG	TACAGGGGCA	GAGTGTCTCC	TCTGGCAGCT	CTGAGATCAA	1740
	ATCCGATGAC	AGGGGTGATG	AGAACCCTGA	AGACACGAAA	TCTTCGGAGG	ACAAGAAATT	1800
	AGATGACGAC	AAGAAGGATA	TCAAATCAAT	TACTAGCAAT	AATGACGATG	AGGACCTGAC	1860
25	ACCAGAGCAG	AAGGCAGAGC	GTGAGAAGGA	GCGGAGGATG	GCCAACAATG	CCCAGAGCGG	1920
	TCTGCGGGTC	CGTGACATCA	ACGAGGCTTT	CAAAGAGCTC	GGCCGCATGG	TGCAGCTCCA	1980
	CCTCAAGAGT	GACAAGCCCC	AGACCAAGCT	CCTGATCCTC	CACCAGGCGG	TGGCCGTCAT	2040
	CCTCAGTCTG	GAGCAGCAAG	TCCGAGAAAG	GAATCTGAAT	CCGAAAGCTG	CGTGTCTGAA	2100
	AAGAAGGGAG	GAAGAGAAGG	TGTCCTCGGA	GCCTCCCCCT	CTCTCCTTGG	CCGGCCACAC	2160
30	CCCTGGAATG	GGAGACGCAT	CGAATCACAT	GGGACAGATG	TAAAGGGTGC	CAAGTTGCCA	2220
	CATTGCTTCA	TTAAACAACG	AGACCACTTC	CTTAACAGCT	GTATTATCTT	AAACCCACAT	2280
	AAACACTTCT	CCTTAACCCC	CATTTTTGTA	ATATAAGACA	AGTCTGAGTA	GTTATGAATC	2340
	GCAGACGCAA	GAGGTTTTCG	CATTCCCAAT	TATCAAAAAA	CAGAAAAACA	AAAAAAGAAA	2400
35	AGAAAAAAGT	GCAACTTGAG	GGACGACTTT	CTTTAACATA	TCATTAGAAA	TGTGCAAAGC	2460
	AGTATGTACA	GGCTGAGACA	CAGCCAGAG	ACTGAACGGC			

Seq ID NO: 199 Protein sequence:
Protein Accession #: NP_003190.1

40	1	11	21	31	41	51	
	MHHQQRMAAL	GTDKELSDL	DFSAMFSPPV	SSGKNGPTSL	ASGHFTGSNV	EDRSSSGSWG	60
	NGGHPSPSRN	YGDGTPYDHM	TSRDLGSHDN	LSPPFVNSRI	QSKTERGSYS	SYGRESNLQG	120
	CHQQSLGGD	MDMGNPGTSL	PTKPGSQYYQ	YSSNNPRRRP	LHSSAMEVQT	KKVRKVPPGL	180
45	PSSVYAPSAS	TADYNRDSFG	YPSSKPATST	FPSSFPMQDG	HHSSDPWSSS	SGMNQPGYAG	240
	MLGNSSHIPQ	SSSYCSLPH	ERLSYPSSH	ADINSSLPPM	STFHRSGTNH	YSTSSCTPPA	300
	NGTDSIMANR	GSGAAGSSQT	GDALGKALAS	IYSPDHTNNS	FSSNPSTPVG	SPPSLSAGTA	360
	VWSRNGGQAS	SSPNYEGPLH	SLQSRIEDRL	ERLDDAIHVL	RNHAVGPSTA	MPGGHGMHMG	420
	IIGPSHNGAM	GGLGSGYGTG	LLSANRHSLS	VGTHREDGVA	LRGSHSLLPN	QVPVPQLPVQ	480
50	SATSPDLNPP	QDPYRGMPPG	LQQQSVSSGS	SEIKSDDEGD	ENLQDTKSSE	DKKLDDDKKD	540
	IKSITSNNDD	EDLTPEQKAE	REKERRMANN	ARERLRVRDI	NEAFKELGRM	VQLHLKSDKP	600
	QTKLLILHQA	VAVILSLEQQ	VRERNLNPKA	ACLKRREEEK	VSSEPPPLSL	AGPHPGMGDA	660
	SNHMQQM						

55 Seq ID NO: 200 DNA sequence
Nucleic Acid Accession #: BC005987 (1-1286), BE888744 (1287-1756)
Coding sequence: 124-525 (underlined sequences correspond to start and stop codons)

60	1	11	21	31	41	51	
	GGCAGAAGAG	GAAGATTTC	GAAGAGTGCA	GCTGCCTGAA	CCGAGCCCTG	CCGAACAGCT	60
	GAGAATTGCA	CTGCAACCAT	GAGTGAGAAC	AATAAGAATT	CCTTGGAGAG	CAGCCTACGG	120
	CAACTAAAA	GCCATTTTCA	CTGGAACCTG	ATGGAGGGAG	AAAACCTCCT	GGATGATTTT	180
	GAAGACAAAG	TATTTTACCG	GACTGAGTTT	CAGAATCGTG	AATTCAAAGC	CACAATGTGC	240
65	AACCTACTGG	CCTATCTAAA	GCACCTCAAA	GGGCAAAACG	AGGCAGCCCT	GGAATGCTTA	300
	CGTAAAGCTG	AAGAGTTAAT	CCAGCAAGAG	CATGCTGACC	AGGCAGAAAT	CAGAAGTCTG	360
	GTACCTGGGG	GAAACTATGC	CTGGGTCTAC	TATCACATGG	GCCGACTCTC	AGACGTTTCA	420
	ATTTATGTAG	ACAAGGTGAA	ACATGTCTGT	GAGAAGTTTT	CCAGTCCCTA	TAGAATTGAG	480
	AGTCCAGAGC	TTGACTGTGA	GGAAGGGTGG	ACACGGTTAA	AGTGTGGARG	AAACCAAAT	540
70	GAAAGAGCGA	AGGTGTGCTT	TGAGAAGGCT	CTGGAAGAGA	AGCCAAAGAA	CCCAGAAATC	600
	ACCTCTGGAC	TGGCAATAGC	AAGCTACCGT	CTGGACAAC	GGCCACCATC	TCAGAACGCC	660
	ATTGACCCTC	TGAGGCAAGC	CATTCCGGCT	AATCCTGACA	ACCAGTACCT	TAAAGTCCTC	720
	CTGGCTCTGA	AGCTTCATAA	GATGCGTGAA	GAAGGTGAAG	AGGAAGGTGA	AGGAGAGAAG	780
	TTAGTTGAAG	AAGCTTTGGA	GAAAGCCCAA	GGTGTAAACG	ATGTACTTCG	CAGTGCAGCC	840
75	AAGTTTTATC	GAAGAAAAGA	TGAGCCAGAC	AAAGCGATTG	AACTGCTTAA	AAAGGCTTTA	900
	GAATACATAC	CAAACAATGC	CTACCTGCAT	TGCCAAATTG	GGTGTGCTA	TAGGGCAAAA	960

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GTCTTCCAAG TAATGAATCT AAGAGAGAAT GGAATGTATG GGAAAAGAAA GTTACTGGAA 1020
CTAATAGGAC ACGCTGTGGC TCATCTGAAG AAAGCTGATG AGGCCAATGA TAATCTCTTC 1080
CGTGCTCTGT CCATTCTTGC CAGCCTCCAT GCTCTAGCAG ATCAGTATGA AGAAGCAGAG 1140
TATTACTTCC AAAAGGAATT CAGTAAAGAG CTTACTCCTG TAGCGAAACA ACTGCTCCAT 1200
CTGCGGTATG GCAACTTTCA GCTGTACCAA ATGAAGTGTG AAGACAAGGC CATCCACCAC 1260
TTTATAGAGG GTGTAAAAAT AAACCAGAAA TCAAGGGAGA AAGAAAAGAT GAAAGACAAA 1320
CTGCAAAAAA TTGCCAAAAT GCGACTTTCT AAAAATGGAG CAGATTCTGA GGCTTTGCAT 1380
GTCTTGGCAT TCCTTCAGGA GCTGAATGAA AAAATGCAAC AAGCAGATGA AGACTCTGAG 1440
AGGGGTTTGG AGTCTGGAAG CCTCATCCCT TCAGCATCAA GCTGGAATGG GGAATGAAGA 1500
ATAGAGATGT GGTGCCCCACT AGGCTACTGC TGAAGGGGAG CTGAAATTC TCCACAAGTT 1560
GGTATTCAAA ATATGTAATG ACTGGTATGG CAAAAGATTG GACTAAGACA CTGGCCATAC 1620
CACTGGACAG GGTATATGTT AACCTGAATT GCTGGGTCTT AAAAGAGCCC AAGGAGTTCT 1680
GGGAGAGGGA CAGATGGGGG GGTCGTCCAG GGCTGCGCTA AATTATTCTC AATGATTTGT 1740
CTCTTTGCGG AACTTC
  
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Seq ID NO: 201 Protein sequence:
Protein Accession #: AAA59191

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1      11      21      31      41      51
|      |      |      |      |      |
MSENNKNSLE SSLRQLKCHF TWNLMEGENS LDDFEDKVFY RTEFQNRFEK ATMCNLLAYL 60
KHLKGQNEAA LECIRKAEEL IQQEHADQAE IRSLVTWGNY AWVYYHMGRL SDVQIYVDKV 120
KHVCEKFSSP YRIESPCLDC EEGWTRLKCG GNQNERAKVC FEKALEKKPK NPEFTSGLAI 180
ASYRLDNWPP SQNAIDPLRQ AIRLNPNDQY LKVLALAKLH KMREEGEEEG EGEKLVEEAL 240
EKAPGVTDLV RSAAKFYRRK DEPDKAIELL KKALEYIPNN AYLHCQIGCC YRAKVQVMN 300
LRENGMYGKR KLELELIGHAV AHLKKADEAN DNLFRVCSIL ASLHALADQY EDAEYVFQKE 360
FSKELTPVAK QLLHLRYGNF QLYQMKCEDK AIHHFIEGVK INQKSREKEK MKDKLQKIAK 420
MRLSKNGADS EALHVLAFILQ ELNEKMQQAD EDSERGLESG SLIPSASSWN GE
  
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Seq ID NO: 202 DNA sequence
Nucleic Acid Accession #: NM_003090
Coding sequence: 57-824 (underlined sequences correspond to start and stop codons)

35
 40
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1      11      21      31      41      51
|      |      |      |      |      |
GAATTCCGCG GGAGGCCACG GGCTTTCCAC AGCGCGGGGG AACGGGAGGC TGCAGGATGG 60
TCAAGCTGAC GCGCGAGCTG ATCGAGCAGG CCGCGCAGTA CACCAACGCG GTGCGCGACC 120
GGGAGCTGGA CCTCCGGGGG TATAAAATTC CCGTCATTGA AAATCTAGGT GCTACGTTAG 180
ACCAAGTTGA TGCTATTGAT TTTTCTGACA ATGAGATCAG GAAACTGGAT GGTTTTCCTT 240
TGTTGAGAAG ACTGAAACAA TTGTTAGTGA ACAACAACAG AATATGCCGT ATAGGTGAGG 300
GACTTGATCA GGCTCTGCCC TGTCTGACAG AACTCATCTC CACCAATAAT AGTCTCGTGG 360
AACTGGGTGA TCTGGACCTC CTGGCATCTC TCAAATCGCT GACTTACCTA AGTATCCTAA 420
GAAATCCGGT AACCAATAAG AAGCATTACA GATTGTATGT GATTTATAAA GTTCCGCAAG 480
TCAGAGTACT GGATTTCCAG AAAGTGAACG TAAAGAGCGC TCAGGAAGCA GAGAAAATGT 540
TCAAGGGCAA ACGGGGTGCA CAGCTTGCAA AGGATATTGC CAGGAGAAGC AAAACTTTTA 600
ATCCAGGTGC TGGTTTGCCA ACTGACAAAA AGAGAGGTGG GCCATCTCCA GGGGATGTAG 660
AAGCAATCAA GAATGCCATA GCAAATGCTT CAACTCTGGC TGAAGTGGAG AGGCTGAAGG 720
GGTTGCTGCA GTCTGGTCAG ATCCCTGGCA GAGAACGCAG ATCAGGGCCC ACTGATGATG 780
GTGAAGAAGA GATGAAGAA GACACAGTCA CAAACGGGTC CTGAGCAGTG AGGCAGATGT 840
ATAATAATAG GCCCTCTTGG AACAACTCTT GCTTTTCGAA CATGGTATAA TAGCCTTGTT 900
TGTGTTAGCA AAGTGAATC TATCAGCATT GTTGAAATGC TTAAGACTGC TGCTGATAAT 960
TTGTAAATAT AAGTTTGAAT ATCTAAATGT CAATTTCTA CAAATTATAA AAATAAACTC 1020
CACTCTCTAT GCTAAAAAAA AAAAAAAGGA ATTC
  
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Seq ID NO: 203 Protein sequence:
Protein Accession #: NP_003081.1

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1      11      21      31      41      51
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MVKLTAEIE QAAQYTNVR DRELDLRGYK IPVIENTGAT LDQFDAIDFS DNEIRKLDGF 60
PLLRLRLKTL VNNNRICRIG EGLDQALPCL TELILTNNSL VELGDLDPPLA SLKSLTYLSI 120
LRNPVTNKKH YRLYVIYKVP QVRVLDQKLV KLKERQEAEL MFKGKRGQAL AKDIARRSKT 180
FNPAGLPTD KKRGGPSPGD VEAIKNAIAN ASTLAEVERL KGLLQSQQIP GRERRSGPTD 240
DGEEEMEEDT VTNGS
  
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Seq ID NO: 204 DNA sequence
Nucleic Acid Accession #: NM_017643.1
Coding sequence: 169-1401 (underlined sequences correspond to start and stop codons)

70
 75

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TGGGAGGAGC CTGAGGTGGA CCTCGCGTCC TGAGTCTGGA AGGCACCTAT GGGGACCTGC 180
TGGGGTGATA TCTCAGAAAA TGTGAGAGTA GAAGTTCCCA ATACAGACTG CAGCCTACCT 240
  
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	CAGCATAAAT	ATACAAACTG	GAAAGCTTTT	CTAGTGAAAC	GACTTACTGG	TGCCAAAACA	480
5	CTGCCTCCTG	ATTTCTCCCA	AAAGGTTTCA	GAGAGTATGC	AGTATCCTTT	CAAACCTTGC	540
	ATGAGAGTAG	AAGTGGTTGA	CAAGAGGCAT	TTGTGTCGAA	CACGAGTAGC	AGTGGTGGAA	600
	AGTGTAAATTG	GAGGAAGATT	AAGACTAGTG	TATGAAGAAA	GCGAAGATAG	AACAGATGAC	660
	TTCTGGTGCC	ATATGCACAG	CCCATTAATA	CATCATATTG	GTGGTCTCG	AAGCATAGGT	720
10	CATCGATTCA	AAAGATCTGA	TATTACAAAG	AAACAGGATG	GACATTTTGA	TACACCACCA	780
	CATTTATTTG	CTAAGGTAAA	AGAAGTAGAC	CAGAGTGGGG	AATGGTTCAA	GGAAGGAATG	840
	AAATTGGAAG	CTATAGACCC	ATTAAATCTT	TCTACAATAT	GTGTCGCAAC	CATTAGAAAG	900
	GTGCTAGCTG	ACGGATTCTCT	GATGATTGGG	ATCGATTGGC	CAGAAGCAGC	AGACGGATCT	960
	GACTGGTTCT	GTTACCATGT	AACCTCTCCT	TCTATTTTCC	CTGTGCGTTT	CTGTGAAATT	1020
	AACATGATTG	AACCTACTCC	ACCCAGAGGT	TACACAAAAC	TTCTTTTAA	ATGGTTTGAC	1080
15	TACCTCAGGG	AAACTGGCTC	CATTGCAGCA	CCAGTAAAC	TATTTAATAA	GGATGTTCCA	1140
	AATCACGGAT	TTGCTGTAGG	AATGAAATTA	GAAGCAGTAG	ATCTCATGGA	GCCACGTTTA	1200
	ATATGTGTAG	CCACAGTAAC	TGCAATTATT	CATCGTCTCT	TGAGGATACA	TTTTGATGGA	1260
	TGGGAAGAAG	AGTATGATCA	GTGGGTAGAC	TGTGAGTCAC	CTGACCTCTA	TCCTGTAGGG	1320
	TGGTGTCACT	TAACTGGATA	TCAACTACAG	CCTCCAGCAT	CACAGTGTA	GTGGTATAC	1380
20	AGAAAAGGTG	TCCTTTTGTGA	AAAATCAGCA	ATTCTCCAGA	GGACTATCTC	ACATAAGTCA	1440
	TCTTATGAGC	TCACAGGACA	AGAATATACC	TATGTCTGAT	TGGTTGCCAG	GTAAGACATT	1500
	AAGACTCAAC	AACAATATCA	CAGAATCAGA	CCATGTGTCC	CATGGCAATG	TGAATCCAAT	1560
	AGTCAATTAC	ATAATGACTA	TAGAAACACA	ACAGTCACCA	AATTAAACTA	GACTTACTAT	1620
25	TTTAGTGAGT	TAAAAATTAC	ATACTAAAAG	TTTATTGGTA	GGTAATAAAT	GCTTTTGTAGT	1680
	AAATAGTGGA	AAATGTCTCA	TGTTGAGGCT	ATGGTTTGT	AGGAACAAGT	ACCCTTATTT	1740
	TCAGAGCATC	ATGTAATTAA	GTATAATGGT	CTTGGTAAAG	ATAGTTCATA	TAAGTTGTAT	1800
	CTAGCAAACT	GTATCGTCTA	AATTGTAAAC	AATTATCTAG	TACCAATTTT	CCCTTTTAT	1860
	TTTTCAGCAT	CAAGAGAAAA	CCAATCAGCT	TCATCAAAAC	AGAAGAAAAA	GGCTAAGTCC	1920
	CAGCAATACA	AAGGACATAA	GAAAAGTGGG	TCACCACGTG	GTGTTACAT	ACATTTTCTA	1980
30	ATTGTAACT	AATTGGAGTC	ACAGTATTCT	TGGACAGAAA	ATGATATATC	TTGTGAGAAC	2040
	TGATGATTGT	CATTATGTGA	TTATGCTTAA	AGGTGCAGTA	TGCCATAAAA	GGCAAACCCT	2100
	TGCAATAATG	AGAAACACTG	ATATTTTACT	AACAGGAGAA	ATGATTACCA	CAGTATTTAA	2160
	AGTATACGTG	GTAAAGAATA	GAGTCTGTGA	ATGATTCTTG	AAATAATATG	TAAAACCTAC	2220
35	TGAAAGTTAA	TCCTTTTAA	AAACTTTATT	TAAAAAGAAA	AATTAGCAGC	CAGGTGCAGT	2280
	GGCTCACGCC	TGTAATCCCA	GCACTTTAGG	AGGCCGAGGC	TGGCAGATCA	CAAGGTCAGG	2340
	AGATCGAGAC	CATCTGGCT	AACACGGTGA	AACCTGTCT	CCACCAAAAA	TACAAAAAAT	2400
	CTGCCGGGCG	TGGTGGCACA	CGCCTGAAGT	CCCAGCTACT	CAGGAGGCTG	AGGCAAGAGA	2460
	ATCACTTGAA	CCCAGGAGGC	AGAGGTTGCA	GTGGGCCAAG	ATCACGCCAC	TACATTCCAG	2520
40	CTGGGCAACA	CAGCAAGACT	CTGTCTCAAA	AAAAAATAAA	AAAA		

Seq ID NO: 205 Protein sequence:

Protein Accession #: NP_060113.1

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	CGSDIHPVGW	CAASGKPLVP	PRTIQHKYTN	WKAFLVKRLT	GAKTLPPDFS	QKVSSEMQYP	120
	FKPCMRVEVV	DKRHLCRTRV	AVVESVIGGR	LRLVYEESD	RTDDFWCHMH	SPLIHHIGWS	180
	RSIGHRFKRS	DITKKQDGHF	DTPPHLFAKV	KEVDQSGEWF	KEGMKLEAID	PLNLSTICVA	240
50							
	TIRKVLADGF	LMIGIDGSEA	ADGSDWFCYH	ATSPSIFPVG	FCEINMIELT	PPRGYTKLPF	300
	KWFDYLRLEF	SIAEPVKLFN	KDVPNHGFRV	GMKLEAVDLM	EPRLICVATV	TRIIHRLRLI	360
	HFDGWEEYD	QWVDCESPD	YPVGCQLT	YQLQPPASQC	KLVRKGVLL		

55

Seq ID NO: 206 DNA sequence

Nucleic Acid Accession #: NM_012334

Coding sequence: 223-6399 (underlined sequences correspond to start and stop codons)

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	TGAGAAGGAC	AAGAAGGGAC	CGGGCGATGG	CAGCAGGGGA	GCCCCGCGGG	CGCGCGTCCT	120
	CGGGAGTGCG	GCCGTGACAC	GCATGGTTTC	CCCCGACCGG	CGGCGGCGCT	GACTTCCGCG	180
65							
	AGTCGGAGCG	GCACTCGGCG	AGTCCGGGAC	TGCGCTGGAA	CAATGGATAA	CTTCTTCACC	240
	GAGGGAACAC	GGGTCTGGCT	GAGAGAAAAT	GGCCAGCATT	TTCCAAGTAC	TGTAAATTCC	300
	TGTGCAGAAG	GCATCGTCGT	CTTCCGGACA	GACTATGGTC	AGGTATTAC	TTACAAGCAG	360
	AGCACAAATTA	CCCACAGAA	GGTGACTGCT	ATGCACCCCA	CGAACGAGGA	GGGCGTGGAT	420
	GACATGGCGT	CCTTGACAGA	GCTCCATGGC	GGCTCCATCA	TGTATAACTT	ATTCCAGCGG	480
70							
	TATAAGAGAA	ATCAAATATA	TACCTACAT	GGCTCCATCC	TGGCCTCCGT	GAACCCCTAC	540
	CAGCCCATCG	CCGGGCTGTA	CGAGCCTGCC	ACCATGGAGC	AGTACAGCCG	GCGCCACCTG	600
	GGCGAGCTGC	CCCCGCACAT	CTTCGCCATC	GCCAACGAGT	GCTACCGCTG	CCTGTGGAAG	660
	CGTACGACAC	ACCAGTGCAT	CCTCATCAGT	GGTGAAGATG	GGGCAGGTAA	AACCGAAAGC	720
75							
	ACTAAATTGA	TCCTCAAGTT	TCTGTCACT	ATCAGTCAAC	AGTCTTTGGA	ATTGTCCTTA	780
	AAGGAGAAGA	CATCCTGTGT	TGAACGAGCT	ATTCTTGAAA	CGAGCCCAT	CATGGAAGCT	840
	TTCGGCAATG	CGAAGACCGT	GTACAACAAC	AACTTAGTCT	GCTTTGGGAA	GTTTGTTCAG	900

	CTGAACATCT	GTCAGAAAGG	AAATATTTCAG	GGCGGGAGAA	TTGTAGATTA	TTTATTAGAA	960
	AAAAACCGAG	TAGTAAGGCA	AAATCCCGGG	GAAAGGAATT	ATCACATATT	TTATGCACTG	1020
	CTGGCAGGGC	TGGAACATGA	AGAAAGAGAA	GAATTTTATT	TATCTACGCC	AGAAACTAC	1080
5	CACTACTTGA	ATCACTCTGG	ATGTGTAGAA	GACAAGACAA	TCAGTGACCA	GGAATCCTTT	1140
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	TCGAGGCTGC	TTGCTGTAT	ACTGCATCTT	GGGAACATAG	AAATTATCAC	TGCTGGTGGG	1260
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	ACACAGCTCA	CAGATGCTTT	GACCCAGAGA	TCATGTTC	TCAGGGGAGA	AGAGATCCTC	1380
10	ACGCCTCTCA	ATGTTCAACA	GGCAGTAGAC	AGCAGGGACT	CCCTGGCCAT	GGCTCTGTAT	1440
	CGGTCTGTCT	TTGAGTGGGT	AATCAAGAAG	ATCAACAGCA	GGATCAAAGG	CAATGAGGAC	1500
	TTCAAGTCTA	TTGGCATCCT	CGACATCTTT	GGATTGAAA	ACTTTGAGGT	TAATCACTTT	1560
	GAACAGTTCA	ATATAAATA	TGCAAAACGAG	AAACTTCAGG	AGTACTTCAA	CAAGCATATT	1620
	TTTTCTTTAG	AACAACCTAGA	ATATAGCCGG	GAAGGATTAG	TGTGGGAAGA	TATTGACTGG	1680
	ATAGACAATG	GAGAAATGCCT	GGACTTGATT	GAGAAGAAAC	TTGGCCTCCT	AGCCCTTATC	1740
15	AATGAAGAAA	GCCATTTTCC	TCAAGCCACA	CACAGCACCT	TATTGGAGAA	GCTACACAGT	1800
	CAGCATGCGA	ATAACCACTT	TTATGTGAAG	CCCAGAGTTG	CAGTTAACAA	TTTGGAGTG	1860
	AAGCACTATG	CTGGAGAGGT	GCAATATGAT	GTCCGAGGTA	TCTTGGAGAA	GAACAGAGAT	1920
	ACATTTGAG	ATGACCTTCT	CAATTTGCTA	AGAGAAAGCC	GATTTGACTT	TATCTACGAT	1980
20	CTTTTGAAC	ATGTTTCAAG	CCGCAACAAC	CAGGATACCT	TGAAATGTGG	AAGCAAACAT	2040
	CGGCGGCTTA	CAGTCAGCTC	ACAGTTCAAG	GACTCACTGC	ATTCTTAAAT	GGCAACGCTA	2100
	AGCTCCTCTA	ATCCTTTCTT	TGTTCCGCTGT	ATCAAGCCAA	ACATGCAGAA	GATGCCAGAC	2160
	CAGTTTGACC	AGGCGGTGTG	GCTGAACACC	CTGCGGTACT	CAGGGATGCT	GGAGACTGTG	2220
	AGAATCCGCA	AAGCTGGGTA	TGCGGTCCGA	AGACCTTTC	AGGACTTTTA	CAAAAGGTAT	2280
	AAAGTGCTGA	TGAGGAATCT	GGCTCTGCCT	GAGGACGTC	GAGGGAAGTG	CACGAGCCTG	2340
25	CTGCAGCTCT	ATGATGCCTC	CAACAGCGAG	TGGCAGCTGG	GGAAGACCAA	GGTCTTTCTT	2400
	CGAGAATCCT	TGGAACAGAA	ACTGGAGAAG	CGGAGGGAAG	AGGAAGTGAG	CCACGCGGCC	2460
	ATGGTGATTG	GGGCCCATGT	CTTGGGCTTC	TAGCACGAA	AACAATACAG	AAAGGTCCTT	2520
	TATTGTGTGG	TGATAATACA	GAAGAATTAC	AGAGCATTC	TCTGAGGAG	GAGATTTTGT	2580
30	CACCTGAAAA	AGCGAGCCAT	AGTTTCCAG	AAGCAACTCA	GAGGTCAGAT	TGCTCGGAGA	2640
	GTTTACAGAC	AATTGCTGGC	AGAGAAAAGG	GAGCAAGAA	AAAAGAAAG	ACAGGAAGAG	2700
	GAAGAAAAGA	AGAAACGGGA	GGAAGAAGAA	AGAGAAGAG	AGAGAGAGCG	AAGAGAAGCC	2760
	GAGCTCCGCG	CCGACGAGGA	AGAAGAAACG	AGGAAGCAGC	AAGAACTCGA	AGCCTTGCA	2820
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35	GTGGAAGAGA	TCCTCCGTCT	GGAGAAAGAA	ATCGAGGACC	TGCAGCGCAT	GAAGGAGCAG	2940
	CAGGAGCTGT	CGCTGACCGA	GGCTTCCCTG	CAGAAGCTGC	AGGAGCGGCG	GGACCAAGGAG	3000
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40	CCCTACCCAG	AGGAGGAGGT	CGATGAGGGC	TTGGAAGCCG	ACGACGACGC	CTTCAAGGAC	3240
	TCCCCAACCC	CCAGCGAGCA	CGGCCACTCA	GACCAGCGAA	CAAGTGCCAT	CCGACCAAGC	3300
	GATGACTCTT	CAGAGGAGGA	CCCATACATG	AACGACACGG	TGGTGCCAC	CAGCCCCAGT	3360
	GCGGACAGCA	CGGTGCTGCT	CGCCCCATCA	GTGCAAGGACT	CCGGGAGCCT	ACACAACCTC	3420
	TCCAGCGGCG	AGTCCACCTA	CTGCATGCC	CAGAACGCTG	GGGACTTGCC	CTCCCCAGAC	3480
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	ACCTACAACA	GCTCGGGTGC	CTACCGGTTT	AGCTCTGAGG	GGGCGCAGTC	CTCGTTTGAA	3660
	GATAGTGAAG	AGGACTTTGA	TTCCAGGTTT	GATACAGATG	ATGAGCTTTC	ATACCGGCGT	3720
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55	ACTTTCCACC	TGATTGCAGA	GTCCCCAGAA	GATGCCAGCC	AGTGGTTTCAG	CGTGTGAGT	4140
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	ACCGTGTACG	GGCGCAAGCA	CTGTTACCGG	CTCTACACCA	AGCTGCTCAA	CGAGGCCACC	4680
65	CGGTGGTCCA	GTGCCATTCA	AAACGTGACT	GACACCAAGG	CCCCGATCGA	CACCCCCACC	4740
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	TACAAGCGGA	ACCCGATCCT	TCGATACACC	CATCAACCTT	TGCACTCCCC	GCTCCTGCC	4860
	CTTCCGTATG	GGGACATAAA	TCTCAACTTG	CTCAAAGACA	AAGGCTATAC	CACCCTTCAG	4920
	GATGAGGCCA	TCAAGATATT	CAATTCCCTG	CAGCAACTGG	AGTCCATGTC	TGACCCAATT	4980
70	CCAATAATCC	AGGGCATCCT	ACAGACAGGG	CATGACCTGC	GACCTCTGCG	GGACGAGCTG	5040
	TACTGCCAGC	TTATCAAACA	GACCAACAAA	GTGCCCCACC	CCGGCAGTGT	GGGCAACCTG	5100
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	AAATACGCTC	TCTTCACTTA	CGAATCTCTT	AAGAAAACCA	AATGCCGAGA	GTTTGTGCTT	5280
75	TCCCGAGATG	AAATAGAAGC	TCTGATCCAC	AGGCAGGAAA	TGACATCCAC	GGTCTATTGC	5340
	CATGGCGGCG	GCTCCTGCAA	GATCACCATC	AACTCCACCA	CCACTGCTGG	GGAGGTGGTG	5400
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	AAAATAATCT	GGTCTTGGAC	TTTTTATTTT	TATATGGAAA	AGTTTTTAAG	ACTTGGGCCA	7680
	ACTAAGTCTA	CCCACACGAA	AAAAGAAATT	TGCCTTGTCC	CTTTGTGTAC	AACCATGCAA	7740
40	AACTGTTTGT	TGGCTCACAG	AAGTTCTGAC	AATAAAAGAT	ACTAGCT		

Seq ID NO: 207 Protein sequence:
Protein Accession #: NP_036466

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	YSRRHLGELP	PHIFAIANEC	YRCLWKRYDN	QCILISGESG	AGKTESTKLI	LKFLSVISQQ	180
	SLELSLKEKT	SCVERAILLES	SPIMEAFGNA	KTVYNNNSSR	FGKFVQLNIC	QKGNIOGGRI	240
50	VDYLLLEKNR	VRQNPGERNY	HIFYALLLAG	EHEEREEFYI	STPENYHYLN	QSGCVEDKTI	300
	SDQESFREVI	TRMDVMQFSK	EEVREVSRLI	AGILHLGNIE	FITAGGAQVS	FKTALGRSAE	360
	LLGLDPTQLT	DALTQRMFEL	RGEIILTPLN	VQQAVIDSRDS	LAMALYACCF	EWVIKKINSR	420
	IKGNEDPFKSI	GILDFGFEN	FEVNHFEQFN	INYANEKLQE	YFNKHIFSLE	QLEYSREGLV	480
	WEDIDWIDNG	ECLDLIEKKL	GLLALINEES	HFPQATDSTL	LEKLHSQHAN	NHFVVKPRVA	540
55	VNNFGVKHYA	GEVQYDVRGI	LEKNRDTFRD	DLNLLRESR	FDFIYDLFEH	VSSRNNQDTL	600
	KCGSKHRRPT	VSSQFKDSLH	SLMATLSSSN	PFFVRCIKPN	MQKMPDQFDQ	AVVLNQLRYS	660
	GMLETVRIRK	AGYAVRRPFQ	DFYKRYKVLN	RNLALPEDVR	GKCTSLQLLY	DASNSEWQLG	720
	KTKVFLRESL	EQKLEKRREE	EVSHAAMVIR	AHVLGFLARK	QYRKVLYCVV	IIQKNYRAFL	780
	LRRRFLHLKK	AAIVFQKQLR	GQIARRVYRQ	LLAEKREQUE	KKKQEEEEKK	KREEEERERE	840
60	REEREAELRA	QEEETRKKQQ	ELEALQKSQK	EAELTRELEK	QKENKQVEEI	LRLEKEIEDL	900
	QRMKEQQELS	LTEASLQKLQ	ERRDQELRRL	EEEACRAAQE	FLESILNFDEI	DECVRNIERS	960
	LSVGSEFSSE	LAESACEEKP	NFNFSQPYPE	EEVDEGFED	DDAFKDSNP	SEHGHSQDRT	1020
	SGIRTSDDSD	EEDPYMNDTV	VPTSPSADST	VLLAPSVDQS	GSLHNSSSGE	STYCMPQNA	1080
	DLPSPDGDYD	YDQDDYEDGA	ITSGSSVTFE	NSYGSQWSPD	YRCSVGTVNS	SGAYRFSSEG	1140
65	AQSSFEDSEE	DFDSRFDTDD	ELSYRRDSVY	SCVTLPPYFHS	FLYMKGGLMN	SWKRRWCVLK	1200
	DETFLWFRSK	QALKQGWLH	KKGGSSSTLS	RRNWKRWFW	LRQSKLMYFE	NDSEKCLKGT	1260
	VEVRTAKEII	DNTTKENGID	IIMADRTFHL	IAESPEDASQ	WFSVLSQVHA	STDQEIQEMH	1320
	DEQANPQNAV	GTLDVGLIDS	VCSADSPDRP	NSFVIITANR	VLCNADTPE	EMHHWITLLQ	1380
	RSKGDTRVEG	QEFIVRGWLH	KEVKNSPKMS	SLKLKKRWFV	LTHNSLDYYK	SSEKNALKLG	1440
70	TLVLNLSLCS	VDPDEKIFKE	TGYWNVTVYG	RKHCYRLYTK	LLNEATRWS	AIQNVTDTKA	1500
	PIDTPTQLLI	QIKENCLNS	DVVEQIYKRN	PILRYTHHPL	HSPILLPLPYG	DINLNLKDK	1560
	GYYTLQDEAI	KIFNSLQQL	SMSDPIPIIQ	GILQTGHDLR	PLRDELYCQL	IKQTNKVPHP	1620
	GSVGNLYSWQ	ILTCLSCFTL	PSRGILKYLK	FHLKRIREQF	PGTEMEKYAL	FTYESLKKTK	1680
	CREFVPSRDE	IEALIHREQM	TSTVYCHGGG	SCKITINSHT	TAGEVVEKLI	RGLAMEDSRN	1740
75	MFALFEYNHG	VDAKIESRTV	VADVLAKFEK	LAATSEVGLD	PWKFYFKLYC	FLDTONVPKD	1800
	SVEFAFMFEQ	AHEAVIHGHH	PAPEENLQVL	AALRLQYLQ	DYTLHAAIPP	LEEVSLSQRL	1860

KARISQSTKT FTPCERLEKR RTSFLEGLTLR RSFRTGSSVVR QKVVEEQMLD MWIKEEVSSA 1920
 RASIIDKWRK PQGMNQEQAM AKYMALIKEW PGYGSTLFDV ECKEGGFQPE LWLGVSADAV 1980
 SVYKRGEGRP LEVFQYEHIL SFGAPLANTY KIVVDERELL FETSEVVDVA KLMKAYISMI 2040
 VKKRYSTTRS ASSQGSSR

Seq ID NO: 208 DNA sequence

Nucleic Acid Accession #: XM_059761.1

Coding sequence: 124-525 (underlined sequences correspond to start and stop codons)

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10      1      11      21      31      41      51
      |      |      |      |      |      |
CGAAGATCTA TCCAAAATCA AGAAGCCTTT GATTTAGATG TTGCTGTAAA AGAAAATAAA 60
GATGATCTCA ATCATGTGGA TTTGAATGTG TGTACAAGCT TTTCGGGCCC GGGTAGGAGT 120
15      GGCATGGCTC TTATGGAAGT TAACCTATTA AGTGGCTTTA TGGTGCCCTC AGAAGCAATT 180
      TCTCTGAGCG AGACAGTGAA GAAAGTGGAA TATGATCATG GAAAACCTCA CCTCTATTTA 240
      GATTCTGTAA ATGAAACCCA GTTTTGTGTT AATATTCTCT CTGTGAGAAA CTTTAAAGTT 300
      TCAAATACCC AAGATGCTTC AGTGTCCATA GTGGATTACT ATGAGCCAAG GAGACAGGCG 360
      GTGAGAAGTT ACAACTCTGA AGTGAAGCTG TCCTCCTGTG ACCTTTGCAG TGATGTCCAG 420
      GGCTGCCGTC CTTGTGAGGA TGGAGCTTCA GGCTCCCATC ATCACTCTTC AGTCATTTT 480
20      ATTTTCTGTT TCAAGCTTCT GTACTTTATG GAACCTTGGC TGTGATTAT TTTTAAAGGA 540
      CTCTGTGTAA CACTAACATT TCCAGTAGTC ACATGTGATT GTTTTGTTTT CGTAGAAGAA 600
      TACTGCTTCT ATTTTGA AAAA AAGAGTTTTT TTTCTTTCTA TGGGGTTGCA GGGATGGTGT 660
      ACAACAGGTG TAGCTCATGTA TAGCTGCATA GATTTCCTCA CCGATCTTT GTGTGGAAGA 720
25      TCAGAAATGAA TGCAGTTGTG TGTCTATATT TTCCCTCTC AAAATCTTTT AGAATTTT 780
      TGGAGGTGTT TGTTTTCTCC AGAATAAAGG TATTACTTTA G
  
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Seq ID NO: 209 Protein sequence

Protein Accession #: XP_059761.1

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30      1      11      21      31      41      51
      |      |      |      |      |      |
MALMEVNLLS GFMVPSEAIS LSETVKKVEY DHGKLNLYLD SVNETHQFCVN IPAVRNFKVS 60
      NTQDASVSIV DYEPERRQAV RSYNSEVKLS SCDLCSDVQG CRPCEDGASG SHHHSSVIFI 120
35      FCFKLLYFME LWL
  
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Seq ID NO: 210 DNA sequence

Nucleic Acid Accession #: NM_015472

Coding sequence: 258-1460 (underlined sequences correspond to start and stop codons)

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40      1      11      21      31      41      51
      |      |      |      |      |      |
GACACACTCC TCTACAACAC CAGAGACTCC CAAACACAAG GCCTTATATT GACTCATTTT 60
      AGCTCACATC CTGGCGACTC TCAAGAGAGA AACCTCAGAG TGAATAAAT CTCCATAATG 120
45      AGAAGACATG TACATTCACT ATCTATTTTG GCATTTTCCC CAATACATCT CTGCTCATCT 180
      GACTCTTATC TTGGCATCTG CTTCCTGGTG GATCTGAACT GACCCATAAG CCACGCTTAC 240
      TGGTGATTTT CCAGAAGATG AATCCGGCCT CGGCGCCCCC TCCGCTCCCG CCGCTGGGCG 300
      AGCAAGTGAT CCACGTCACG CAGGACCTAG ACACAGACCT CGAAGCCCTC TTCAACTCTG 360
      TCATGAATCC GAAGCCTAGC TCGTGGCGGA AGAAGATCCT GCCGAGTCT TTCTTTAAGG 420
50      AGCCTGATTC GGGCTCGCAC TCGCGCCAGT CCAGCACCAG CTCGTCGGGC GGCCACCCGG 480
      GGCCTCGACT GGCTGGGGGT GCCCAGCATG TCCGCTCGCA CTCGTCGCCG GCGTCCCTGC 540
      AGCTGGGCAC CGGCGCGGGT GCTGCGGGTA GCCCGCGCA GCAGCACGCG CACCTCCGCC 600
      AGCAGTCCTA CGACGTGACC GACGAGCTGC CACTGCCCCC GGGCTGGGAG ATGACCTTCA 660
      CGGCCACTGG CCAGAGGTAC TTCTCAATC ACATAGAAAA AATCACCACA TGGCAAGACC 720
55      CTAGGAAGGC GATGAATCAG CCTCTGAATC ATATGAACCT CCACCTTGCC GTCAGTTCCA 780
      CACCAGTGCC TCAGAGGTCC ATGGCAGTAT CCCAGCCAAA TCTCGTGATG AATCACCAC 840
      ACCAGCAGCA GATGGCCCCC AGTACCCTGA GCCAGCAGAA CCACCCACT CAGAACCAC 900
      CCGCAGGGCT CATGAGTATG CCAATGCGC TGACCACTCA GCAGCAGCAG CAGCAGAAAC 960
      TGCGGCTTCA GAGAATCCAG ATGGAGAGAG AAAGGATTCT AATGCGCCAA GAGGAGCTCA 1020
60      TGAGGCAGGA AGTGCCTCT TGTGACAGC TCCCCATGGA AGCTGAGACT CTGCCCCAG 1080
      TTCAGGCTGC TGTCAACCCA CCCACGATGA CCCAGACATC GAGATCCATC ACTAATAATA 1140
      GCTCAGATCC TTTCTCAATC GGAGGGCCAT ATCATTGAGG GGAGCAGAGC ACTGACAGTG 1200
      GCCTGGGGTT AGGGTGCTAC AGTGTCCCCA CAACTCCGGA GGAATTCCTC AGCAATGTGG 1260
      ATGAGATGGA TACAGGAGAA AACGCAGGAC AAACACCCAT GAACATCAAT CCCCACACAG 1320
65      CCCGTTTCCC TGATTTCTTT GACTGTCTTC CAGGAACAAA CGTTGACTTA GGAACCTTGG 1380
      AATCTGAAGA CCTGATCCCC CTCTTCAATG ATGTAGAGTC TGCTCTGAAC AAAAGTGAGC 1440
      CCTTTCTAAC CTGGCTGTAA TCACTACCAT TGTAACCTGG ATGTAGCCAT GACCTTACAT 1500
      TTCTGGGCC TCTTGGAAAA AGTGATGGAG CAGAGCAAGT CTGCAGGTGC ACCACTTCCC 1560
70      GCCTCCATGA CTCGTGCTCC CTCCTTTTTA TGTGTCAGT TTAATCATTT CCTGGTTT 1620
      ATTGAGAGTA ACTTAAGTTA AACATAAATA AATATTCTAT TTTCATTTTC
  
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Seq ID NO: 211 Protein sequence

Protein Accession #: NP_056287.1

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75      1      11      21      31      41      51
      |      |      |      |      |      |
  
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MNPASAPPPL PPPGQQVIHV TQDLDTLEA LFNSVMNPKP SSWRKILPE SFFKEPDSGS 60
 HSRQSTDS GHTGPRLAG GAQHVRSRSS PASLQLGTGA GAAGSPAQQH AHLRQQSYDV 120
 TDELPLPPGW EMTFTATGQR YFLNHIKQIT TWQDPRKAMN QPLNHNMLHP AVSSTPVFQR 180
 SMAVSQPNLV MNHQHQQMA PSTLSQQNHP TQNPPAGLMS MPNALTQQQ QQQKRLQRI 240
 QMERERIMR QEELMRQEA LCRQLPMEAE TLAPVQAAVN PPTMTPTMRS ITNNSSDPFL 300
 NGGPVHSREQ STDSGLGLGC YSVPTTPEDF LSNVDEMDTG ENAGQTFMNI NPQQTRFPDF 360
 LDCLPGTNVD LGTLESEDLI PLFNDVESAL NKSEPFLTWL

Seq ID NO: 212 DNA sequence

Nucleic Acid Accession #: NM_018174

Coding sequence: 176-2194 (underlined sequences correspond to start and stop codons)

15 CATCTCCCC AACCTGGGG TCGTGTCTT CAACGCCTGC GAGGCCGCGT CGCGGCTGGC 60
 GCGCGGCGAG GATGAGGCGG AGCTGGCGCT GAGCCTCTG GCGCAGCTGG GCATCACGCC 120
 TCTGCCACTC AGCCGCGGQR CCGTGCCAGC CAAACCCACC GTGCTCTTCG AGAAGATGGG 180
 CGTGGGCGCG CTGGACATGT ATGTGCTGCA CCCGCCCTCC GCGGCGCGCG AGCGCACGCT 240
 GGCTCTGTGT TCGCGCCTGC TGGTGTGGCA CCGCGCCGGC CCGGCGGAGA AGGTGTGTGCG 300
 CGTGTCTGTT CCCGTTGCA CCGCGCCCGC CTGCCTCTG GACGGCCTGG TCCGCTGCA 360
 20 GCACCTGAGG TTCTGTGCG AGCCCGTGGT GACGCCCCAG GACCTGGAGG GGCCGCGGCG 420
 AGCCGAGAGC AAAGAGAGCG TGGGCTCCCG GGACAGCTCG AAGAGAGAGG GCCTCCTGGC 480
 CACCCACCCT AGACTTGGCC AGGAGCGCCC TGGGGTGGCC CGCAAGGAGC CAGCACGGCG 540
 TGAGGCCCCA CGCAAGACTG AGAAAGAACG CAAGACCCCG CGGGAGTTGA AGAAAGACCC 600
 CAAACCGAGT GTCTCCCGGA CCCAGCCGCG GGAGGTGCGC CGGGCAGCCT CTCTGTGTG 660
 25 CAACCTCAAG AAGACGAATG CCCAGGCGGC ACCCAAGCCC CGCAAAGCGC CCAGCACGTC 720
 CCACTCTGGC TTCCCGCCGG TGGCAAATGG ACCCCGCGAG CCGCCAGGCC TCCGATGTGG 780
 AGAAGCCAGC CCCCCAGTG CAGCCTGCGG CTCTCCGCGC TCCAGCTGGG TGGCCACGCC 840
 CAGCCTGGAG CTGGGCGCGA TCCAGCCGCG GGAGGAGAAG GCACTGGAGC TGCCTTTGGC 900
 CGCCAGCTCA ATCCCAAGGC CAGGCACACC CTCCCCTGAG TCCACCGGGA GCGCCGCGA 960
 30 GGGCAGCGAG CGGCTGTGCG TGAGCCCACT GCGGGGCGGG GAGGCGGGC CAGACGCCTC 1020
 ACCCACAGTG ACCACACCCA CGGTGACCAC GCCCTACTA CCCGAGAGG TGGGCTCCCC 1080
 GCACTCGAGC GAGGTGGAGC AGTCCCTGTC GGTGTCTTT GAGCAGGTGC TGCCGCCATC 1140
 CGCCCCCACC AGTGAAGGCT GGCTGAGCCT CCCGCTGCGT GGCCCCCGGG CGCGGCGCTC 1200
 GGCTTCCCCA CACGATGTGG ACCTGTGCTT GGTGTACACC TGTGAATTG AGCATCGCAA 1260
 35 GCGGTGCGCA ATGGCACCGG CACCTGCGTC CCGCGGCAGC TCGAATGACA GCAGTGCCCG 1320
 GTCACAGGAA CGGGCAGGTG GGCTGGGGGG CGAGGAGAGC CCACCCACAT CGGTACGCGA 1380
 GTCCCTGCCC ACCCTGTCTG ACTCGGATCC CGTGCCCTG GCGCCCGGTG CGGCAGACTC 1440
 AGACGAAGAC ACAGAGGGCT TTGGAGTCCC TCGCCACGAC CCTTTGCTG ACCCCCTCAA 1500
 GGTCCCCCAG CCACTGCTGT ACCCATCCAG CATCTGCATG GTGGACCCCG AGATGTGTGCC 1560
 40 CCCCCAAGACA GCACGGCAAA CCGAGAAGCT CAGCCGCACC CGGAAGCCCC TGGCCCGCCC 1620
 CAACTCACGC GCTGCCGCCC CCAAAGCCAC TCCAGTGGCT GCTGCCAAAA CCAAGGGGCT 1680
 TGCTGTGGG GACCGTGCCA GCCGACCACT CAGTGCCCGG AGTGAGCCCA GTGAGAAGGG 1740
 AGGCCGGGGA CCCCTGTCCA GAAAGTCTCT AACCCCCAAG ACTGCCACTC GAGGCCCGTC 1800
 GGGGTGAGCC AGCAGCGCGC CCGGGGTGTC AGCCACCCCA CCAAGTCCC CGGTCTACCT 1860
 45 GGACCTGGCC TACCTGCCCC GCGGGAGCAG CGCCACCTG GTGGATGAGG AGTTCTTCCA 1920
 GCGCGTGGCG GCGCTCTGCT ACGTCATCAG TGGCCAGGAC CAGCGCAAGG AGGAAGGCAT 1980
 GCGGGCGGTC CTGGACGCGC TACTGGCCAG CAAGCAGCAT TGGGACCGTG ACCTGCAGGT 2040
 GACCTGTATC CCCACTTTCG ACTCGGTGGC CATGCATACG TGGTACGAG AGACGCACGC 2100
 CCGGCACCA GCGCTGGGCA TCACGGTGTG GGGCAGCAAC GGCATGGTGT CCATGCAGGA 2160
 50 TGACGCCTTC CCGGCTGTGA AGGTGGAGTT CTAGCCCCAT CGCCGACACG CCCCCCACTC 2220
 AGCCAGAGCC GCGCTGTCTT AGATTCAGCC ACATCAGAAA TAAACTGTGA CTACACTTG

Seq ID NO: 213 Protein sequence:

Protein Accession #: NP_060644.1

55 MGVGRLDMYV LHPPSAGAER TLASVCALLV WHPAGPGEKV VRVLFPGCTP PACLLDGLVR 60
 LQHLRFLREP VVTPOLEGP GRAESKESVG SRDSSKREGL LATHPRPGQE RPGVARKEPA 120
 RAEAPRKTEK EAKTPRELKK DPKPSVSRTQ PREVRRRASS VPNLKKTNQA AAPKPRKAPS 180
 TSHSGFPFVA NGPRSPPSLR CGEASPPSAA CGSPASQLVA TPSLELGPFP AGEKALELP 240
 60 LAASSIPRPR TSPESHRSR AEGSERLSLS PLRGGEAGPD ASPTVTPTTV TTPSLPAEVG 300
 SPHSTEVDES LSVSFEQVLP PSAPTSEAGL SLPLRGPRAR RSASPHDIDL CLVSPCEFEH 360
 RKAVPMAPAP ASPGSSNDSS ARSQERAGGL GAEETPPTSV SESLPTLSDS DPVPLAPGAA 420
 DSEDTEGFG VPRHDLPLDP LKVPPLPDP SSICMVDPEM LPPKTARQTE NVSRTRKPLA 480
 65 PPSRAAAPK ATPVAAATK GLAGGDARS PLSARSEPSE KGGRAPLSRK SSTPKTATRG 540
 PSASASSRPG VSATPPKSPV YLDLAYLPSG SSAHLVDEEF FQRVRLCYV ISGQDQRKEE 600
 GMRVLDALL ASKQHWDRDL QVTLIPTFDS VAMHTWYAE HARHQAIGIT VLGSNGMVSM 660
 QDDAFPACKV EF

Seq ID NO: 214 DNA sequence

Nucleic Acid Accession #: NM_002019.1

Coding sequence: 250-4266 (underlined sequences correspond to start and stop codons)

75 1 11 21 31 41 51
 | | | | | |
 GCGGACACTC CTCTCGGCTC CTCCCCGCA GCGGCGGCGG CTCGGAGCGG GCTCCGGGGC 60
 TCGGGTGCAG CGGCCAGCGG GCCTGGCGGC GAGGATTACC CGGGGAAGTG GTTGTCTCTT 120

	GGCTGGAGCC	GCGAGACGGG	CGCTCAGGGC	GCGGGGCGCG	CGGCGGCGAA	CGAGAGGACG	180
	GACTCTGGCG	GCCGGGTCGT	TGGCCGGGGG	AGCGCGGGCA	CCGGGCGGAGC	AGGCCGCGTC	240
	GCGCTCACC	TGGTCAGCTA	CTGGGACACC	GGGGTCCTGC	TGTGCGCGCT	GCTCAGCTGT	300
5	CTGCTTCTCA	CAGGATCTAG	TTCAGGTTCA	AAATTAAAG	ATCCTGAACT	GAGTTTAAAA	360
	GGCACCAGC	ACATCATGCA	AGCAGGCCAG	ACACTGCATC	TCCAATGCAG	GGGGGAAGCA	420
	GCCCATAAAT	GGTCTTTGCC	TGAAATGGTG	AGTAAGGAAA	GCGAAAGGCT	GAGCATAACT	480
	AAATCTGCCT	GTGGAAGAAA	TGGCAAACAA	TTCTGCAGTA	CTTTAACCTT	GAACACAGCT	540
	CAAGCAAACC	ACACTGGCTT	CTACAGCTGC	AAATATCTAG	CTGTACCTAC	TTCAAAGAAG	600
10	AAGGAAACAG	AATCTGCAAT	CTATATATTT	ATTAGTGATA	CAGGTAGACC	TTTCGTAGAG	660
	ATGTACAGTG	AAATCCCCGA	AAATTATACAC	ATGACTGAAG	GAAGGGAGCT	CGTCATTCCC	720
	TGCCGGGTTA	CGTCACCTAA	CATCACTGTT	ACTTTAAAAA	AGTTTCCACT	TGACACTTTG	780
	ATCCCTGATG	GAAAAACGCAT	AATCTGGGAC	AGTAGAAAGG	GCTTCATCAT	ATCAAATGCA	840
	ACGTACAAAG	AAATAGGGCT	TCTGACCTGT	GAAGCAACAG	TCAATGGGCA	TTTGTATAAG	900
15	ACAAACTATC	TCACACATCG	ACAAACCAAT	ACAATCATAG	ATGTCCAAAT	AAGCACACCA	960
	CGCCAGTCA	AAATTAATAG	AGGCCATACT	CTTGTCTCTA	ATTGTACTGC	TACCACTCCC	1020
	TTGAACACGA	GAGTTCAAAAT	GACCTGGAGT	TACCTGTATG	AAAAAATAA	GAGAGCTTCC	1080
	GTAAGGCGAC	GAATTGACCA	AAGCAATTCC	CATGCCAACA	TATTCACAG	TGTTCTTACT	1140
	ATTGACAAAA	TGAGAACAA	AGACAAAGGA	CTTTTACTTT	GTCGTGTAAG	GAGTGGACCA	1200
20	TCATTCAAAT	CTGTTAACAC	CTCAGTGCAT	ATATATGATA	AAGCATTCAT	CACTGTGAAA	1260
	CATCGAAAAA	AGCAGGTGCT	TGAAACCGTA	GCTGGCAAGC	GGTCTTACCG	TGCTCTATG	1320
	AAAGTGAAGG	CATTTCCCTC	GCCGGAAGTT	GTATGGTTAA	AAGATGGGTT	ACCTGCGACT	1380
	GAGAAATCTG	CTCGCTATTT	GACTCGTGCG	TACTCGTTAA	TTATCAAGGA	CGTAACTGAA	1440
	GAGGATGCAG	GGAATTATAC	AATCTTGCTG	AGCATAAAAC	AGTCAAAATG	GTTTAAAAAC	1500
25	CTCACTGCCA	CTCTAATTGT	CAATGTGAAA	CCCCAGATTT	ACGAAAAGGC	CGTGTCTATG	1560
	TTTCCAGACC	CGGCTCTCTA	CCCACTGGGC	AGCAGACAAA	TCCTGACTTG	TACCGCATAT	1620
	GGTATCCCTC	AACCTACAAT	CAAGTGGTTC	TGGCACCCTT	GTAACCATAA	TCATTCCGAA	1680
	GCAAGGTGTG	ACTTTTGTTC	CAATAATGAA	GAGTCCTTTA	TCCTGGATGC	TGACAGCAAC	1740
	ATGGGAAACA	GAATTGAGAG	CATCACTCAG	CGCATGGCAA	TAATAGAAGG	AAAGAATAAG	1800
	ATGGCTAGCA	CCTTGGTGTG	GGCTGACTCT	AGAAATTTCTG	GAATCTACAT	TTGCATAGCT	1860
30	TCCAATAAAG	TTGGGACTGT	GGAAGAAAC	ATAAGCTTTT	ATATCACAGA	TGTGCCAAAT	1920
	GGGTTTTCATG	TTAACTTGA	AAAAATGCCG	ACGGAAGGAG	AGGACCTGAA	ACTGTCTTGC	1980
	ACAGTTAACA	AGTTCTTATA	CAGAGACGTT	ACTTGGATTT	TACTGCGGAC	AGTTAATAAC	2040
	AGAACAATGC	ACTACAGTAT	TAGCAAGCAA	AAAATGGCCA	TCATAAGGA	GCACTCCATC	2100
35	ACTCTTAATC	TTACCATCAT	GAATGTTTCC	CTGCAAGATT	CAGGCACCTA	TGCCTGCAGA	2160
	GCCAGGAATG	TATACACAGG	GGAAGAAATC	CTCCAGAAGA	AAGAAATTAC	AATCAGAGAT	2220
	CAGGAAGCAC	CATACCTCCT	GCGAAACCTC	AGTGATCACA	CAGTGGCCAT	CAGCAGTTCC	2280
	ACCACCTTAG	ACTGTCATGC	TAATGGTGTC	CCCGAGCCTC	AGATCACTTG	GTTTAAAAAC	2340
	AACCACAAAA	TACAACAAGA	GCCTGGAATT	ATTTTAGGAC	CAGGAAGCAG	CACGCTGTTT	2400
40	ATTGAAAGAG	TCACAGAAGA	GGATGAAGGT	GTCTATCACT	GCAAAGCCAC	CAACCAGAAG	2460
	GGCTCTGTGG	AAAGTTCAGC	ATACCTCACT	GTTCAGGAA	CCTCGGACAA	GTCTAATCTG	2520
	GAGCTGATCA	CTCTAACATG	CACCTGTGTG	GCTGCGACTC	TCTTCTGGCT	CCTATTAACC	2580
	CTCCTTATCC	GAAAAATGAA	AAGGTCTTCT	TCTGAAATAA	AGACTGACTA	CCTATCAATT	2640
	ATAATGGACC	CAGATGAAGT	TCCTTTGGAT	GAGCAGTGTG	AGCGGCTCCC	TTATGATGCC	2700
45	AGCAAGTGGG	AGTTTGCCCG	GGAGAGACTT	AAACTGGGCA	AATCACTTGG	AAGAGGGGCT	2760
	TTTGGAAGAG	TGGTTCAAGC	ATCAGCATTT	GGCATTAAAG	AATCACCTAC	GTGCCGGACT	2820
	GTGGCTGTGA	AAATGTGTA	AGAGGGGGCC	ACGGCCAGCG	AGTACAAAGC	TCTGATGACT	2880
	GAGCTAAAAA	TCTTGACCCA	CATTGGCCAC	CATCTGAACG	TGGTTAACCT	GCTGGGAGCC	2940
	TGCACCAAGC	AAGGAGGGCC	TCTGATGGTG	ATTGTTGAAT	ACTGCAATAA	TGGAAATCTC	3000
50	TCCAACCTACC	TCAAGAGCAA	ACGTGACTTA	TTTTTTCTCA	ACAAGGATGC	AGCACTACAC	3060
	ATGGAGCCTA	AGAAAGAAAA	AATGGAGCCA	GGCCTGGAAC	AAGGCAAGAA	ACCAAGACTA	3120
	GATAGCGTCA	CCAGCAGCGA	AAGCTTTGCG	AGCTCCGGCT	TTCAAGGAAG	TAAAGTCTG	3180
	AGTGATGTTG	AGGAAGAGGA	GGATTCTGAC	GGTTTCTACA	AGGAGCCCAT	CACTATGGAA	3240
	GATCTGATTT	CTTACAGTTT	TCAAGTGGCC	AGAGGCATGG	AGTTCTCTGC	TTCCAGAAAG	3300
55	TGCATTCAATC	GGGACCTGGC	AGCGAGAAAC	ATTCTTTTAT	CTGAGAACAA	CGTGGTGAAG	3360
	ATTTGTGATT	TTGGCCTTGC	CCGGGATATT	TATAAGAAC	CCGATTATGT	GAGAAAAGGA	3420
	GATACTCGAC	TTCTCTGTA	ATGGATGGCT	CCCGAATCTA	TCTTTGACAA	AATCTACAGC	3480
	ACCAAGAGCG	ACGTGTGGTC	TTACGGAGTA	TTGCTGTGGG	AAATCTTCTC	CTTAGGTGGG	3540
	TCTCCATACC	CAGGAGTACA	AATGGATGAG	GACTTTTGCA	GTCGCCTGAG	GGAAGGCATG	3600
60	AGGATGAGAG	CTCCTGAGTA	CTCTACTCCT	GAAATCTATC	AGATCATGCT	GGACTGCTGG	3660
	CACAGAGACC	CAAAAGAAAG	GCCAAGATTT	GCAGAACTTG	TGGAAAAACT	AGGTGATTTG	3720
	CTTCAAGCAA	ATGTACAACA	GGATGGTAAA	GACTACATCC	CAATCAATGC	CATACTGACA	3780
	GGAATAGTGT	GGTTTACATA	CTCAACTCCT	GCCTTCTCTG	AGGACTTCTT	CAAGGAAAGT	3840
	ATTTTCACTC	CGAAGTTTAA	TTTCAAGGAG	TCTGATGATG	TCAGATATGT	AAATGCTTTT	3900
65	AAGTTTATGA	GCCTGGAAG	AATCAAAACC	TTTGAAGAAC	TTTTACCGAA	TGCCACCTCC	3960
	ATGTTTATGA	ACTACCAAGG	CGACAGCAGC	ACTCTGTTGG	CCTCTCCCAT	GCTGAAGCGC	4020
	TTCACCTGGA	CTGACAGCAA	ACCCAAGGCC	TCGCTCAAGA	TTGACTTGAG	AGTAACCAGT	4080
	AAAAGTAAGG	AGTCGGGGCT	GTCTGATGTC	AGCAGGCCCA	GTTTCTGCCA	TTCCAGCTGT	4140
	GGGCACGTCA	GCGAAGGCCA	GCGCAGGTTT	ACCTACGACC	ACGCTGAGCT	GGAAGGAAA	4200
70	ATCGCGTGCT	GCTCCCGGCC	CCCAGACTAC	AACCTCGGTG	TCTGTACTC	CACCCACCCC	4260
	ATCTAGAGTT	TGACACGAAG	CCTTATTTCT	AGAAGCACAT	GTGTATTTAT	ACCCCCAGGA	4320
	AACTAGCTTT	TGCCAGTATT	ATGCATATAT	AAGTTTACAC	CTTTATCTTT	CCATGGGAGC	4380
	CAGCTGCTTT	TTTAAATAGT	CTTTTTTTTT	TTGACTAACA	AGAATGTAA	AGAAATGTAA	4440
	TCCAGATAGA	GAAATAGTGA	CAAGTGAAGA	ACACTACTGC	TAAATCTCTA	TGTTACTCAG	4500
75	TGTTAGAGAA	ATCCTTCCTA	AACCCAAATG	CTTCCCTGCT	CCAACCCCGC	CCACCTCAGG	4560
	GCACGCAGGA	CCAGTTTGAT	TGAGGAGCTG	CAGTATCATC	CCAATGCATC	ACGTACCCCA	4620
	CTGGGCCAGC	CCTGCAGCCC	AAAACCCAGG	GCAACAAGCC	CGTTAGCCCC	AGGGGATCAC	4680

	TGGCTGGCCT	GAGCAACATC	TCGGGAGTCC	TCTAGCAGGC	CTAAGACATG	TGAGGAGGAA	4740
	AAGGAAAAAA	AGCAAAAAGC	AAGGGAGAAA	AGAGAAACCG	GGAGAAGGCA	TGAGAAAGAA	4800
	TTTGAGACGC	ACCATGTGGG	CACGGAGGGG	GACGGGGCTC	AGCAATGCCA	TTTCAGTGGC	4860
5	TTCCACAGTC	TGACCCTTCT	ACATTGTAGG	GCCCAGCCAG	GAGCAGATGG	ACAGCGATGA	4920
	GGGGACATTT	TCTGGATTCT	GGGAGGCAAG	AAAAGGACAA	ATATCTTTTT	TGGAACATAA	4980
	GCAAAATTTT	GACCTTTACC	TATGGAAGTG	GTTCTATGTC	CATTCTCATT	CGTGGCATGT	5040
	TTTGATTTGT	AGCACTGAGG	GTGGCACTCA	ACTCTGAGCC	CATACTTTTG	GCTCCTCTAG	5100
	TAAGATGCAC	TGAAAACCTA	GCCAGAGTTA	GGTTGTCTCC	AGGCCATGAT	GGCCTTACAC	5160
10	TGAAAATGTC	ACATCTATTT	TTGGGTATTA	ATATATAGTC	CAGACACTTA	ACTCAATTTT	5220
	TTGGTATTAT	TCTGTTTTGC	ACAGTTAGTT	GTGAAAGAAA	GCTGAGAAGA	ATGAAAATGC	5280
	AGTCTGAGG	AGAGTTTTCT	CCATATCAAA	ACGAGGGCTG	ATGGAGGAAA	AAGGTCAATA	5340
	AGGTCAAGGG	AAGACCCCGT	CTCTATACCA	ACCAAACCAA	TTCACCAACA	CAGTTGGGAC	5400
	CCAAAACACA	GGAAGTCAGT	CACGTTTCCT	TTTCATTAA	TGGGGATTCC	ACTATCTCAC	5460
15	ACTAATCTGA	AAGGATGTGG	AAGAGCATT	GCTGGCGCAT	ATTAAGCACT	TTAAGCTCCT	5520
	TGAGTAAAAA	GGTGGTATGT	AATTTATGCA	AGGTATTCT	CCAGTTGGGA	CTCAGGATAT	5580
	TAGTTAATGA	GCCATCAGTA	GAAGAAAAGC	CCATTTTCAA	CTGCTTTGAA	ACTTGCTCTG	5640
	GGTCTGAGCA	TGATGGGAAT	AGGGAGACAG	GGTAGGAAAG	GGCGCCTACT	CTTCAGGGTC	5700
	TAAAGATCAA	GTGGGCCTTG	GATCGCTAAG	CTGGCTCTGT	TGATGCTAT	TTATGCAAGT	5760
20	TAGGGTCTAT	GTATTTAGGA	TGCGCCTACT	CTTCAGGGTC	TAAAGATCAA	GTGGGCCTTG	5820
	GATCGCTAAG	CTGGCTCTGT	TTGATGCTAT	TTATGCAAGT	TAGGGTCTAT	GTATTTAGGA	5880
	TGCTGTCACC	TTCTGCAGCC	AGTCAGAAGC	TGGAGAGGCA	ACAGTGGATT	GCTGCTTCTT	5940
	GGGGAGAAGA	GTATGCTTCC	TTTTATCCAT	GTAATTTAAC	TGTAGAACCT	GAGCTCTAAG	6000
	TAACCGAAGA	ATGTATGCCT	CTGTTCTTAT	GTGCCACATC	CTTGTTTAA	GGCTCTCTGT	6060
25	ATGAAGAGAT	GGGACCGTCA	TCAGCACATT	CCCTAGTGAG	CCTACTGGCT	CCTGGCAGCG	6120
	GCTTTTGTGG	AAGACTCACT	AGCCAGAAGA	GAGGAGTGGG	ACAGTCTCTT	CCACCAAGAT	6180
	CTAAATCCAA	ACAAAAGCAG	GCTAGAGCCA	GAAGAGAGGA	CAAATCTTTG	TTGTTCTCTT	6240
	TCTTTTACCA	TACGCAAAAC	ACCTGTGACA	GCTGGCAATT	TTATAAATCA	GGTAACTGGA	6300
	AGGAGGTTAA	ACTCAGAAAA	AAGAAGACCT	CAGTCAATT	TCTACTTTTT	TTTTTTTTTT	6360
30	TCCAAATCAG	ATAATAGCCC	AGCAAAATAGT	GATAACAAAT	AAAACCTTAG	CTGTTTCTAT	6420
	CTTGATTCCA	ATAATTAATT	CTTAATCATT	AAGAGACCAT	AATAAATAT	CCTTTTCAAG	6480
	AGAAAAGCAA	AACCATTAGA	ATTGTTACTC	AGCTCCTTCA	AACTCAGGTT	TGTAGCATAC	6540
	ATGAGTCCAT	CCATCAGTCA	AAGAATGGTT	CCATCTGGAG	TCTTAATGTA	GAAAGAAAAA	6600
	TGGAGACTTG	TAATAATGAG	CTAGTTACAA	AGTGCTTGTT	CATTAAATA	GCACTGAAAA	6660
35	TTGAAAACAT	GAATTAACCT	TAATATTCCA	ATCATTGGCC	ATTTATGACA	AAAATGGTTG	6720
	GCACTAACAA	AGAACGAGCA	CTTCCTTTCA	GAGTTTCTGA	GATAATGTAC	GTGGAACAGT	6780
	CTGGGTGGAA	TGGGGCTGAA	ACCATGTGCA	AGTCTGTGTC	TTGTCACTCC	AAGAAGTGAC	6840
	ACCGAGATGT	TAAATTTAGG	GACCCGTGCC	TTGTTTCCCTA	GCCCAACAAG	ATGCAACAT	6900
	CAACACAGATA	CTCGCTAGCC	TCATTTAAAT	TGATTAAAGG	AGGAGTGCAT	CTTTGGCCGA	6960
40	CAGTGGTGTA	ACTGTGTGTG	TGTGTGTGTG	TGTGTGTGTG	TGTGTGTGTG	TGTGGGTGTG	7020
	GGTGTATGTG	TGTTTGTGTG	ATACTATT	AAGGAACTG	GAATTTTAA	GTTACTTTTA	7080
	TACAAACCAA	GAATATATGC	TACAGATATA	AGACAGACAT	GGTTTGGTCC	TATATTCTTA	7140
	GTCATGATGA	ATGTATTTTG	TATACCATCT	TCATATAATA	TACTTAAAAA	TATTTCTTAA	7200
	TTGGGATTTG	TAATCGTACC	AACTTAATTG	ATAAACTTGG	CAACTGCTTT	TATGTTCTGT	7260
45	CTCCTTCCAT	AAATTTTCCA	AAATACTAAT	TCAACAAAGA	AAAAGCTCTT	TTTTTTCCTA	7320
	AAATAAACTC	AAATTTATCC	TTGTTTAGAG	CAGAGAAAAA	TTAAGAAAAA	CTTTGAAATG	7380
	TGCTCAAAAA	ATTGCTAAAT	ATTTTCAATG	GAAAACTAAA	TGTTAGTTTA	GCTGATGTGA	7440
	TGGGGTTTTC	GACCTTTTCA	CTTTTGTGTT	GTTTTACCTA	TTTCACAACT	GTGTAAATTG	7500
	CCAATAATTC	CTGTCCATGA	AAATGCAAAAT	TATCCAGTGT	AGATATATTT	GACCATCACC	7560
50	CTATGGATAT	TGGCTAGTTT	TGCCTTATT	AAGCAAATTC	ATTTACAGCT	GAATGTCTGC	7620
	CTATATATTC	TCTGCTCTTT	GTATTCTCCT	TTGAACCCGT	TAAACATCC	TGTGGCACTC	

Seq ID NO: 215 Protein sequence:
Protein Accession #: NP_002010.1

55	1	11	21	31	41	51	
	MVSYNDTGVL	LCALLSCLLL	TGSSSGSKLK	DPESLSLKGTO	HIMQAGQTLH	LQCRGEAAHK	60
	WSLPENVSKE	SERLSITKSA	CGRNGKQFCS	TLTLNTAQAN	HTGFYSCKYL	AVPTSKKKET	120
60	ESAIYIFISD	TGRPFVEMYS	EIPEIHMTE	GRELVI PCR	TSPNITVTLK	KFPLDTLIPD	180
	GKRIIWDSRK	GFIISNATYK	EIGLLTCEAT	VNGHLYKTNY	LTHRQNTNII	DVQISTPRPV	240
	KLLRGHTLVL	NCTATPLNT	RVQMTWSYPD	EKNKRASVRR	RIDQSN SHAN	IFYSVLTIDK	300
	MQNKDKGLYT	CRVRSGPSFK	SVNTSVHIYD	KAFITVKHRK	QQVLETVAGK	RSYRLSMKVK	360
	AFNSPEVVLW	KDGLPATEKS	ARYLTRGYSL	IKDVTEDDA	GNYTILSLIK	QSNVFKNLTA	420
65	TLIVNVKQPI	YEKAVSSFPD	PALYPLGSRQ	ILTCTAYGIP	QPTIKWFHP	CNNHNSHARC	480
	DFCSNNEESF	ILDADSNMGN	RIESITQORMA	IEBKKNKMAS	TLVVADSRIS	GIYICIASNK	540
	VGTVGRNISF	YITDVPNGFH	VNLEKMPTEG	EDLKLSTCVN	KFLYRDVTWI	LLRTVNNRTM	600
	HYISKQKMA	ITKEHSITLN	LTIMNVSLQD	SGTYACRARN	VYTGEELQK	KEITIRDQEA	660
70	PYLLRNLSDH	TVAISSSTTL	DCHANGVPEP	QITWFKNNHK	IQQEPGIIIG	PGSSTLFIER	720
	VTEEDBGVYH	CKATNQKGSV	ESSAYLTVQG	TSKSNLELI	TLTCTCVAAT	LFWLLLTLLI	780
	RKMKRSSEI	KDGLPATEKS	PDEVPLDEQC	ERLPYDASKW	EFARERLKLK	KSLGRGAFGK	840
	VVQASAFGIK	KSPTCRTVAV	KMLKEGATAS	BYKALMTELK	ILTHIGHHLN	VVNLLGACTK	900
	QGGPLMVIVE	YCKYGNLSNY	LKSKRDLFFL	NKDAALHMEP	KKEKMEPGLE	QGGKPRLDSV	960
75	TSSESFASSG	FQEDKSLSDV	EEEDSDGFFY	KEPITMEDLI	SYSFQVARGM	EFLSSRKCIH	1020
	RDLAARNILL	SENNVVKICD	FGLARDIYKN	PDYVRKGDTR	LPLKWMAPES	IFDKIYSTKS	1080
	DVWSYGVLLW	BIFSLGGSPY	PGVQMDDEFC	SRLREGMRMR	APEYSTPEIY	QIMLDCWHRD	1140

PKERPRFAEL VEKLGDLLQA NVQODGKDYI PINAILTGNS GFTYSTPAFS EDFFKESISA 1200
 PKFNSGSSDD VRYVNAFKFM SLERIKTFEE LLPNATSMFD DYQGDSTLL ASPMLKRFTW 1260
 TDSKPKASLK IDLRVTSKSK ESGLSDVSRP SFCHSSCGHV SEGKRRFTYD HAELEKRIAC 1320
 CSPPPDYNSV VLYSTPPI

Seq ID NO: 216 DNA sequence

Nucleic Acid Accession #: NM_024689

Coding sequence: 76-624 (underlined sequences correspond to start and stop codons)

10 1 11 21 31 41 51
 | | | | | |
 CTCTTTGGCC AAGCCCTGCC TCTGTACAGC CTCGAGTGGA CAGCCAGAGG CTGCAGCTGG 60
 AGCCCAGAGC CCAAGATGGA GCCCCAGCTG GGGCCTGAGG CTGCCGCCCT CCGCCCTGGC 120
 TGGCTGGCCC TGCTGCTGTG GGTCTCAGCC CTGAGCTGTT CTTTCTCCTT GCCAGCTTCT 180
 15 TCCCTTTCTT CTCTGGTGCC CCAAGTCAGA ACCAGCTACA ATTTTGGAAG GACTTTCCTC 240
 GGTCTTGATA AATGCAATGC CTGCATCGGG ACATCTATT TCAAGAAAGT CTTTAAAGAA 300
 GAAATAAGAT CTGACAACTG GCTGGCTTCC CACCTTGGAC TGCCTCCCGA TTCCTTGCTT 360
 TCTTATCCTG CAAATTACTC AGATGATTCC AAAATCTGGC GCCCTGTGGA GATCTTTAGA 420
 CTGGTCAGCA AATATCAAAA CGAGATCTCA GACAGGAAAA TCTGTGCCCT TGCAATCAGC 480
 20 CCAAAGACCT GCAGCATTGA GCGTGTCTCG CGGAAAACAG AGAGGTTCCA GAAATGGCTG 540
 CAGGCCAAGC GCCTCAGGCC GGACCTGGTG CAGGACTGTC ACCAGGGCCA GAGAGAATA 600
 AAGTTCTGTG GTATGCTGAG ATAACACCA TGAAGAAAGC TGGCATGGAG CCCAGCACTG 660
 AGAACTTCCA GAAAGTGTTA GCCTTCTCCC AACTGTGTTA TACCAACCAC ATTTTCAAAT 720
 AGTAATCATT AAAGAGGCTT CTGCATCAAA CCTTCACATG CAGCTCCCAT GCCACCCTCC 780
 25 AGAATTCACC AACACACAGG CCCACCAGCA ACAGGCTACC TTTGCACAAT ATTCTCTGAT 840
 GACAACCTCA AAGCCCCGGC TCTTTCCACC ACCTGTGGT CCCCTAGATG GGGCTGTTGC 900
 TGAGCCCAAC CCAATCCAGA TGTGATCCCC CTGTGATCTA CTCTGGCAA GATTCTCAGT 960
 CTGGACAGGT CTTCCCTATG AGATAGAACC TGATAAGGAG CTAGGGCAAT TCTGACAACA 1020
 TTACCAAAGG CCCACATAAC TTCTAAATT TGGTCTGGTC TGAAGGAAAA CCTGTTCTCG 1080
 30 CCCTAGTGAT GGATGAACCT TCTTATCTCT GCCTTCTAGA GGGAAAAAAA AAGCATACTT 1140
 CTTTACTTTT TTAAGTACCT CCATCAGAGT CATGAAATCA CCTGTCAAGA CTATCTATCT 1200
 TTTATGTTTC CATTCTGGTA AGAACTCTTT AAATGAGGAC ACTGCTGATT GCTGGTGATG 1260
 TTTTGTGAGC AAACACTCGG GGGTATGGAT GAAAGCCAAT CGCAGGTCAA ATGACTCCTT 1320
 35 GGGGAAGCTA CTTCTCTCTT ATTCAGATTT CACTAAAATC TTCCAAGATG AAAGCAAATC 1380
 TAGATTTGCG TCTTCATTGC TGTCCATTTT TGTAATGAAC GAGTGTTTT CTTTAGCTA 1440
 GTGTATCAGG CAGGGTTCTA CCAGAGAAAC AGAACCAGTA GGAGATACAT ATACATGTCC 1500
 AGATTTATTT CAAAGAATTG ATTTACATGA TTGTGGGGAT TGGCAAGTCC AAAATCCATA 1560
 TGGTAGGCCT GCAATCTGTA AACCTTTGGG CAGGAGCTGA TGCTGTAGTT TGCAGATAGA 1620
 40 ATTCCTTGTT CCTTAAAAA ATCTGTTTTT GTTCTTAAAG GCTTTGAATG ATTGGATCAG 1680
 GCCCACCAG ATTACCTAGA TAATCTCTTT TACTTAAAGT AAATGATTG TAGGTGCTAA 1740
 TCACATCTAT GAAATGCCTT CACAGCAACA CCTAGATTAG CATTCAATTG AATAACTGGG 1800
 GAATACAGCC TAGCCAAGTT GACACATAAA ATTAACCATC ACAGCAACAT GCCTGTCTAA 1860
 TTTTATCGAC CGTCTTCAGA CTGTTAAGGA TTGTGGTAGA GAACTGTGAC AGCCACTCTC 1920
 45 AGCATCACCC TGAACCAAAG GCCCTATCA AGTAACAATA TAGCCAAGCA AAATCCAGT 1980
 CAATAGAGAC ATTGACTGGT TGGCTGGCTT CCCAAGGGAT AGCACCAGAC AAGAAATGCA 2040
 AGGATGAGGA AACCAGGCAC GGGAGAGGGA GGGGCAACAG AGGTCCAGGG TTTGGTTATC 2100
 TTTTATTTT TCACTGGGGG GTGGTAAGTT AGCCCTGTTG CCCATGTATG CAGATGGGAG 2160
 AAGTGATTTA GAAACTCCAA AGCAATTGGT AATCCCCAAA ATGGGTGTAT CTGGTTTGAA 2220
 50 ATGAAACCTT ATTTTATTGG AAATGGTTGG TTTCCCAATT CTGTTTGCCA TTGGCCAATA 2280
 TAATTTGTGG TTTGCACATG GCCAGCACAT GCCAAACAGA AGTAGACAAA GGTCTCACTC 2340
 TGTAAGTGGG ACCTTGGGGA GGAGCTGCCT CCATCATAAA GGGAGGGGTT AGTAAAAATG 2400
 GTCTCTTAAG CCTGTTCTCG CTACAGTTAT AGAGGTGCT CAGAACCTTC TCAGCAAATA 2460
 TAGCAGTTAT CTATTGTTGT GTATTAAACC ATTTCAACAC AT

Seq ID NO: 217 Protein sequence:

Protein Accession #: NP_078965.1

1 11 21 31 41 51
 | | | | | |
 60 MEPQLGPEAA ALRPGWLALL LNVSAALSCSF SLPASSLSSL VPQVRTSYNF GRTFLGLDKC 60
 NACIGTSICK KPFKEIRSD NWLASHLGLP PDSLLSY PAN YSDDSKIWRP VEIFRLVSKY 120
 QNEISDRKIC ASASAPKTCS IERVLRKTER FQKWLQAKRL TPDLVQDCHQ GQRELKFLCM 180
 LR

Seq ID NO: 218 DNA sequence

Nucleic Acid Accession #: AF075027.1

Coding sequence: 3-269 (underlined sequences correspond to start and stop codons)

70 1 11 21 31 41 51
 | | | | | |
 GATTAAATTA GTGCTTTAAA CCGTCTTGGT AAATATTCCG CGGGAGCTGG GGAGGACCGT 60
 TGGGATGGCT GTAGCTTGAG TTGAATTTTA ACTGTCTCTA TTCTGGGTTT TGTCGCTCTG 120
 CTTTCTGTGC CAAGGTGCTG TGTACGGGA GAGAGTGACT GGAAGTAAC AAAGCTGAAT 180
 75 CTTTCTCCCT GGAGTAAGGC CGAAGACTGG ATTACTACAC GCCTAGACGT GACACTACAC 240
 CCATAGATCT CATGCATCAT TAATGCCATA TGACATTGCC ATTTCTTTC TCAGTTTACG 300
 GACAAAAGTG GTGGGTTTTC ATTGTCTTCA CTGATTGTCA ATGCATTAAT AAAGAAGATG 360

TGTGGT

Seq ID NO: 219 Protein sequence:
Protein Accession #: AF075027

1	11	21	31	41	51	
ERKWQCHMAL	MMHEIYGCSV	TSRRVVIQSS	ALLQGERFSF	VTFQSLSPVT	QHLGTESRAT	60
KPRMRTVKIQ	LKLQPSQRSS	PAPAEYLRPR	FKALN			

Seq ID NO: 220 DNA sequence
Nucleic Acid Accession #: AL133411.8
Coding sequence: 1-1395 (underlined sequences correspond to start and stop codons)

1	11	21	31	41	51	
ATGGGCAAGG	ACTTCATGAC	TAAAACACTA	AAAGCAATGG	CAACAAAAGC	CAAAATTGAC	60
AAATGGGATC	TAATCAAAAT	AAAGAGCTTC	CGCACAGCAA	AAGAACTAT	TATCAGAGTG	120
AAAGGGCAAC	CTACAGAATG	GGAGAAAAAT	TTTGCAATGT	ATCCATCTGA	CAAAGGGCTG	180
ACATCCAGAA	TCTATAAGGA	ACTTAAACAA	TTTTACAAGA	AAAAACCAA	CAACGCCATC	240
AAAAAGGACA	TGGATGAAGC	TGGAAACCGT	CATTCTCAGA	AACTAACAC	AGGAACAGAA	300
AACCAAACAC	CACATGTTCT	CACTCATAAG	TGGGAGTTGA	ACAATGAGAA	CACATGGACA	360
CAGGGAGGGG	AACATCACAC	ACTGGGGCCT	GTCAGAAGCC	CCTCTGGCCT	CCTGGCTGGC	420
CTTGAACATG	CTGGGAGGAA	ATTACAATTC	ATCCATGGGC	TGTTTACCCT	TGAAAATGAA	480
TGGGCCCAGG	AACAATCCAT	AATCAAAAAG	AAATATGCAT	TATGGATTGG	AACCAAGCAG	540
ATCTGGGTGG	CACAAACTCC	TGGTGAATCT	ATCTCCAGTT	CACCAGCATT	GCCTAATGTG	600
CTACCTTTAA	ATGAAGATGT	TAATAAGCAG	GAAGAAAAGA	ATGAAGATCA	TACTCCCAAT	660
TATGCTCCTG	CTAATGAGAA	AAATGGCAAT	TATTATAAAG	ATATAAAACA	ATATGTGTTT	720
ACAACACAAA	ATCCAAATGG	CAGTGAATCT	GAAATATCTG	TGAGAGCCAC	AACTGACCTG	780
AATTTTGCTC	TAAAAACGTA	TAAACTGTGC	AATGCAACTA	CATATGAAAA	ATCCACCATT	840
GAAGAAGAAA	CAACTACTAG	CGAACCCCTC	CATAAAAATA	TTCAAAGATC	AACCCCAAAC	900
GTGCTGTCAT	TTTGAGCAAT	GTTAGCTAAA	GCTATAAATG	GAACAGCAGT	GGTCATGGAT	960
GATAAAGATC	AATTATTTCA	CCCAATTCCA	GAGTCTGATG	TGAATGCTAC	ACAGGGAGAA	1020
AATCAGCCAG	ATCTAGAGGA	TCTGAAGATC	AAAATAATGC	TGGGAATCTC	GTTGATGACC	1080
CTCCTCCTCT	TTGTGGTCTT	CTTGGCATTG	TGTAGTGCTA	CACTGTACAA	ACTGAGGCAT	1140
CTGAGTTATA	AAAGTTGTGA	GAGTCAGTAC	TCTGTCAACC	CAGAGCTGGC	CACGATGTCT	1200
TACTTTTCATC	CATCAGAAGG	TGTTTCAGAT	ACATCCTTTT	CCAAGAGTGC	AGAGAGCAGC	1260
ACATTTTGTG	GTACCACTTC	TTCAGATATG	AGAAGATCAG	GCACAAGAAC	ATCAGAATCT	1320
AAGATAATGA	CGGATATCAT	TTCCATAGGC	TCAGATAATG	AGATGCATGA	AAACGATGAG	1380
TCGGTTACCC	GGTGA					

Seq ID NO: 221 Protein sequence:
Protein Accession #: AL133411.8

1	11	21	31	41	51	
MGKDFMTKTL	KAMATKAKID	KWDLIKLKSF	RTAKETIIRV	NRQPTWEKN	FAMYP SDKGL	60
TSRIYKELKQ	FYKKKPNNAI	KKDMDEAGNR	HSQKNTNGTE	NQTPHVLTHK	WELNNENTWT	120
QGGEHHTLGP	VRSPGSLLAG	LEHAGRKLQF	IHGLFTLENE	WAQEQSIIQK	KYALWIGTKQ	180
IWVAQTPGES	ISSSPALPNV	LPLNEDVNKQ	BEKNEDHTPN	YAPANEKNGN	YKDIKQYVF	240
TTQNPNGTES	EISVRATDDL	NFALKNDKTV	NATTYKSTI	EEETTTSEPS	HKNIQRSTPN	300
VPAFTWMLAK	AINGTAVVMD	DKDQLFHPPI	ESDVNATQGE	NQPDLEDLKI	KIMLGISLMT	360
LLLFVVLAF	CSATLYKLRLH	LSYKSCESQY	SVNPELATMS	YFHPSEGVSD	TSFSKSAESS	420
TFLGTTSSDM	RRSGTRTSES	KIMTDIISIG	SDNEMHENDE	SVTR		

Seq ID NO: 222 DNA sequence
Nucleic Acid Accession #: AL050295.1
Coding sequence: 237-2073 (underlined sequences correspond to start and stop codons)

1	11	21	31	41	51	
GAAGGGGACA	GAAGGCAGTT	CACCTCTGCT	CCCGACAGCC	TGGGAACCCG	CAAGAGCCCC	60
AGCATTTGAA	GTCTGTGCTT	GTGAAACCCC	ACCCTCCTCT	GGCTGTGTGA	TGAATGGGA	120
TGCCCTCGAG	GTACACCTCA	CCTGAGAGGG	TTTGGGCGAG	ATCAGCAGTA	AGGTGTTAAA	180
TTTTAGAAAG	CTGAAALACT	CAGAAGAGAA	AGGCCAACCA	ACTCAAACCT	GAAGACATGA	240
AATCCCAAG	GAGAACCACT	TTGTGCCTCA	TGTTTATTGT	GATTTATTCT	TCCAAAGCTG	300
CACTGAACATG	GAAATACGAG	TCTACTATTC	ATCCTTTGAG	TCTTCATGAA	CATGAACCAG	360
CTGGTGAAGA	GGCACTGAGG	CAAAAACGAG	CCGTTGCCAC	AAAAAGTCCT	ACGGCTGAAG	420
AATACACTGT	TAATATTGAG	ATCAGTTTTG	AAAATGCATC	CTTCCTGGAT	CCTATCAAAG	480
CCTACTTGAA	CAGCCTCAGT	TTTCCAATTC	ATGGGAATAA	CACTGACCAA	ATTACTGACA	540
TTTTTGAGCAT	AAATGTGACA	ACAGTCTGCA	GACCTGCTGG	AAATGAAATC	TGGTGTCTCT	600
GCGAGACAGG	TTATGGGTGG	CCTCGGGAAA	GGTGTCTTCA	CAATCTCATT	TGTCAAGAGC	660
GTGACGTCTT	CCTCCAGGG	CACCATTGCA	GTTGCCTTAA	AGAACTGCCT	CCCAATGGAC	720

CTTTTCGCT GCTTCAGGAA GATGTTACCC TGAACATGAG AGTCAGACTA AATGTAGGCT 780
 TTCAAGAAGA CCTCATGAAC ACTTCCTCCG CCTCTATAG GTCCTACAAG ACCGACTTGG 840
 AAACAGCGTT CCGGAAGGGT TACGGAATTT TACCAGGCTT CAAGGGCGTG ACTGTGACAG 900
 5 GGTTCAAGTC TGGAAAGTGTG GTTGTGACAT ATGAAGTCAA GACTACACCA CCATCACTTG 960
 AGTTAATACA TAAAGCCAAT GAACAAGTTG TACAGAGCCT CAATCAGACC TACAAAATGG 1020
 ACTACAATC CTTTCAAGCA GTTACTATCA ATGAAAGCAA TTTCTTTGTC ACACCAGAAA 1080
 TCATCTTTGA AGGGGACACA GTCAGTCTGG TGTGTGAAA GGAAGTTTGT TCCTCCAATG 1140
 TGTCTTGGCG CTATGAAGAA CAGCAGTTGG AAATCCAGAA CAGCAGCAGA TTCTCGATT 1200
 10 ACACCGCACT TTTCAACAAC ATGACTTCGG TGTCCAAGCT CACCATCCAC AACATCACTC 1260
 CAGGTGATGC AGGTGAATAT GTTTGCAAA TGAATATTAGA CATTTTGTAA TATGAGTGCA 1320
 AGAAGAAAAAT AGATGTTATG CCCATCCAAA TTTTGGCAAA TGAAGAAATG AAGGTGATGT 1380
 GCGACAACAA TCCTGTATCT TTGAAGTCT GCAGTCAGGG TAATGTTAAT TGGAGCAAG 1440
 TAGAATGGAA GCAGGAAGGA AAAATAAATA TTCCAGGAAC CCTGAGACA GACATAGATT 1500
 15 CTAGCTGCAG CAGATACACC CTCAAGGCTG ATGGAACCCA GTGCCAAGC GGGTCGTCTG 1560
 GAACAACAGT CATCTACACT TGTGAGTTCA TCAGTGCCTA TGGAGCCAGA GGCAGTGCAA 1620
 ACATAAAAGT GACATTATC TCTGTGGCCA ATCTAACAA AACCCTGGAG CCAATTTCTG 1680
 TTTCTGAGGG ACAAACCTTT TCTATAAAAT GCATCAGTGA TGTGAGTAAC TATGATGAGG 1740
 TTTATTGGAA CACTTCTGCT GGAATTAAAA TATACCAAAG ATTTTATACC ACGAGGAGGT 1800
 20 ATCTTGATGG AGCAGAATCA GTACTGACAG TCAAGACCTC GACCAGGGAG TGAATGGAA 1860
 CCTATCACTG CATATTTAGA TATAAGAAAT CATACAGTAT TGCAACCAA GACGTCATTG 1920
 TTCACCCGCT GCCTCTAAAG CTGAACATCA TGATTGATCC TTTGGAAGCT ACTGTTTCAT 1980
 CAGTGGTTC CCATCACATC AAGTGCTGCA TAGAGGAGGA TGGAGACTAC AAAGTTACTT 2040
 TCCATATGGG TTCTCATCTC CTTCCTGCTG TAAAAA AAAAAA A

25 Seq ID NO: 223 Protein sequence
 Protein Accession #: CAB43394.1

1 11 21 31 41 51
 30 MKSPRRITLC LMFIVYSSK AALNWNVEST IHPLSLHEHE PAGEEALRQK RAVATKSPTA 60
 EEYTVNIEIS FENASFLDPI KAYLNSLSFP IHGNNTDQIT DILSINVTTV CRPAGNEIWC 120
 SCETGYGWPR ERCILHNLICQ ERDVFLPGHH CSCLKELPPN GPFCLLQEDV TLNMRVRLNV 180
 GFQEDLMNTS SALYRSYKTD LETAFRKGYG ILPGFKGVTV TGFKSGSVVV TYEVKTTTPPS 240
 35 LELIHKANEQ VVQSLNQTYK MDYNSFQAVT INESNFFVTP EIIFEGDTS LVCEKEVLSS 300
 NVSWRYEEQQ LEIQNSSRFS IYALFNMT SVSKLTIHNI TPGDAGEYVC KLILDIFEYE 360
 CKKKIDVMPI QILANEEMKV MCDNNPVS LN CCSQGNVNS KVEWKQEGKI NIPGTPETDI 420
 DSSCSRYTLK ADGTQCPSPS SGTTVIYTCE FISAYGARG ANIKVTFISV ANLTITPDPI 480
 SVSEGNFQSI KCISDVSNYD EVYWNYSAGI KIYQRFYTR RYLDGAESVL TVKTTSTREWN 540
 40 GTHYICIFRYK NSYSIATKDV IVHPLPLKLN IMIDPLEATV SCSGSHHIK CIEEDGDYKV 600
 TFHMGSSSLP AVKKKKKK

Seq ID NO: 224 DNA sequence
 Nucleic Acid Accession #: NM_007268

45 Coding sequence: 46-1245 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 50 GGTAGCAGGA GGCTGGAAGA AAGGACAGAA GTAGCTCTGG CTGTGATGGG GATCTTACTG 60
 GGCCTGTACT TCCTGGGGCA CCTAACAGTG GACACTTATG GCCGTCCCAT CCTGGAAGTG 120
 CCAGAGAGTG TAACAGGACC TTGGAAGGGG GATGTGAATC TTCCCTGCAC CTATGACCCC 180
 CTGCAAGGCT ACACCCAGT CTGGTGAAG TGGCTGGTAC AACGTGGCTC AGACCTGTG 240
 ACCATCTTTC TACGTGACTC TTCTGGAGAC CATATCCAGC AGGCAAAGTA CCAGGGCCGC 300
 CTGCATGTGA GCCACAAGGT TCCAGGAGAT GTATCCCTCC AATTGAGCAC CCTGGAGATG 360
 55 GATGACCGGA GCCACTACAC GTGTGAAGTC ACCTGGCAGA CTCCTGATGG CAACCAAGTC 420
 GTGAGAGATA AGATTACTGA GCTCCGTGTC CAGAAACTCT CTGTCTCCAA GCCACAGTG 480
 ACAACTGGCA GCGGTTATGG CTTCACGGTG CCCAGGGGAA TGAGGATTAG CCTTCAATGC 540
 CAGGCTCGGG GTTCTCCTCC CATCAGTTAT ATTTGGTATA AGCAACAGAC TAATAACCG 600
 GAACCCATCA AAGTAGCAAC CCTAAGTACC TTAATCTTCA AGCCTGCGGT GATAGCCGAC 660
 60 TCAGGCTCCT ATTTCTGCAC TGCCAAGGGC CAGGTTGGCT CTGAGCAGCA CAGCGACATT 720
 GTGAAGTTTG TGGTCAAAGA CTCCTCAAAG CTAATCAAGA CCAAGACTGA GGCACCTACA 780
 ACCATGACAT ACCCCTTGAA AGCAACATCT ACAGTGAAGC AGTCCTGGGA CTGGACCACT 840
 GACATGGATG GCTACCTTGG AGAGACCAGT GCTGGGCCAG GAAAGAGCCT GCCTGTCTTT 900
 GCCATCATCC TCATCATCTC CTGTGTCTGT ATGGTGGTTT TTACCATGGC CTATATCATG 960
 65 CTCTGTGCGA AGACATCCCA ACAAGAGCAT GTCTACGAAG CAGCCAGGGC ACATGCCAGA 1020
 GAGGCCAACG ACTCTGGAGA AACCATGAGG GTGGCCATCT TCGCAAGTGG CTGCTCCAGT 1080
 GATGAGCCAA CTTCCAGAA TCTGGCAAC AACTACTCTG ATGAGCCCTG CATAGGACAG 1140
 GAGTACCAGA TCATCGCCCA GATCAATGGC AACTACGCCC GCCTGTCTGA CACAGTCTCT 1200
 CTGATTATG AGTTCTGGC CACTGAGGGC AAAAGTGTCT GTTAAAAATG CCCATTAGG 1260
 70 CCAGGATCTG CTGACATAAT TGCCTAGTCA GTCCTTGCTC TCTGCATGGC CTCTTCCCT 1320
 GCTACCTCTC TTTCTGGATA GCCCAAAGTG TCCGCCTACC AACTCTGGAG CCGCTGGGAG 1380
 TCACTGGCTT TGCCCTGGAA TTTGCCAGT GCATCTCAAG TAAGCCAGCT GCTGGATTG 1440
 GCTCTGGGCC CTTCTAGTAT TTTGCCGGG GGCTTCTGGT ACTCTCTCT AAATACCAGA 1500
 GGGAAGATGC CCATAGCACT AGGACTTGGT CATCATGCCT ACAGACACTA TTCAACTTTG 1560
 75 GCATCTTGCC ACCAGAAGC CCGAGGGAGG CTCAGCTCTG CCAGCTCAGA GGACCACTT 1620
 TATCCAGGAT CATTTCTCTT TCTTCAGGGC CAGACAGCTT TTAATTGAAA TTGTTATTTC 1680
 ACAGGCCAGG GTTCAGTTCT GCTCTCCAC TATAAGTCTA ATGTTCTGAC TCTCTCTGG 1740

TGCTCAATAA ATATCTAATC ATAACAGCAA AAAAAAAAAA AAAAAA

Seq ID NO: 225 Protein sequence:

Protein Accession #: NP_009199.1

	1	11	21	31	41	51	
	MGILLGLLLL	GHLTVDTYGR	PILEVPESVT	GPWKGDVNL	CTYDPLQGYT	QVLVKWLVQR	60
	GSDPVTIFLR	DSSGDHIQQA	KYQGRHLVSH	KVPGDVSLLQ	STLEMDDRS	YTCEVTWQTP	120
10	DGNQVVRDKI	TELRVQKLSV	SKPTVTGSG	YGFTVPQGM	ISLQCQARG	PPISYIWKQ	180
	QTNNQEPKIV	ATLSTLLFKP	AVIADSGSYF	CTAKGQVGSE	QHSDIVKFV	KDSSKLLKTK	240
	TEAPTMTYP	LKATSTVKQS	WDWTTDMGY	LGETSAGPGK	SLPVFAILL	ISLCCMVVFT	300
	MAYIMLCRKT	SQGEHVYEA	RAHAREANDS	GETMRVAIFA	SGCSSDEPTS	QNLGNNSYDE	360
15	PCIGQEYQII	AQINGNYARL	LDTVPLDYEF	LATEGKSVC			

Seq ID NO: 226 DNA sequence

Nucleic Acid Accession #: XM_64321

Coding sequence: 1-2079 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
	<u>ATGGTCGCCA</u>	GTTCCGATCA	AGACAGAGCC	CCGTATCTTC	CAGGGACACT	AGACAAGATG	60
	CCAGGACCAC	GCTCCGCTC	TGCCAGAGG	CCAAAAGCAG	CCCAACAAGA	GCCCCGCATT	120
25	GAGCCTGTGA	CTTACAGGGA	GGGTGGTGGA	GCCATCGTCC	TCACGTATGC	GCTGGGGATC	180
	GGGGTTGGGA	TCACGGGAAA	CACAGTTCAA	CAACCACCTC	AACTCACTGA	CTCCGCCAGC	240
	ATCCGTCAGG	AGGATGCTCT	TGATAACAAA	ATTGACATTG	CTGAAGATGG	TGGCCAGACA	300
	CCATACGAAG	CTACCTTGCA	GCAAAGCTTT	CAATACTCAC	CTACAACAGA	TCTTCCTCCA	360
	CTCACAAATG	GCTACCTGCC	ATCAATCAGC	ATGTATGAAA	TTCAAACCAA	ATACCAGTCG	420
30	CATAATCAAT	ATCCTAATGG	AAATTCATAA	CAGAAGACCA	CATTAAATTC	TAGAAAACCC	480
	TTCCCTTCCA	CAGCCACCCAC	TTCCGTACCA	CAAACTGTGA	TTCCAAAGAA	GAGTGGCTCA	540
	CCTGAAGTTA	AACATAAAAT	AACCAAAACT	ATCCAGAATG	GCAGGGAATT	GTTCAAGTCT	600
	TCCCTTTGTG	GAGACCTTTT	AAATGAAGTA	CAGGCAAGTG	AGCACACGAA	GTCAAAGCAT	660
	GAAAGCAGAA	AAGAAAAGAG	GAATAAACCC	AAAAAGCATG	ACTCATCAAG	ATCTGAAGAG	720
35	CGCAAGTCAC	ACAAAATCCC	CAAATTAGAA	CCAGAGGAAC	AAAATAGACC	AAATGAGAGG	780
	GTTCACACCA	TATCAGAAAA	ACCAAGGGAA	GATCCAGTAC	TAAAAGAGGA	AGCCCCAGTT	840
	CAGCCAATAC	TATCTTCTGT	TCCAACAACA	GAAGTGTCCA	CTGGTGTAA	GTTTCAAGTT	900
	GGTGATCTTG	TGTGGTCCAA	GGTGACGGTC	ACACCCTGTT	GGGTGCCCCG	CCTGCGAGGA	960
	CGGAGGAGCC	ATCACTGTTC	CAGCTGCCTG	GAGATCTTGG	TGCTGGTGCC	AGCCCTCAGC	1020
40	CTCAAGAGGT	CTTTCATGGT	TTCTTCCTTG	AAGTTCCTCA	CCTCCACGGG	CAAACAGAAG	1080
	CCACATTTCA	AGGGAACCTG	CCAGATGGGC	TGGTCACCTA	TGGCCTCCAC	GACCAATGTC	1140
	TCCTTGCTCC	TTGGTCATTG	GGAAGGAACA	GACCAGATGT	CATCCAGGGG	CCCGGAATTT	1200
	GGGGGGCGCC	GCTGGGTGTG	GCAGCATCAG	AAGCCTCAGA	TCCGCATCTC	CATCTGCCAC	1260
	AGGCCAGGGA	AGGAACCTCT	GAGACTCAGT	TTCCCTACGAT	GTGAAGTGGA	GAGAAGAATC	1320
45	TCCTCTTTAG	CCACCTCTCA	GGGCTGCTGG	TGTTCCGCCC	CAGACCACGT	CTGTGAGAAA	1380
	TGCTTAGAAG	ACTATGCAGG	CGCGCGCCAT	TTGACACTCA	GAGCCCAGGA	AGCCTTCTTT	1440
	GGTCCAGACA	CGAGGACTGG	AAGCCTTAGA	GCTGTGCGCA	AGAGATACTG	CAGGAACAGC	1500
	CAGCACCAGA	GATATCTCCT	GCAAGGCCTC	CTAGGTGGGT	TCTTGGGAAG	AAGGAATGCC	1560
	AATGAATATG	ATTGCAAGCT	AGAGACGAGA	GAAGCGCGGT	CCTCAACTCC	AAGAATCCCG	1620
50	TATTCCCCAA	CCACATCCTT	TCAGTCTGAA	AGTGCCCTTA	ACCACTACTT	TCCCTACCAC	1680
	GTCTCCCTTT	CCAAAGTTCT	CAAAACGCAA	ATTTCTGTGA	CCTGTGTGCA	CCTGTGTGCA	1740
	GTCGTAGCAG	TACGTAGGAG	ATCCAATATG	CCTGGCACAA	GGGGGTGGGG	TGGCCACAAA	1800
	CAGAAGCAGC	CCGTGCTTGC	CAAGTACACG	CCTGCCTGCC	ACGCACAATG	GGAGACATTC	1860
	CGCAAGTTCC	ACGTGATGGC	TCAGAAGAGG	GGCCTGTGAG	GAAGATGTAG	GGGCCAGCAG	1920
55	CCCCCGGCGG	CGCCCCGCAA	GGTGGCTGAC	AGACGCCAGC	AGCTGCCGGG	GGCTCCGGGC	1980
	TGCTCCTGCT	CCCAGGATGT	GTATCTGACT	GGAGTTCTG	GATTAAAGGC	CAGTCGTGGC	2040
	TTCAATCCAC	ATCCTTGGGT	GCCCTTCGGC	TCCTCCTAG			

Seq ID NO: 227 Protein sequence:

Protein Accession #: XP_064321.1

	1	11	21	31	41	51	
	MVASSDQDRA	PYLPGLDKM	PGPRLRSAQR	PKAAQQEPGI	EPGTYREGGG	AIVLTALGI	60
	GVGITGNTVQ	QPPQLTDSAS	IRQEDAFDNK	IDIAEDGGQT	PYEATLQGSF	QYSPTDLPP	120
	LTNGYLPIS	MYEIQTKYQS	HNQYPNGNSK	QKTTLNSRKP	FPSTATTSVP	QTVIPKSGS	180
	PEVKLKIKTK	IQNRELFKS	SLCGDLLNEV	QASEHTKSKH	ESRKEKRKKP	KKHDSSRSEE	240
70	RKSHKIPKLE	PEEQNRPNR	VHTISEKPRE	DPVLKEEAPV	QPILSSVPTT	EVSTGVKFQV	300
	GDLVWSKVTV	TPCWVPLRLG	RRSHHCSSCL	EILVLVPALS	LKRSFMVSSL	KFLTSTGKQK	360
	PTFKGTAQMG	WSPMASTTNV	SLLLGHWEGT	DOMSSRGPEF	GGRRWVWQHQ	KPQIRISICH	420
	RPGKEPLRLS	FLRCEVERRI	SSLATSQGCW	CSPPDHVCEK	CLEDYAGRRH	LTLRAQEAF	480
	GPDSRTGSLR	AVGKRYCRNS	QHQRVLLQGL	LGGFLEERNA	NEYDCKLETR	EAASSTPRIP	540
	YSPTHILQSE	SAPNHYFPYH	VLSKFLKRK	ANSHFLHLCA	VVAVRRRSNM	PGTRGWGGHK	600
75	QKQPCPAKYT	PACHAQWETF	RKFHVMAQKR	GLSGRCRGQQ	PPAAPRKVAD	RRQQLPGAPG	660
	CSCSQDVYLT	GVSGLKASRG	FIPHPVVPFG	SS			

Seq ID NO: 228 DNA sequence

Nucleic Acid Accession #: NM_006033

Coding sequence: 253-1752 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
10	AGCAGCGAGT	CCTTGCCTCC	CGGCGGCTCA	GGACGAGGGC	AGATCTCGTT	CTGGGGCAAG	60
	CCGTTGACAC	TCGCTCCCTG	CCACCGCCCG	GGCTCCGTGC	CGCCAAGTTT	TCATTTTCCA	120
	CCTTCTCTGC	CTCCAGTCCC	CCAGCCCCTG	GCCGAGAGAA	GGGTCTTACC	GGCCGGGATT	180
	GCTGGAAACA	CCAAGAGGTG	GTTTTGTGTT	TTTAAACTT	CTGTTTCTTG	GGAGGGGGTG	240
	TGGCGGGGCA	GGATGAGCAA	CTCCGTTTCT	CTGCTCTGTT	TCTGGAGCCT	CTGCTATTGC	300
	TTTGCTGCGG	GGAGCCCCGT	ACCTTTTGGT	CCAGAGGGAC	GGCTGGAAGA	TAAGTCCAC	360
15	AAACCCAAAG	CTACACAGAC	TGAGGTCAAA	CCATCTGTGA	GGTTTAACTT	CCGCACCTCC	420
	AAGGACCCAG	AGCATGAAGG	ATGCTACCTC	TCCGTCGGCC	ACAGCCAGCC	CTTAGAAGAC	480
	TGCAGTTTCA	ACATGACAGC	TAAACCTTT	TTCATCATTC	ACGGATGGAC	GATGAGCGGT	540
	ATCTTTGAAA	ACTGGCTGCA	CAAACTCGTG	TCAGCCCTGC	ACACAAGAGA	GAAAGACGCC	600
	AATGTAGTTG	TGGTTGACTG	GCTCCCCCTG	GCCACCAGC	TTTACACGGA	TGCCGTCAAT	660
20	AATACCAGGG	TGGTGGGACA	CAGCATTGCC	AGGATGCTCG	ACTGGCTGCA	GGAGAAGGAC	720
	GATTTTTCTC	TCGGGAAATG	CCACTTGATC	GGCTACAGCC	TCGGAGCGCA	CGTGGCCGGG	780
	TATGCAGGCA	ACTTCGTGAA	AGGAACGGTG	GGCCGAATCA	CAGGTTTGGG	TCCTGCCGGG	840
	CCCATGTTTG	AAGGGGCCGA	CATCCACAAG	AGGCTCTCTC	CGGACGATGC	AGATTTTGTG	900
	GATGTCCTCC	ACACCTACAC	GCCTTCCTTC	GGCTTGAGCA	TTGGTATTCA	GATGCCTGTG	960
25	GGCCACATTG	ACATCTACCC	CAATGGGGGT	GACTTCCAGC	CAGGCTGTGG	ACTCAACGAT	1020
	GTCTTGGGAT	CAATTGCATA	TGGAACAATC	ACAGAGGTGC	TAAATGTGTA	GCATGAGCGA	1080
	GCCGTCCACC	TCTTTGTGTA	CTCTCTGGTG	AATCAGGACA	AGCCGAGTTT	TGCCCTCCAG	1140
	TGCACTGACT	CCAATCGCTT	CAAAAAGGGG	ATCTGTCTGA	GCTGCCGCAA	GAACCGTTGT	1200
	AATAGCATTG	GCTACAATGC	CAAGAAAATG	AGGAACAAGA	GGAACAGCAA	AATGTACCTA	1260
30	AAAACCCGGG	CAGGCATGCC	TTTCAGAGTT	TACCATTATC	AGATGAAAAT	CCATGTCTTC	1320
	AGTTACAAGA	ACATGGGAGA	AATTGAGCCC	ACCTTTTACG	TCACCCTTTA	TGGCACTAAT	1380
	GCAGATTCCC	AGACTCTGCC	ACTGGAAATA	GTGGAGCGGA	TCGAGCAGAA	TGCCACCAAC	1440
	ACCTTCTCGG	TCTACACCGA	GGAGGACTTG	GGAGACCTCT	TGAAGATCCA	GCTCACCTGG	1500
35	GAGGGGGCCT	CTCAGTCTTG	GTACAACCTG	TGGAAGGAGT	TTGCGAGCTA	CCTGTCTCAA	1560
	CCCCGCAACC	CCGGACGGGA	GCTGAATATC	AGGCGCATCC	GGGTGAAGTC	TGGGGAAACC	1620
	CAGCGGAAAC	TGACATTTTG	TACAGAAGAC	CCTGAGAACA	CCAGCATATC	CCCAGGCCGG	1680
	GAGCTCTGGT	TTGCGAAGTG	TCGGGATGGC	TGGAGGATGA	AAAACGAAAC	CAGTCCCACT	1740
	GTGGAGCTTC	CCTGAGGGTG	CCCGGGCAAG	TCTTGCCAGC	AAGGCAGCAA	GACTTCCTGC	1800
40	TATCCAAGCC	CATGGAGGAA	AGTTACTGCT	GAGGACCCAC	CCAATGGAAG	GATTCTTCTC	1860
	AGCCTTGACC	CTGGAGCACT	GGGAACAAC	GGTCTCTGT	GATGGCTGGG	ACTCCTCGCG	1920
	GGAGGGGACT	GCGCTGCTAT	AGCTCTTGCT	GCCTCTCTTG	AATAGCTCTA	ACTCCAAACC	1980
	TCTGTCCACA	CCTCCAGAGC	ACCAAGTCCA	GATTTGTGTG	TAAGCAGCTG	GGTGCCTGGG	2040
	GCCTCTCTGT	CACACTGGAT	TGGTTCTCA	GTGCTGGGC	GAGCCTGTAC	TCTGCCTGAC	2100
45	GAGGAACGCT	GGCTCCGAAG	AGGCCCTGTG	TAGAAGGCTG	TCAGCTGCTC	AGCCTGCTTT	2160
	GAGCCTCAGT	GAGAAGTCCT	TCCGACAGGA	GCTGACTCAT	GTGAGGATGG	CAGGCCTGGT	2220
	ATCTTGCTCG	GGCCCTAGCT	GTTGGGGTTC	TCATGGGTTG	CACTGACCAT	ACTGCTTACG	2280
	TCTTAGCCAT	TCCGTCCTGC	TCCCCAGCTC	ACTCTCTGAA	GCACACATCA	TTGGCTTTCC	2340
	TATTTTCTCT	TTTCTTTTCT	AATTGAGCAA	ATGTCTATTG	AACACTTAAA	ATTAATTAGA	2400
50	ATGTGGTAAT	GGACATATTA	CTGAGCCTCT	CCATTTGGAA	CCCAGTGGAG	TTGGGATTTC	2460
	TAGACCTCTC	TTCTGTGTTG	ATGGTGTATG	TGTATATGCA	TGGGGAAAGG	CACCTGGGGC	2520
	CTGGGGGAGG	CTATAGGATA	TAAGCATTAG	GGACCCTGAG	GCTTTAAGTG	GTTTCTATTT	2580
	CTTCTTAGTT	ATTATGTGCC	ACCTTCTTAG	TTATTATGTG	CCACCTCCCC	TATGAGTGAC	2640
	GTGTTTGATC	ACTAGCAGAA	TAGCAAGCAG	AGTATCATTC	ATGCTGGGGC	CAGAATGATG	2700
55	GCCGGTTGCC	AGATATAACT	GCTTTGGAGC	AAATCTCTTC	TGTTTAGAGA	GATAGAAGTT	2760
	ATGACATATG	TAATACACAT	CTGTGTACAC	AGAAACCGGC	ACCTGCCAGA	CAGAGCTGGT	2820
	TCTAAGATTT	AATACAGTGC	TTTTTTTCTT	CTTTGAAATA	TTTACTTTA	ATACCAGTGC	2880
	CTTTTCTTGT	TGAACCTTCT	GGAAAAGCCA	CCAATTCTAG	ATCTTGATTT	GAATTAATAC	2940
	ACACAATATC	TGAGACACTT	ACACTTTTCA	AAAGATTTGT	GTATGCATTG	CCTAATTAGA	3000
60	GTAGGGGGAG	AAGGGCAACT	ATTATTATCC	CTATTTTACA	AAACTGAGGC	TTAGTGAGGT	3060
	TCAGCCACAT	GCCTAGACTT	ATATACTAGT	TAGTGGTGCA	GCCAGGGAGA	GGACTCAGAT	3120
	TTCTTGAGAG	CAAAGTCTAT	CTCTGAAACT	CCATGAAGAC	TTTTGCAGCC	AGTTCCACAC	3180
	AATATGCCCC	AGACGTGAGA	CAAAACAAGG	CTTTTCTTTT	TATATAGAGC	CATCCATAAA	3240
	ATCCTAAGCC	CTTTTATTAA	TGTATAACCA	GGAGAACATC	TGTGCCAACG	GTTGGACTTT	3300
65	TTATGGCTGA	GATTCGGGAG	GAAGTGTGAC	ACCAAGCAGG	AGAGGAAGAA	TGATTTTCTT	3360
	TGTACTTAGG	TTTTCTAAGG	ACATTGTTTT	AATCTGTATC	GTGCCAAAGT	TGTATCACTG	3420
	TTAAACTTCT	GAAGACATAA	CCAGTTGAGT	CTTATTTCAA	GATATGTTCT	CAAGCCAATT	3480
	GTGTGCTTCT	CTTGTTTCTG	TGATTGCTTT	CTAGCCAAAG	CGAAGCTTGT	ACAGGTTGAG	3540
	TATCCCTTAT	CCAAAATGCT	TGGAACCAGA	AGTGTPTCAA	ATTTTAGATT	ATTTTCAGAT	3600
70	TTTGGAATGT	TTGCATATAC	ATAATGAGAT	ATTTTGGGAA	TAGGACCCGA	GCCTAAACAC	3660
	AAAATTCATT	GATGTGTCAG	TTACACCTTA	TCCACATAGC	CTGAGGGTAA	TTTATACGTA	3720
	TATTTTAAAT	AGTTGTGTAC	ATGAAGCATG	GTTTGTGGTA	ACTTATGTGA	GGGGTTTCC	3780
	CATTTTGTGT	CTTGTTGGTG	CTCAAAAAGT	TTTGGATTTT	GGAGCATTTT	GGATTTTGA	3840
	TTTTTGGATT	AGGGTTGCTC	AACCCATATT	ATTGGCTGTA	CATCTGGTGC	ACTTCTGACT	3900
75	TCTGTTTTTA	CTAATGGAAG	CTTTGCA				

Seq ID NO: 229 Protein sequence:

Protein Accession #: NP_006024.1

1 11 21 31 41 51
| | | | |
5 MSNSVPLLCF WSLCYCFAAG SPVPFGPEGR LEDKLHKPKA TQTEVKPSVR FNLRTSKDPE 60
HEGCVLSVGH SQPLEDCSFN MTAKTFPIIH GWTMSGIFEN WLHKLVSAIH TREKDANVVV 120
VDWLPLAHQL YTDAVNNTRV VGHSIARMLD WLQEKDDFSL GNVHLIGYSL GAHVAGYAGN 180
FVKGTVGRIT GLDPAGPMFE GADIIHKRLSP DDADFVDVLH TYTRSFGLSI GIQMPVGHID 240
10 IYPNGGDFQP GCGLNDVLGS IAYGTITEVV KCEHERAVHL FVDSLVDQDK PSFAFQCTDS 300
NRFKKGICLS CRKNRCNSIG YNAKKMRNKR NSKMYLKTRA GMPFRVYHYQ MKIHVFSYKN 360
MGEIEPTFYV TLYGTNADSQ TLPLEIVERI EQNATNTFLV YTEEDLGDLL KIQLTWEGAS 420
QSWYNLWKEF RSYLSQPRNP GRELNIRIR VKSGETQRKL TFCTEDPENT SISPGRELWF 480
RKCRDGWRMK NETSPTVELP

15

It is understood that the examples described above in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All publications, sequences of accession numbers, and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent
5 application were specifically and individually indicated to be incorporated by reference.

WHAT IS CLAIMED IS:

- 1 1. A method of detecting an angiogenesis-associated transcript in a cell in
2 a patient, the method comprising contacting a biological sample from the patient with a
3 polynucleotide that selectively hybridized to a sequence at least 80% identical to a sequence
4 as shown in Tables 1-8.
- 1 2. The method of claim 1, wherein the biological sample is a tissue
2 sample.
- 1 3. The method of claim 1, wherein the biological sample comprises
2 isolated nucleic acids.
- 1 4. The method of claim 3, wherein the nucleic acids are mRNA.
- 1 5. The method of claim 3, further comprising the step of amplifying
2 nucleic acids before the step of contacting the biological sample with the polynucleotide.
- 1 6. The method of claim 1, wherein the polynucleotide comprises a
2 sequence as shown in Tables 1-8 .
- 1 7. The method of claim 1, wherein the polynucleotide is labeled.
- 1 8. The method of claim 7, wherein the label is a fluorescent label.
- 1 9. The method of claim 1, wherein the polynucleotide is immobilized on
2 a solid surface.
- 1 10. The method of claim 1, wherein the patient is undergoing a therapeutic
2 regimen to treat a disease associated with angiogenesis.
- 1 11. The method of claim 1, wherein the patient is suspected of having
2 cancer.
- 1 12. An isolated nucleic acid molecule consisting of a polynucleotide
2 sequence as shown in Tables 1-8.
- 1 13. The nucleic acid molecule of claim 12, which is labeled.
- 1 14. The nucleic acid of claim 13, wherein the label is a fluorescent label

- 1 15. An expression vector comprising the nucleic acid of claim 12.
- 1 16. A host cell comprising the expression vector of claim 15.
- 1 17. An isolated polypeptide which is encoded by a nucleic acid molecule
2 having polynucleotide sequence as shown in Tables 1-8
- 1 18. An antibody that specifically binds a polypeptide of claim 17.
- 1 19. The antibody of claim 18, further conjugated or fused to an effector
2 component.
- 1 20. The antibody of claim 19, wherein the effector component is a
2 fluorescent label.
- 1 21. The antibody of claim 19, wherein the effector component is a
2 radioisotope.
- 1 22. The antibody of claim 19, which is an antibody fragment.
- 1 23. The antibody of claim 19, which is a humanized antibody
- 1 24. A method of detecting a cell undergoing angiogenesis in a biological
2 sample from a patient, the method comprising contacting the biological sample with an
3 antibody of claim 18.
- 1 25. The method of claim 24, wherein the antibody is further conjugated or
2 fused to an effector component.
- 1 26. The method of claim 25, wherein the effector component is a
2 fluorescent label.
- 1 27. The method of detecting antibodies specific to angiogenesis in a
2 patient, the method comprising contacting a biological sample from the patient with a
3 polypeptide which is encoded by a nucleotide sequence of Tables 1-8.

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Published:

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(54) Title: METHODS OF DIAGNOSIS OF ANGIOGENESIS, COMPOSITIONS AND METHODS OF SCREENING FOR ANGIOGENESIS MODULATORS

(57) Abstract:

WO 2002/079492 A2

PATENT COOPERATION TREATY

PCT

DECLARATION OF NON-ESTABLISHMENT OF INTERNATIONAL SEARCH REPORT

(PCT Article 17(2)(a), Rule 13ter.1(c) and 39)

Applicant's or agent's file reference 18501-62PC	IMPORTANT DECLARATION	Date of mailing (day/month/year) 10 APRIL 2003
International application No. PCT/US02/04915	International filing date (day/month/year) 14 February 2002 (14.02.2002)	(Earliest) Priority date (day/month/year) 14 February 2001 (14.02.2001)
International Patent Classification (IPC) or both national classification and IPC IPC(7): A61K 39/395 and US Cl.: 424/145.100		
Applicant EOS BIOTECHNOLOGY, INC.		

This International Searching Authority hereby declares, according to Article 17(2)(a), that no international search report will be established on the international application for the reasons indicated below.

1. ☒ The subject matter of the international application relates to:
 - a. ☐ scientific theories.
 - b. ☐ mathematical theories
 - c. ☐ plant varieties.
 - d. ☐ animal varieties.
 - e. ☐ essential biological processes for the production of plants and animals, other than microbiological processes and the products of such processes.
 - f. ☐ schemes, rules or methods of doing business.
 - g. ☐ schemes, rules or methods of performing purely mental acts.
 - h. ☐ schemes, rules or methods of playing games.
 - i. ☐ methods for treatment of the human body by surgery or therapy.
 - j. ☐ methods for treatment of the animal body by surgery or therapy.
 - k. ☒ diagnostic methods practised on the human or animal body.
 - l. ☐ mere presentations of information.
 - m. ☐ computer programs for which this International Searching Authority is not equipped to search prior art.
2. ☒ The failure of the following parts of the international application to comply with prescribed requirements prevents a meaningful search from being carried out:

☐ the description

☒ the claims

☐ the drawings
3. ☒ The failure of the nucleotide and/or amino acid sequence listing to comply with the standard provided for in Annex C of the Administrative Instructions prevents a meaningful search from being carried out:

☒ the written form has not been furnished or does not comply with the standard.

☐ the computer readable form has not been furnished or does not comply with the standard.

4. Further comments:
Please See Continuation Sheet

Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703)305-3230	Authorized officer  Khatol Shalman-Shah Telephone No. (703)308-0196
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Form PCT/ISA/203 (July 1998)

**DECLARATION OF NON-ESTABLISHMENT OF
INTERNATIONAL SEARCH REPORT**
Form PCT/ISA/203 (July 1998)

International application No.
PCT/US02/04915

4. Further comments:

Applicant failed to comply with the standards provided in Annex C of administrative instruction in regard to nucleotide and/or amino acid sequence identifiers in the claims. Applicant was not fully responsive to the PCT/ISA/225. A meaningful search can not be carried out.

Additionally there are other problems with the claims.

Claims 1, 6, 12, 17 and 27 are unsearchable under PCT Article 17(2)(b) because claims are improper for referring to tables in the specification.

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